

```

Asp Leu Val Leu Gly Gly His Asp His Ile Tyr Thr Arg Ser His Leu
    100                      105                      110

Met Asn Gly Phe Thr Pro Val Asp Ala Gly Arg Glu Ala Val Val Gly
    115                      120                      125

Glu Thr Leu Asn Pro Lys Ala Gly Glu Val Val Tyr Leu Ala Thr Asn
    130                      135                      140

Ser Ser Ser Gly Ser Lys Phe Tyr Asp Phe Tyr Asp Phe Gln Leu Gly
    145                      150                      155                      160

Gln Arg Tyr Asp Thr Gly Leu Asp Phe Gln Glu Thr Val Asp Gln Lys
    165                      170                      175

Lys Ile Arg Thr Tyr Thr Ala Val Trp Asn Gln Asp Gln Val Gln Asp
    180                      185                      190

Tyr Thr Asn Val Glu Leu Thr Pro Glu Gly Leu Thr Val Thr Thr Lys
    195                      200                      205

Asp Ala Val Ser Gly Glu Leu Val Asp Gln Phe Thr Leu Ser Lys Gln
    210                      215                      220

Asp Arg Asp Glu Glu Ser Glu Val Pro Val Glu Asp Asp Lys Asp Gly
    225                      230                      235                      240

Asp Asn Ala Thr Gly Ser Ser Asn Leu Gly Leu Ala Ala Ile Leu Ala
    245                      250                      255

Pro Val Leu Ala Ile Phe Gly Phe Val Gly Gly Leu Phe Val Gly Gly
    260                      265                      270

Gly Ser Leu Ala Glu Phe Phe Ala Asn Leu Gly Val Lys Met Pro Phe
    275                      280                      285

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<210> 879

<211> 969

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(946)

<223> RXN01908

<400> 879

tccacgacat ctgcacacaga aagaagattc accatgtcta agaacaacgc agctcacccg 60

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                Met His Ser Asp Arg
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ttt gag cac cca gac aac ggc tat ggc tac acc att cgt cag gac act 163
Phe Glu His Pro Asp Asn Gly Tyr Gly Tyr Thr Ile Arg Gln Asp Thr
                10                      15                      20

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gat gca gag aac ccg atg acc cat cac gat acg aaa gat gca gct ctc	211
Asp Ala Glu Asn Pro Met Thr His His Asp Thr Lys Asp Ala Ala Leu	
25 30 35	
tgg gtt cac aac cga cca cga cgc gga gat acc gtc gcc gat aag cca	259
Trp Val His Asn Arg Pro Arg Arg Gly Asp Thr Val Ala Asp Lys Pro	
40 45 50	
gaa ggc aat gag att ctc gac atc ttt gcc aag ttc atc tgc ggc cag	307
Glu Gly Asn Glu Ile Leu Asp Ile Phe Ala Lys Phe Ile Cys Gly Gln	
55 60 65	
cac gat aat gat gac aac ccg ttc gaa gtc tgg tcc gac ggt gac tcg	355
His Asp Asn Asp Asp Phe Glu Val Trp Ser Asp Gly Asp Ser	
70 75 80 85	
gat gca tca ctc atc cgc acc aag gcg tat gtt gcc gag cac cac ccc	403
Asp Ala Ser Leu Ile Arg Thr Lys Ala Tyr Val Ala Glu His His Pro	
90 95 100	
gaa ctt ata ttc gac atc tct gcg aaa acc atc acg ggt tat tcc caa	451
Glu Leu Ile Phe Asp Ile Ser Ala Lys Thr Ile Thr Gly Tyr Ser Gln	
105 110 115	
ggc gat tgg ctc gat gtg gtc tgt gtt act act gcc gcc act tgc gac	499
Gly Asp Trp Leu Asp Val Val Cys Val Thr Thr Ala Ala Thr Cys Asp	
120 125 130	
gaa ctt atc cct gct gac agt ctt att gac atc tac cgc cag tgg gct	547
Glu Leu Ile Pro Ala Asp Ser Leu Ile Asp Ile Tyr Arg Gln Trp Ala	
135 140 145	
ttt ggt gat gtg tgg aca gtg att cct gat tct cag cca ggt ctc gca	595
Phe Gly Asp Val Trp Thr Val Ile Pro Asp Ser Gln Pro Gly Leu Ala	
150 155 160 165	
ggt att tat gct gac gat cca gct gac gcc ctt gcg tac tat caa gag	643
Gly Ile Tyr Ala Asp Asp Pro Ala Asp Ala Leu Ala Tyr Tyr Gln Glu	
170 175 180	
aat ttc gaa gat gaa ccc atc tgg gat ctc tta agc cgc cac gac gct	691
Asn Phe Glu Asp Glu Pro Ile Trp Asp Leu Leu Ser Arg His Asp Ala	
185 190 195	
gac aaa gac gcc gca gca ctg gca gct gcc tct gct gca gaa aac cac	739
Asp Lys Asp Ala Ala Ala Leu Ala Ala Ala Ser Ala Ala Glu Asn His	
200 205 210	
gca cta gcg cga ggt act acc cca gtc gtt atc cgt acc caa gac atc	787
Ala Leu Ala Arg Gly Thr Thr Pro Val Val Ile Arg Thr Gln Asp Ile	
215 220 225	
atc act aac gcg cga tac ctc atg tct gat agt gct gat gac aat cca	835
Ile Thr Asn Ala Arg Tyr Leu Met Ser Asp Ser Ala Asp Asp Asn Pro	
230 235 240 245	
gaa tac gat cgc gcc ttg gtc gaa ctt agt gct tat ctc tta agt atc	883
Glu Tyr Asp Arg Ala Leu Val Glu Leu Ser Ala Tyr Leu Leu Ser Ile	
250 255 260	

gac ctc gat gat cgc gtt gct gca gag atg acc att tta ggt cgc cct 931
 Asp Leu Asp Asp Arg Val Ala Ala Glu Met Thr Ile Leu Gly Arg Pro
 265 270 275

gtg cct aaa gaa gga taaccaccac accagaaaag aag 969
 Val Pro Lys Glu Gly
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<210> 880

<211> 282

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 880

Met His Ser Asp Arg Phe Glu His Pro Asp Asn Gly Tyr Gly Tyr Thr
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Ile Arg Gln Asp Thr Asp Ala Glu Asn Pro Met Thr His His Asp Thr
 20 25 30

Lys Asp Ala Ala Leu Trp Val His Asn Arg Pro Arg Arg Gly Asp Thr
 35 40 45

Val Ala Asp Lys Pro Glu Gly Asn Glu Ile Leu Asp Ile Phe Ala Lys
 50 55 60

Phe Ile Cys Gly Gln His Asp Asn Asp Asp Asn Pro Phe Glu Val Trp
 65 70 75 80

Ser Asp Gly Asp Ser Asp Ala Ser Leu Ile Arg Thr Lys Ala Tyr Val
 85 90 95

Ala Glu His His Pro Glu Leu Ile Phe Asp Ile Ser Ala Lys Thr Ile
 100 105 110

Thr Gly Tyr Ser Gln Gly Asp Trp Leu Asp Val Val Cys Val Thr Thr
 115 120 125

Ala Ala Thr Cys Asp Glu Leu Ile Pro Ala Asp Ser Leu Ile Asp Ile
 130 135 140

Tyr Arg Gln Trp Ala Phe Gly Asp Val Trp Thr Val Ile Pro Asp Ser
 145 150 155 160

Gln Pro Gly Leu Ala Gly Ile Tyr Ala Asp Asp Pro Ala Asp Ala Leu
 165 170 175

Ala Tyr Tyr Gln Glu Asn Phe Glu Asp Glu Pro Ile Trp Asp Leu Leu
 180 185 190

Ser Arg His Asp Ala Asp Lys Asp Ala Ala Ala Leu Ala Ala Ser
 195 200 205

Ala Ala Glu Asn His Ala Leu Ala Arg Gly Thr Thr Pro Val Val Ile
 210 215 220

Arg Thr Gln Asp Ile Ile Thr Asn Ala Arg Tyr Leu Met Ser Asp Ser
 225 230 235 240

Ala Asp Asp Asn Pro Glu Tyr Asp Arg Ala Leu Val Glu Leu Ser Ala

245

250

255

Tyr Leu Leu Ser Ile Asp Leu Asp Asp Arg Val Ala Ala Glu Met Thr
 260 265 270

Ile Leu Gly Arg Pro Val Pro Lys Glu Gly
 275 280

<210> 881

<211> 583

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(583)

<223> FRXA01908

<400> 881

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cagtcgtgtct tccatatattc atatcccagc acataccact atg cac tct gac cgc 115
 Met His Ser Asp Arg
 1 5

ttt gag cac cca gac aac ggc tat ggc tac acc att cgt cag gac act 163
 Phe Glu His Pro Asp Asn Gly Tyr Gly Thr Ile Arg Gln Asp Thr
 10 15 20

gat gca gag aac ccg atg acc cat cac gat acg aaa gat gca gct ctc 211
 Asp Ala Glu Asn Pro Met Thr His His Asp Thr Lys Asp Ala Ala Leu
 25 30 35

tgg gtt cac aac cga cca cga cgc gga gat acc gtc gcc gat aag cca 259
 Trp Val His Asn Arg Pro Arg Arg Gly Asp Thr Val Ala Asp Lys Pro
 40 45 50

gaa ggc aat gag att ctc gac atc ttt gcc aag ttc atc tgc ggc cag 307
 Glu Gly Asn Glu Ile Leu Asp Ile Phe Ala Lys Phe Ile Cys Gly Gln
 55 60 65

cac gat aat gat gac aac ccg ttc gaa gtc tgg tcc gac ggt gac tgc 355
 His Asp Asn Asp Asp Asn Pro Phe Glu Val Trp Ser Asp Gly Asp Ser
 70 75 80 85

gat gca tca ctc atc cgc acc aag gcg tat gtt gcc gag cac cac ccc 403
 Asp Ala Ser Leu Ile Arg Thr Lys Ala Tyr Val Ala Glu His His Pro
 90 95 100

gaa ctt ata ttc gac atc tct gcg aaa acc atc acg ggt tat tcc caa 451
 Glu Leu Ile Phe Asp Ile Ser Ala Lys Thr Ile Thr Gly Tyr Ser Gln
 105 110 115

ggc gat tgg ctc gat gtg gtc tgt gtt act act gcc gcc act tgc gac 499
 Gly Asp Trp Leu Asp Val Val Cys Val Thr Thr Ala Ala Thr Cys Asp
 120 125 130

gaa ctt atc cct gct gac agt ctt att gac atc tac cgc cag tgg gct 547
 Glu Leu Ile Pro Ala Asp Ser Leu Ile Asp Ile Tyr Arg Gln Trp Ala
 135 140 145

ttt ggt gat gtg tgg aca gtg att cct gat tct cag
 Phe Gly Asp Val Trp Thr Val Ile Pro Asp Ser Gln
 150 155 160

583

<210> 882

<211> 161

<212> PRT

<213> Corynebacterium glutamicum

<400> 882

Met His Ser Asp Arg Phe Glu His Pro Asp Asn Gly Tyr Gly Tyr Thr
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Ile Arg Gln Asp Thr Asp Ala Glu Asn Pro Met Thr His His Asp Thr
 20 25 30

Lys Asp Ala Ala Leu Trp Val His Asn Arg Pro Arg Arg Gly Asp Thr
 35 40 45

Val Ala Asp Lys Pro Glu Gly Asn Glu Ile Leu Asp Ile Phe Ala Lys
 50 55 60

Phe Ile Cys Gly Gln His Asp Asn Asp Asp Asn Pro Phe Glu Val Trp
 65 70 75 80

Ser Asp Gly Asp Ser Asp Ala Ser Leu Ile Arg Thr Lys Ala Tyr Val
 85 90 95

Ala Glu His His Pro Glu Leu Ile Phe Asp Ile Ser Ala Lys Thr Ile
 100 105 110

Thr Gly Tyr Ser Gln Gly Asp Trp Leu Asp Val Val Cys Val Thr Thr
 115 120 125

Ala Ala Thr Cys Asp Glu Leu Ile Pro Ala Asp Ser Leu Ile Asp Ile
 130 135 140

Tyr Arg Gln Trp Ala Phe Gly Asp Val Trp Thr Val Ile Pro Asp Ser
 145 150 155 160

Gln

<210> 883

<211> 970

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (69)..(947)

<223> RXN01909

<400> 883

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tttgtatcatg gct aat ttt cga agc aag gat aaa gat ggc aat gtc atc 110
 Met Ala Asn Phe Arg Ser Lys Asp Lys Asp Gly Asn Val Ile

1	5	10	
aat ccg aac gcg tct act aaa ggt gta gat ctt gtt gtc aac gtc tac Asn Pro Asn Ala Ser Thr Lys Gly Val Asp Leu Val Val Asn Val Tyr 15 20 25 30			158
gac agc gcc aag cat gtg acc gaa aag ggt aac act gtc cac ttt gtg Asp Ser Ala Lys His Val Thr Glu Lys Gly Asn Thr Val His Phe Val 35 40 45			206
gat gtt cag gta gcg caa att ccg att gac gct gac ggc act cgt gcg Asp Val Gln Val Ala Gln Ile Pro Ile Asp Ala Asp Gly Thr Arg Ala 50 55 60			254
aat gcg aat ctt gca cca cag act atg cct cat ctg cat ctt gac act Asn Ala Asn Leu Ala Pro Gln Thr Met Pro His Leu His Leu Asp Thr 65 70 75			302
aag gac ggt cag cgc aac aca ggt gtt gcg tat tct gat gcg cag att Lys Asp Gly Gln Arg Asn Thr Gly Val Ala Tyr Ser Asp Ala Gln Ile 80 85 90			350
caa gcg atg cag acg gtg gca gca cag ggg cgc aac cat atg acc ccg Gln Ala Met Gln Thr Val Ala Ala Gln Gly Arg Asn His Met Thr Pro 95 100 105 110			398
ctc ttg agc aaa gac ggt gag aca gtt ggt tac tcc atg ttg gtc aag Leu Leu Ser Lys Asp Gly Glu Thr Val Gly Tyr Ser Met Leu Val Lys 115 120 125			446
gct gat gtc atg ttc ccg aag acc aag gac ggc aag tct ctc cct gcg Ala Asp Val Met Phe Pro Lys Thr Lys Asp Gly Lys Ser Leu Pro Ala 130 135 140			494
gtc atg aac act aag tct ctg cag cca tct ggg gtt cct att tcg gac Val Met Asn Thr Lys Ser Leu Gln Pro Ser Gly Val Pro Ile Ser Asp 145 150 155			542
gcg atg aat att cag cag cag cag ttt atg gct gtg gca atg aat cgc Ala Met Asn Ile Gln Gln Gln Gln Phe Met Ala Val Ala Met Asn Arg 160 165 170			590
caa gca gca gaa gcg cag aag gct gca caa gcc caa gcg acc cag gct Gln Ala Ala Glu Ala Gln Lys Ala Ala Gln Ala Thr Gln Ala 175 180 185 190			638
caa gca cca cag gtg gca ccg cag cca gtt atg cag aat cag caa ttc Gln Ala Pro Gln Val Ala Pro Gln Pro Val Met Gln Asn Gln Gln Phe 195 200 205			686
cag gca cca gtg cca cag ggc cag cag cca gca tat gca gga gcc cct Gln Ala Pro Val Pro Gln Gly Gln Gln Pro Ala Tyr Ala Gly Ala Pro 210 215 220			734
gtc tat gca gac gcg gta gct cat gca acc gcg cag cag cag gca gca Val Tyr Ala Asp Ala Val Ala His Ala Thr Ala Gln Gln Gln Ala Ala 225 230 235			782
gca gct cag gca ccg cag gca cct gct ggg aat ccg ttt aac cag ccg Ala Ala Gln Ala Pro Gln Ala Pro Ala Gly Asn Pro Phe Asn Gln Pro 240 245 250			830

cca gca gta gca gca gct ctg gca ccg cag acg cag ccg cca gca gta 878
 Pro Ala Val Ala Ala Ala Leu Ala Pro Gln Thr Gln Pro Pro Ala Val
 255 260 265 270

gca gca gct ctg gca ccg cag acg cag cag ccg gca gca caa cct cag 926
 Ala Ala Ala Leu Ala Pro Gln Thr Gln Gln Pro Ala Ala Gln Pro Gln
 275 280 285

atg gat aac gag cca ccg ttt taaaggcgca atacaccaca ccc 970
 Met Asp Asn Glu Pro Pro Phe
 290

<210> 884

<211> 293

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 884

Met Ala Asn Phe Arg Ser Lys Asp Lys Asp Gly Asn Val Ile Asn Pro
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Asn Ala Ser Thr Lys Gly Val Asp Leu Val Val Asn Val Tyr Asp Ser
 20 25 30

Ala Lys His Val Thr Glu Lys Gly Asn Thr Val His Phe Val Asp Val
 35 40 45

Gln Val Ala Gln Ile Pro Ile Asp Ala Asp Gly Thr Arg Ala Asn Ala
 50 55 60

Asn Leu Ala Pro Gln Thr Met Pro His Leu His Leu Asp Thr Lys Asp
 65 70 75 80

Gly Gln Arg Asn Thr Gly Val Ala Tyr Ser Asp Ala Gln Ile Gln Ala
 85 90 95

Met Gln Thr Val Ala Ala Gln Gly Arg Asn His Met Thr Pro Leu Leu
 100 105 110

Ser Lys Asp Gly Glu Thr Val Gly Tyr Ser Met Leu Val Lys Ala Asp
 115 120 125

Val Met Phe Pro Lys Thr Lys Asp Gly Lys Ser Leu Pro Ala Val Met
 130 135 140

Asn Thr Lys Ser Leu Gln Pro Ser Gly Val Pro Ile Ser Asp Ala Met
 145 150 155 160

Asn Ile Gln Gln Gln Gln Phe Met Ala Val Ala Met Asn Arg Gln Ala
 165 170 175

Ala Glu Ala Gln Lys Ala Ala Gln Ala Gln Ala Thr Gln Ala Gln Ala
 180 185 190

Pro Gln Val Ala Pro Gln Pro Val Met Gln Asn Gln Gln Phe Gln Ala
 195 200 205

Pro Val Pro Gln Gly Gln Gln Pro Ala Tyr Ala Gly Ala Pro Val Tyr
 210 215 220

Ala Asp Ala Val Ala His Ala Thr Ala Gln Gln Gln Ala Ala Ala Ala
225 230 235 240

Gln Ala Pro Gln Ala Pro Ala Gly Asn Pro Phe Asn Gln Pro Pro Ala
245 250 255

Val Ala Ala Ala Leu Ala Pro Gln Thr Gln Pro Pro Ala Val Ala Ala
260 265 270

Ala Leu Ala Pro Gln Thr Gln Gln Pro Ala Ala Gln Pro Gln Met Asp
275 280 285

Asn Glu Pro Pro Phe
290

<210> 885

<211> 960

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (59)..(937)

<223> FRXA01909

<400> 885

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gct aat ttt cga agc aag gat aaa gat ggc aat gtc atc aat ccg aac 109
Ala Asn Phe Arg Ser Lys Asp Lys Asp Gly Asn Val Ile Asn Pro Asn
5 10 15

gcg tct act aaa ggt gta gat ctt gtt gtc aac gtc tac gac agc gcc 157
Ala Ser Thr Lys Gly Val Asp Leu Val Val Asn Val Tyr Asp Ser Ala
20 25 30

aag cat gtg acc gaa aag ggt aac act gtc cac ttt gtg gat gtt cag 205
Lys His Val Thr Glu Lys Gly Asn Thr Val His Phe Val Asp Val Gln
35 40 45

gta gcg caa att ccg att gac gct gac ggc act cgt gcg aat gcg aat 253
Val Ala Gln Ile Pro Ile Asp Ala Asp Gly Thr Arg Ala Asn Ala Ala
50 55 60 65

ctt gca cca cag act atg cct cat ctg cat ctt gac act aag gac ggt 301
Leu Ala Pro Gln Thr Met Pro His Leu His Leu Asp Thr Lys Asp Gly
70 75 80

cag gcg aac aca ggt gtt gcg tat tct gat gcg cag att caa gcg atg 349
Gln Arg Asn Thr Gly Val Ala Tyr Ser Asp Ala Gln Ile Gln Ala Met
85 90 95

cag acg gtg gca gca cag ggg cgc aac cat atg acc ccg ctc ttg agc 397
Gln Thr Val Ala Ala Gln Gly Arg Asn His Met Thr Pro Leu Leu Ser
100 105 110

aaa gac ggt gag aca gtt ggt tac tcc atg ttg gtc aag gct gat gtc 445

Lys Asp Gly Glu Thr Val Gly Tyr Ser Met Leu Val Lys Ala Asp Val
 115 120 125
 atg ttc ccg aag acc aag gac ggc aag tct ctc cct gcg gtc atg aac 493
 Met Phe Pro Lys Thr Lys Asp Gly Lys Ser Leu Pro Ala Val Met Asn
 130 135 140 145
 act aag tct ctg cag cca tct ggg gtt cct att tcg gac gcg atg aat 541
 Thr Lys Ser Leu Gln Pro Ser Gly Val Pro Ile Ser Asp Ala Met Asn
 150 155 160
 att cag cag cag cag ttt atg gct gtg gca atg aat cgc caa gca gca 589
 Ile Gln Gln Gln Gln Phe Met Ala Val Ala Met Asn Arg Gln Ala Ala
 165 170 175
 gaa gcg cag aag gct gca caa gcc caa gcg acc cag gct caa gca cca 637
 Glu Ala Gln Lys Ala Ala Gln Ala Gln Ala Thr Gln Ala Gln Ala Pro
 180 185 190
 cag gtg gca ccg cag cca gtt atg cag aat cag caa ttc cag gca cca 685
 Gln Val Ala Pro Gln Pro Val Met Gln Asn Gln Phe Gln Ala Pro
 195 200 205
 gtg cca cag ggc cag cag cca gca tat gca gga gcc cct gtc tat gca 733
 Val Pro Gln Gly Gln Gln Pro Ala Tyr Ala Gly Ala Pro Val Tyr Ala
 210 215 220 225
 gac gcg gta gct cat gca acc gcg cag cag cag gca gca gca gct cag 781
 Asp Ala Val Ala His Ala Thr Ala Gln Gln Gln Ala Ala Ala Ala Gln
 230 235 240
 gca ccg cag gca cct gct ggg aat ccg ttt aac cag ccg cca gca gta 829
 Ala Pro Gln Ala Pro Ala Gly Asn Pro Phe Asn Gln Pro Pro Ala Val
 245 250 255
 gca gca gct ctg gca ccg cag acg cag ccg cca gca gta gca gca gct 877
 Ala Ala Ala Leu Ala Pro Gln Thr Gln Pro Pro Ala Val Ala Ala Ala
 260 265 270
 ctg gca ccg cag acg cag cag ccg gca gca caa cct cag atg gat aac 925
 Leu Ala Pro Gln Thr Gln Gln Pro Ala Ala Gln Pro Gln Met Asp Asn
 275 280 285
 gag cca ccg ttt taaaggcgca atacaccaca ccc 960
 Glu Pro Pro Phe
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<210> 886

<211> 293

<212> PRT

<213> Corynebacterium glutamicum

<400> 886

Met Ala Asn Phe Arg Ser Lys Asp Lys Asp Gly Asn Val Ile Asn Pro
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Asn Ala Ser Thr Lys Gly Val Asp Leu Val Val Asn Val Tyr Asp Ser
 20 25 30

Ala Lys His Val Thr Glu Lys Gly Asn Thr Val His Phe Val Asp Val

35					40					45					
Gln	Val	Ala	Gln	Ile	Pro	Ile	Asp	Ala	Asp	Gly	Thr	Arg	Ala	Asn	Ala
50						55					60				
Asn	Leu	Ala	Pro	Gln	Thr	Met	Pro	His	Leu	His	Leu	Asp	Thr	Lys	Asp
65					70					75				80	
Gly	Gln	Arg	Asn	Thr	Gly	Val	Ala	Tyr	Ser	Asp	Ala	Gln	Ile	Gln	Ala
			85						90				95		
Met	Gln	Thr	Val	Ala	Ala	Gln	Gly	Arg	Asn	His	Met	Thr	Pro	Leu	Leu
			100					105					110		
Ser	Lys	Asp	Gly	Glu	Thr	Val	Gly	Tyr	Ser	Met	Leu	Val	Lys	Ala	Asp
		115						120					125		
Val	Met	Phe	Pro	Lys	Thr	Lys	Asp	Gly	Lys	Ser	Leu	Pro	Ala	Val	Met
		130					135				140				
Asn	Thr	Lys	Ser	Leu	Gln	Pro	Ser	Gly	Val	Pro	Ile	Ser	Asp	Ala	Met
145					150						155				160
Asn	Ile	Gln	Gln	Gln	Gln	Phe	Met	Ala	Val	Ala	Met	Asn	Arg	Gln	Ala
					165					170				175	
Ala	Glu	Ala	Gln	Lys	Ala	Ala	Gln	Ala	Gln	Ala	Thr	Gln	Ala	Gln	Ala
			180					185					190		
Pro	Gln	Val	Ala	Pro	Gln	Pro	Val	Met	Gln	Asn	Gln	Gln	Phe	Gln	Ala
			195					200					205		
Pro	Val	Pro	Gln	Gly	Gln	Gln	Pro	Ala	Tyr	Ala	Gly	Ala	Pro	Val	Tyr
			210				215					220			
Ala	Asp	Ala	Val	Ala	His	Ala	Thr	Ala	Gln	Gln	Gln	Ala	Ala	Ala	Ala
225					230						235				240
Gln	Ala	Pro	Gln	Ala	Pro	Ala	Gly	Asn	Pro	Phe	Asn	Gln	Pro	Pro	Ala
				245					250					255	
Val	Ala	Ala	Ala	Leu	Ala	Pro	Gln	Thr	Gln	Pro	Pro	Ala	Val	Ala	Ala
			260						265					270	
Ala	Leu	Ala	Pro	Gln	Thr	Gln	Gln	Pro	Ala	Ala	Gln	Pro	Gln	Met	Asp
			275					280						285	
Asn	Glu	Pro	Pro	Phe											
			290												

<210> 887

<211> 969

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(946)

<223> RXN01910

<400> 887
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Met Ala Phe Pro Leu
1 5
cta gcg gtt gct ggc aca gtt gcc ccc gtt gca gca gga tgg gca aaa 163
Leu Ala Val Ala Gly Thr Val Ala Pro Val Ala Ala Gly Trp Ala Lys
10 15 20
gat aag ttt ctc agc aac tct cag aat aat cag cag gcc cag aat cag 211
Asp Lys Phe Leu Ser Asn Ser Gln Asn Asn Gln Gln Ala Gln Asn Gln
25 30 35
cag atg agt ttt gga cag gtc aac aac agc gca cag aat tct gga tca 259
Gln Met Ser Phe Gly Gln Val Asn Asn Ser Ala Gln Asn Ser Gly Ser
40 45 50
gaa aac agc ggt ttc atg ggt caa tac ggc aat ctg ggt gca ggt ttg 307
Glu Asn Ser Gly Phe Met Gly Gln Tyr Gly Asn Leu Gly Ala Gly Leu
55 60 65
gca ggt gct gct aca ggc gca ggg ctt gcg tat agc gat ttt gaa gat 355
Ala Gly Ala Ala Thr Gly Ala Gly Leu Ala Tyr Ser Asp Phe Glu Asp
70 75 80 85
ggt caa agt ttg tcc aag ggc cgc aac atg gtc ggc aaa ggg ctc 403
Gly Gln Ser Leu Ser Ser Lys Ala Arg Asn Met Val Gly Lys Gly Leu
90 95 100
gct ggt gcc gga gct ggt gtg ttc acc aag ctt gcc aat gat gca att 451
Ala Gly Ala Gly Ala Gly Val Phe Thr Lys Leu Ala Asn Asp Ala Ile
105 110 115
cag gcc gag ggt ggc tgc atg aag gct agt gct tat tct gcc att gca 499
Gln Ala Glu Gly Gly Ser Met Lys Ala Ser Ala Tyr Ser Ala Ile Ala
120 125 130
ggc ggc ttg gga tgc tat ctc aaa gac ggc ggt ccg ggt gtg att aaa 547
Gly Gly Leu Gly Ser Tyr Leu Lys Asp Gly Gly Pro Gly Val Ile Lys
135 140 145
tcc gcg atg gcc agc ggt gca gcc ggt ttt ggt gcg gat aaa gtg cac 595
Ser Ala Met Ala Ser Gly Ala Ala Gly Phe Gly Ala Asp Lys Val His
150 155 160 165
gat aaa tta gct gag tct ggt cat gag ggg ttg gct gat tcc ttg tgc 643
Asp Lys Leu Ala Glu Ser Gly His Glu Gly Leu Ala Asp Ser Leu Ser
170 175 180
ggc gct att caa gga ggt ggt ctt ggt tac tcc acg ctt ggc ggt gtc 691
Gly Ala Ile Gln Gly Gly Leu Gly Tyr Ser Thr Leu Gly Gly Val
185 190 195
act ggt gct ggt att ggc ggt gcg acg ggc ggt ctc gca gga cta gca 739
Thr Gly Ala Gly Ile Gly Gly Ala Thr Gly Gly Leu Ala Gly Leu Ala
200 205 210
caa aac tac ttt ggt ggt ggc gat gac tac agc aac gct ggg gca tct 787
Gln Asn Tyr Phe Gly Gly Gly Asp Asp Tyr Ser Asn Ala Gly Ala Ser

215	220	225	
gca tgc ggg ttt agt gcc aac cag gtt aat agt gag atc agc acc gag			835
Ala Ser Gly Phe Ser Ala Asn Gln Val Asn Ser Glu Ile Ser Thr Glu			
230	235	240	245
att ccg cag ttt gcg aat ctt ggt caa cca cag cga tcc gag ctt gaa			883
Ile Pro Gln Phe Ala Asn Leu Gly Gln Pro Gln Arg Ser Glu Leu Glu			
250	255		260
caa tta gcg cta cct caa gaa tca cgg tct gta gat aag agc tac gac			931
Gln Leu Ala Leu Pro Gln Glu Ser Arg Ser Val Asp Lys Ser Tyr Asp			
265	270		275
caa ggc tac gaa gcg taagcgcttt ataacaaccc cgt			969
Gln Gly Tyr Glu Ala			
280			

<210> 888

<211> 282

<212> PRT

<213> Corynebacterium glutamicum

<400> 888

Met	Ala	Phe	Pro	Leu	Leu	Ala	Val	Ala	Gly	Thr	Val	Ala	Pro	Val	Ala
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Ala	Gly	Trp	Ala	Lys	Asp	Lys	Phe	Leu	Ser	Asn	Ser	Gln	Asn	Asn	Gln
		20						25					30		

Gln	Ala	Gln	Asn	Gln	Gln	Met	Ser	Phe	Gly	Gln	Val	Asn	Asn	Ser	Ala
		35				40						45			

Gln	Asn	Ser	Gly	Ser	Glu	Asn	Ser	Gly	Phe	Met	Gly	Gln	Tyr	Gly	Asn
	50					55					60				

Leu	Gly	Ala	Gly	Leu	Ala	Gly	Ala	Ala	Thr	Gly	Ala	Gly	Leu	Ala	Tyr
65				70					75					80	

Ser	Asp	Phe	Glu	Asp	Gly	Gln	Ser	Leu	Ser	Ser	Lys	Ala	Arg	Asn	Met
			85						90					95	

Val	Gly	Lys	Gly	Leu	Ala	Gly	Ala	Gly	Ala	Gly	Val	Phe	Thr	Lys	Leu
			100				105						110		

Ala	Asn	Asp	Ala	Ile	Gln	Ala	Glu	Gly	Gly	Ser	Met	Lys	Ala	Ser	Ala
		115					120					125			

Tyr	Ser	Ala	Ile	Ala	Gly	Gly	Leu	Gly	Ser	Tyr	Leu	Lys	Asp	Gly	Gly
	130				135						140				

Pro	Gly	Val	Ile	Lys	Ser	Ala	Met	Ala	Ser	Gly	Ala	Ala	Gly	Phe	Gly
	145				150					155				160	

Ala	Asp	Lys	Val	His	Asp	Lys	Leu	Ala	Glu	Ser	Gly	His	Glu	Gly	Leu
			165						170					175	

Ala	Asp	Ser	Leu	Ser	Gly	Ala	Ile	Gln	Gly	Gly	Gly	Leu	Gly	Tyr	Ser
			180				185							190	

Thr Leu Gly Gly Val Thr Gly Ala Gly Ile Gly Gly Ala Thr Gly Gly
 195 200 205
 Leu Ala Gly Leu Ala Gln Asn Tyr Phe Gly Gly Gly Asp Asp Tyr Ser
 210 215 220
 Asn Ala Gly Ala Ser Ala Ser Gly Phe Ser Ala Asn Gln Val Asn Ser
 225 230 235 240
 Glu Ile Ser Thr Glu Ile Pro Gln Phe Ala Asn Leu Gly Gln Pro Gln
 245 250 255
 Arg Ser Glu Leu Glu Gln Leu Ala Leu Pro Gln Glu Ser Arg Ser Val
 260 265 270
 Asp Lys Ser Tyr Asp Gln Gly Tyr Glu Ala
 275 280

<210> 889

<211> 969

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(946)

<223> FRXA01910

<400> 889

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gtctcagatc atgaacagca caatgttaga gaagattgat atg gca ttt ccg ctt 115
 Met Ala Phe Pro Leu
 1 5

cta gcg gtt gct gcc aca gtt gcc ccc gtt gca gca gga tgg gca aaa 163
 Leu Ala Val Ala Gly Thr Val Ala Pro Val Ala Ala Gly Trp Ala Lys
 10 15 20

gat aag ttt ctc agc aac tct cag aat aat cag cag gcc cag aat cag 211
 Asp Lys Phe Leu Ser Asn Ser Gln Asn Asn Gln Gln Ala Gln Asn Gln
 25 30 35

cag atg agt ttt gga cag gtc aac aac agc gca cag aat tct gga tca 259
 Gln Met Ser Phe Gly Gln Val Asn Asn Ser Ala Gln Asn Ser Gly Ser
 40 45 50

gaa aac agc ggt ttc atg ggt caa tac ggc aat ctg ggt gca ggt ttg 307
 Glu Asn Ser Gly Phe Met Gly Gln Tyr Gly Asn Leu Gly Ala Gly Leu
 55 60 65

gca ggt gct gct aca ggc gca ggg ctt gcg tat agc gat ttt gaa gat 355
 Ala Gly Ala Ala Thr Gly Ala Gly Leu Ala Tyr Ser Asp Phe Glu Asp
 70 75 80 85

ggt caa agt ttg tcc tcg aag gcc cgc aac atg gtc gcc aaa ggg ctc 403
 Gly Gln Ser Leu Ser Ser Lys Ala Arg Asn Met Val Gly Lys Gly Leu
 90 95 100

gct ggt gcc gga gct ggt gtg ttc acc aag ctt gcc aat gat gca att 451

Ala Gly Ala Gly Ala Gly Val Phe Thr Lys Leu Ala Asn Asp Ala Ile
105 110 115

cag gcc gag ggt ggc tcg atg aag gct agt gct tat tct gcc att gca 499
Gln Ala Glu Gly Gly Ser Met Lys Ala Ser Ala Tyr Ser Ala Ile Ala
120 125 130

agc gcc ttg gga tcg tat ctc aaa aac ggc ggt ccg ggt gtg att aaa 547
Ser Gly Leu Gly Ser Tyr Leu Lys Asn Gly Gly Pro Gly Val Ile Lys
135 140 145

tcc gcg atg gcc agc ggt gca gcc ggt ttt ggt gcg gat aaa gtg cac 595
Ser Ala Met Ala Ser Gly Ala Ala Gly Phe Gly Ala Asp Lys Val His
150 155 160 165

gat aaa tta gct gag tct ggt cat gag ggg ttg gct gat tcc ttg tcg 643
Asp Lys Leu Ala Gln Ser Gly His Glu Gly Leu Ala Asp Ser Leu Ser
170 175 180

ggc gct att caa gga ggt ggt ctt ggt tac tcc acg ctt gcc ggt gtc 691
Gly Ala Ile Gln Gly Gly Gly Leu Gly Tyr Ser Thr Leu Gly Gly Val
185 190 195

act ggt gct ggt att ggc ggt gcg acg ggc ggt ctc gca gga cta gca 739
Thr Gly Ala Gly Ile Gly Gly Ala Thr Gly Gly Leu Ala Gly Leu Ala
200 205 210

caa aac tac ttt ggt ggt ggc gat gac tac agc aac gct ggg gca tct 787
Gln Asn Tyr Phe Gly Gly Gly Asp Asp Tyr Ser Asn Ala Gly Ala Ser
215 220 225

gca tcg ggg ttt agt gcc aac cag gtt aat agt gag atc agc acc gag 835
Ala Ser Gly Phe Ser Ala Asn Gln Val Asn Ser Glu Ile Ser Thr Glu
230 235 240 245

att ccg cag ttt gcg aat ctt ggt caa cca cag cga tcc gag ctt gaa 883
Ile Pro Gln Phe Ala Asn Leu Gly Gln Pro Gln Arg Ser Glu Leu Glu
250 255 260

caa tta gcg cta cct caa gaa tca cgg tct gta gat aag agc tac gac 931
Gln Leu Ala Leu Pro Gln Glu Ser Arg Ser Val Asp Lys Ser Tyr Asp
265 270 275

caa gcc tac gaa gcg taagcgcttt ataacaaccc cgt 969
Gln Gly Tyr Glu Ala
280

<210> 890

<211> 282

<212> PRT

<213> Corynebacterium glutamicum

<400> 890

Met Ala Phe Pro Leu Leu Ala Val Ala Gly Thr Val Ala Pro Val Ala
1 5 10 15Ala Gly Trp Ala Lys Asp Lys Phe Leu Ser Asn Ser Gln Asn Asn Gln
20 25 30

Gln Ala Gln Asn Gln Gln Met Ser Phe Gly Gln Val Asn Asn Ser Ala

35 40 45
 Gln Asn Ser Gly Ser Glu Asn Ser Gly Phe Met Gly Gln Tyr Gly Asn
 50 55 60
 Leu Gly Ala Gly Leu Ala Gly Ala Ala Thr Gly Ala Gly Leu Ala Tyr
 65 70 75 80
 Ser Asp Phe Glu Asp Gly Gln Ser Leu Ser Ser Lys Ala Arg Asn Met
 85 90 95
 Val Gly Lys Gly Leu Ala Gly Ala Gly Ala Gly Val Phe Thr Lys Leu
 100 105 110
 Ala Asn Asp Ala Ile Gln Ala Glu Gly Gly Ser Met Lys Ala Ser Ala
 115 120 125
 Tyr Ser Ala Ile Ala Ser Gly Leu Gly Ser Tyr Leu Lys Asn Gly Gly
 130 135 140
 Pro Gly Val Ile Lys Ser Ala Met Ala Ser Gly Ala Ala Gly Phe Gly
 145 150 155 160
 Ala Asp Lys Val His Asp Lys Leu Ala Glu Ser Gly His Glu Gly Leu
 165 170 175
 Ala Asp Ser Leu Ser Gly Ala Ile Gln Gly Gly Gly Leu Gly Tyr Ser
 180 185 190
 Thr Leu Gly Gly Val Thr Gly Ala Gly Ile Gly Gly Ala Thr Gly Gly
 195 200 205
 Leu Ala Gly Leu Ala Gln Asn Tyr Phe Gly Gly Gly Asp Asp Tyr Ser
 210 215 220
 Asn Ala Gly Ala Ser Ala Ser Gly Phe Ser Ala Asn Gln Val Asn Ser
 225 230 235 240
 Glu Ile Ser Thr Glu Ile Pro Gln Phe Ala Asn Leu Gly Gln Pro Gln
 245 250 255
 Arg Ser Glu Leu Glu Gln Leu Ala Leu Pro Gln Glu Ser Arg Ser Val
 260 265 270
 Asp Lys Ser Tyr Asp Gln Gly Tyr Glu Ala
 275 280

<210> 891

<211> 1062

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1039)

<223> RXN01911

<400> 891

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tataattgtg agcgggattc ttagtgcgct cgcgggtctg gtg ttt att att ggc 115
Val Phe Ile Ile Gly
1 5

gcc ggc ttg cca ctg ttg tac gtg ccg att ttt gtg act gtc atc gtc 163
Ala Gly Leu Pro Leu Leu Tyr Val Pro Ile Phe Val Thr Val Ile Val
10 15 20

atg gtg gtg tat gcg cta ttg cgc tat gag cag cgc atg tca ggc aca 211
Met Val Val Tyr Ala Leu Leu Arg Tyr Glu Gln Arg Met Ser Gly Thr
25 30 35

gtc tac gag gaa gca gat cct gtc gaa atg gat tca gtg atc tgg gag 259
Val Tyr Glu Glu Ala Asp Pro Val Glu Met Asp Ser Val Ile Trp Glu
40 45 50

ggc atc aag tgc gat att gcc tcg gat att gca gcc cga gca gaa gcg 307
Gly Ile Lys Cys Asp Ile Ala Ser Asp Ile Ala Ala Arg Ala Glu Ala
55 60 65

aaa aaa gcg aaa aag cca gtt gcg tca gat gct gtt gct gtt ggt aac 355
Lys Lys Ala Lys Lys Pro Val Ala Ser Asp Ala Val Ala Val Gly Asn
70 75 80 85

tat atc gcg tcc ttg cgt cag cat atg ttg gta gaa acc cag cga cgt 403
Tyr Ile Ala Ser Leu Arg Gln His Met Leu Val Glu Thr Gln Arg
90 95 100

tat cac cac aag ctt ggt cgt gag ctg cat aat gat cca gcg caa cta 451
Tyr His His Lys Leu Gly Arg Glu Leu His Asn Asp Pro Ala Gln Leu
105 110 115

gag gat tat ggc tct ggt ctg cgt gac tgt gag tgt cgg gca tgt gtg 499
Glu Asp Tyr Gly Ser Gly Leu Arg Asp Cys Glu Cys Arg Ala Cys Val
120 125 130

gtg gct cag aaa ttg ggt gtc acg gtg cac gct cat ggt gtg gtg cag 547
Val Ala Gln Lys Leu Gly Val Thr Val His Ala His Gly Val Val Gln
135 140 145

gcg agc gca cgt aaa aaa gat cgc gtc att att ggg cga gcc gat ggt 595
Ala Ser Ala Arg Lys Lys Asp Arg Val Ile Ile Gly Arg Ala Asp Gly
150 155 160 165

att gat gtg gcc ggc tgg tgg aac cac cgc caa gaa gct cga cgt aaa 643
Ile Asp Val Ala Gly Trp Trp Asn His Arg Gln Glu Ala Arg Arg Lys
170 175 180

acg agc gcg gct aag cag ttg gag cgc gat gca caa cgc aag cga acc 691
Thr Ser Ala Ala Lys Gln Leu Glu Arg Asp Ala Gln Arg Lys Arg Thr
185 190 195

caa gct gag cgc gat aaa gag att gag cgt aag cgt aag gct caa gaa 739
Gln Ala Glu Arg Asp Lys Glu Ile Glu Arg Lys Arg Lys Ala Gln Glu
200 205 210

ttt gta gcg gag cag tca ggg aaa gct gct gca gca caa cgg cgg gcc 787
Phe Val Ala Glu Gln Ser Gly Lys Ala Ala Ala Ala Gln Arg Arg Ala
215 220 225

gag aaa aag gct gcg aag caa gcg cgt gta gat gaa ctg gtg gcg cag 835

Glu Lys Lys Ala Ala Lys Gln Ala Arg Val Asp Glu Leu Val Ala Gln
 230 235 240 245
 aaa cag gct gct cag gag cag aaa act cac tgt aag cgg gac aag cag 883
 Lys Gln Ala Ala Gln Glu Gln Lys Thr His Cys Lys Arg Asp Lys Gln
 250 255 260
 cgt gcg aag aaa gca caa ggg cgc aaa gtt ggt gcc gtt gat aat tcc 931
 Arg Ala Lys Lys Ala Gln Gly Arg Lys Val Gly Ala Val Asp Asn Ser
 265 270 275
 gct gtg gac gat gtg ttg gcg tat gcg gag aaa acc cgc agt ata gct 979
 Ala Val Asp Asp Val Leu Ala Tyr Ala Glu Lys Thr Arg Ser Ile Ala
 280 285 290
 ggc tgt aga gat gac gac agc gtt gtg cac gtt gat atg gca gcg ggt 1027
 Gly Cys Arg Asp Asp Asp 300 Val Val His Val Asp Met Ala Ala Gly
 295 305
 gtc cgc gat gtc taaatcgac gatgatcgaa aaa 1062
 Val Arg Asp Val
 310

<210> 892

<211> 313

<212> PRT

<213> Corynebacterium glutamicum

<400> 892

Val Phe Ile Ile Gly Ala Gly Leu Pro Leu Leu Tyr Val Pro Ile Phe
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Val Thr Val Ile Val Met Val Val Tyr 25 Ala Leu Leu Arg Tyr Glu Gln
 20 25 30

Arg Met Ser Gly Thr Val Tyr Glu Glu Ala Asp Pro Val Glu Met Asp
 35 40 45

Ser Val Ile Trp Glu Gly Ile Lys Cys Asp Ile Ala Ser Asp Ile Ala
 50 55 60

Ala Arg Ala Glu Ala Lys Lys Ala Lys Lys Pro Val Ala Ser Asp Ala
 65 70 75 80

Val Ala Val Gly Asn Tyr Ile Ala Ser Leu Arg Gln His Met Leu Val
 85 90 95

Glu Thr Gln Arg Arg Tyr His His Lys Leu Gly Arg Glu Leu His Asn
 100 105 110

Asp Pro Ala Gln Leu Glu Asp Tyr Gly Ser Gly Leu Arg Asp Cys Glu
 115 120 125

Cys Arg Ala Cys Val Val Ala Gln Lys Leu Gly Val Thr Val His Ala
 130 135 140

His Gly Val Val Gln Ala Ser Ala Arg Lys Lys Asp Arg Val Ile Ile
 145 150 155 160

Gly Arg Ala Asp Gly Ile Asp Val Ala Gly Trp Trp Asn His Arg Gln

165 170 175
 Glu Ala Arg Arg Lys Thr Ser Ala Ala Lys Lys Gln Leu Glu Arg Asp Ala
 180 185 190
 Gln Arg Lys Arg Thr Gln Ala Glu Arg Asp Lys Glu Ile Glu Arg Lys
 195 200 205
 Arg Lys Ala Gln Glu Phe Val Ala Glu Gln Ser Gly Lys Ala Ala Ala
 210 215 220
 Ala Gln Arg Arg Ala Glu Lys Lys Ala Ala Lys Gln Ala Arg Val Asp
 225 230 235 240
 Glu Leu Val Ala Gln Lys Gln Ala Ala Gln Glu Gln Lys Thr His Cys
 245 250 255
 Lys Arg Asp Lys Gln Arg Ala Lys Lys Ala Gln Gly Arg Lys Val Gly
 260 265 270
 Ala Val Asp Asn Ser Ala Val Asp Asp Val Leu Ala Tyr Ala Glu Lys
 275 280 285
 Thr Arg Ser Ile Ala Gly Cys Arg Asp Asp Asp Ser Val Val His Val
 290 295 300
 Asp Met Ala Ala Gly Val Arg Asp Val
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 <210> 893
 <211> 946
 <212> DNA
 <213> Corynebacterium glutamicum
 <220>
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 <222> (101)..(946)
 <223> FRXA01911
 <400> 893
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 Val Phe Ile Ile Gly
 1 5
 gcc gcc ttg cca ctg ttg tac gtg cgg att ttt gtg act gtc atc gtc 163
 Ala Gly Leu Pro Leu Leu Tyr Val Pro Ile Phe Val Thr Val Ile Val
 10 15 20
 atg gtg gtg tat gcg cta ttg cgc tat gag cag cgc atg tca gcc aca 211
 Met Val Val Tyr Ala Leu Leu Arg Tyr Glu Gln Arg Met Ser Gly Thr
 25 30 35
 gtc tac gag gaa gca gat cct gtc gaa atg gat tca gtg atc tgg gag 259
 Val Tyr Glu Glu Ala Asp Pro Val Glu Met Asp Ser Val Ile Trp Glu
 40 45 50
 gcc atc aag tgc gat att gcc tcg gat att gca gcc cga gca gaa gcg 307
 Gly Ile Lys Cys Asp Ile Ala Ser Asp Ile Ala Ala Arg Ala Glu Ala

55	60	65	
aaa aaa gcg aaa aag cca gtt gcg tca gat gct gtt gct gtt ggt aac	355		
Lys Lys Ala Lys Lys Pro Val Ala Ser Asp Ala Val Ala Val Gly Asn			
70 75 80 85			
tat atc gcg tcc ttg cgt cag cat atg ttg gta gaa acc cag cga cgt	403		
Tyr Ile Ala Ser Leu Arg Gln His Met Leu Val Glu Thr Gln Arg Arg			
90 95 100			
tat cac cac aag ctt ggt cgt gag ctg cat aat gat cca gcg caa cta	451		
Tyr His His Lys Leu Gly Arg Glu His Asn Asp Pro Ala Gln Leu			
105 110 115			
gag gat tat ggc tct ggt ctg cgt gac tgt gag tgt cgg gca tgt gtg	499		
Glu Asp Tyr Gly Ser Gly Leu Arg Asp Cys Glu Cys Arg Ala Cys Val			
120 125 130			
gtg gct cag aaa ttg ggt gtc acg gtg cac gct cat ggt gtg gtg cag	547		
Val Ala Gln Lys Leu Gly Val Thr Val His Ala His Gly Val Val Gln			
135 140 145			
gcg agc gca cgt aaa aaa gat cgc gtc att att ggg cga gcc gat ggt	595		
Ala Ser Ala Arg Lys Lys Asp Arg Val Ile Ile Gly Arg Ala Asp Gly			
150 155 160 165			
att gat gtg gcc ggc tgg tgg aac cac cgc caa gaa gct cga cgt aaa	643		
Ile Asp Val Ala Gly Trp Trp Asn His Arg Gln Glu Ala Arg Arg Lys			
170 175 180			
acg agc gcg gct aag cag ttg gag cgc gat gca caa cgc aag cga acc	691		
Thr Ser Ala Ala Lys Gln Leu Glu Arg Asp Ala Gln Arg Lys Arg Thr			
185 190 195			
caa gct gag cgc gat aaa gag att gag cgt aag cgt aag gct caa gaa	739		
Gln Ala Glu Arg Asp Lys Glu Ile Glu Arg Lys Arg Lys Ala Gln Glu			
200 205 210			
ttt gta gcg gag cag tca ggg aaa gct gct gca gca caa cgg cgg gcc	787		
Phe Val Ala Glu Gln Ser Gly Lys Ala Ala Ala Gln Arg Arg Ala			
215 220 225			
gag aaa aag gct gcg aag caa gcg cgt gta gat gaa ctg gtg gcg cag	835		
Glu Lys Lys Ala Ala Lys Gln Ala Arg Val Asp Glu Leu Val Ala Gln			
230 235 240 245			
aaa cag gct gct cag gag cag aaa act cac tgt aag cgg gac aag cag	883		
Lys Gln Ala Ala Gln Glu Gln Lys Thr His Cys Lys Arg Asp Lys Gln			
250 255 260			
cgt gcg aag aaa gca caa ggg cgc aaa gtt ggt gcc gtt gat aat tcc	931		
Arg Ala Lys Lys Ala Gln Gly Arg Lys Val Gly Ala Val Asp Asn Ser			
265 270 275			
gct gtg gac gat gtg	946		
Ala Val Asp Asp Val			
280			

<210> 894

<211> 282

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 894

Val Phe Ile Ile Gly Ala Gly Leu Pro Leu Leu Tyr Val Pro Ile Phe
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Val Thr Val Ile Val Met Val Val Tyr Ala Leu Leu Arg Tyr Glu Gln
 20 25 30

Arg Met Ser Gly Thr Val Tyr Glu Glu Ala Asp Pro Val Glu Met Asp
 35 40 45

Ser Val Ile Trp Glu Gly Ile Lys Cys Asp Ile Ala Ser Asp Ile Ala
 50 55 60

Ala Arg Ala Glu Ala Lys Lys Ala Lys Lys Pro Val Ala Ser Asp Ala
 65 70 75 80

Val Ala Val Gly Asn Tyr Ile Ala Ser Leu Arg Gln His Met Leu Val
 85 90 95

Glu Thr Gln Arg Arg Tyr His His Lys Leu Gly Arg Glu Leu His Asn
 100 105 110

Asp Pro Ala Gln Leu Glu Asp Tyr Gly Ser Gly Leu Arg Asp Cys Glu
 115 120 125

Cys Arg Ala Cys Val Val Ala Gln Lys Leu Gly Val Thr Val His Ala
 130 135 140

His Gly Val Val Gln Ala Ser Ala Arg Lys Lys Asp Arg Val Ile Ile
 145 150 155 160

Gly Arg Ala Asp Gly Ile Asp Val Ala Gly Trp Trp Asn His Arg Gln
 165 170 175

Glu Ala Arg Arg Lys Thr Ser Ala Ala Lys Gln Leu Glu Arg Asp Ala
 180 185 190

Gln Arg Lys Arg Thr Gln Ala Glu Arg Asp Lys Glu Ile Glu Arg Lys
 195 200 205

Arg Lys Ala Gln Glu Phe Val Ala Glu Gln Ser Gly Lys Ala Ala Ala
 210 215 220

Ala Gln Arg Arg Ala Glu Lys Lys Ala Ala Lys Gln Ala Arg Val Asp
 225 230 235 240

Glu Leu Val Ala Gln Lys Gln Ala Ala Gln Glu Gln Lys Thr His Cys
 245 250 255

Lys Arg Asp Lys Gln Arg Ala Lys Lys Ala Gln Gly Arg Lys Val Gly
 260 265 270

Ala Val Asp Asn Ser Ala Val Asp Asp Val
 275 280

<210> 895

<211> 1074

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> {101}..{1051}

<223> RXN01930

<400> 895

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tgtcattoga	cattattacc	gctcactcac	aatogatgaa	gtg	att	tca	aca	aat	115
				Val	Ile	Ser	Thr	Asn	
				1				5	

gag	att	gaa	aat	att	cac	tca	act	cgt	cgg	gat	att	gaa	ata	gcg	ctt	163
Glu	Ile	Glu	Asn	Ile	His	Ser	Thr	Arg	Arg	Asp	Ile	Glu	Ile	Ala	Leu	
			10						15					20		

gat	gaa	tct	tcc	act	agt	gag	cca	aag	aga	ttt	tcg	gaa	att	tca	cac	211
Asp	Glu	Ser	Ser	Thr	Ser	Glu	Pro	Lys	Arg	Phe	Ser	Glu	Ile	Ser	His	
			25					30						35		

ctt	tac	ctc	gca	ctt	gcc	gaa	ggg	aaa	ata	tcc	ttt	ccg	gaa	agc	cca	259
Leu	Tyr	Leu	Ala	Leu	Ala	Glu	Gly	Lys	Ile	Ser	Phe	Pro	Glu	Ser	Pro	
		40					45					50				

agt	gaa	ctt	cga	gaa	ctc	tat	gac	cat	tta	atg	cac	ggc	gag	cta	ggg	307
Ser	Glu	Leu	Arg	Glu	Leu	Tyr	Asp	His	Leu	Met	His	Gly	Glu	Leu	Gly	
		55				60					65					

aaa	gaa	aat	gaa	tta	gat	ggg	gag	att	ttc	cgc	caa	gga	ccc	gtg	gaa	355
Lys	Glu	Asn	Glu	Leu	Asp	Gly	Glu	Ile	Phe	Arg	Gln	Gly	Pro	Val	Glu	
		70			75				80						85	

atc	cgc	gat	agt	cgg	caa	aaa	gtg	att	cat	tca	ggg	ttt	tct	cca	gaa	403
Ile	Arg	Asp	Ser	Arg	Gln	Lys	Val	Ile	His	Ser	Gly	Phe	Ser	Pro	Glu	
				90					95					100		

tca	cag	atc	atc	gaa	gga	atc	aac	gca	att	att	aag	ctg	gcg	cac	tca	451
Ser	Gln	Ile	Ile	Glu	Gly	Ile	Asn	Ala	Ile	Ile	Lys	Leu	Ala	His	Ser	
			105					110						115		

gaa	gag	gaa	tcc	aac	ctt	gtt	ggc	atc	atg	atg	tca	cac	ttc	atg	ttt	499
Glu	Glu	Glu	Ser	Asn	Leu	Val	Gly	Ile	Met	Met	Ser	His	Phe	Met	Phe	
		120					125						130			

gaa	tca	att	cac	ccg	ttt	tat	gat	gga	aac	gga	aga	act	ggg	cgc	tac	547
Glu	Ser	Ile	His	Pro	Phe	Tyr	Asp	Gly	Asn	Gly	Arg	Thr	Gly	Arg	Tyr	
		135				140					145					

ctt	ctc	ggg	ata	caa	tta	agc	aaa	att	ctc	tcc	cct	gct	aca	gca	ctg	595
Leu	Leu	Gly	Ile	Gln	Leu	Ser	Lys	Ile	Leu	Ser	Pro	Ala	Thr	Ala	Leu	
		150				155					160				165	

aca	atg	tct	tcg	gca	att	aat	caa	ttt	cga	aac	aag	tac	tac	aaa	gcg	643
Thr	Met	Ser	Ser	Ala	Ile	Asn	Gln	Phe	Arg	Asn	Lys	Tyr	Tyr	Lys	Ala	
				170				175						180		

ttt	cat	gcc	gta	gaa	cac	cga	tta	aat	cgc	gga	gac	gga	aca	ccg	ttt	691
Phe	His	Ala	Val	Glu	His	Arg	Leu	Asn	Arg	Gly	Asp	Gly	Thr	Pro	Phe	

185	190	195	
gtt att tcc atg ctt gag ctg tta att gca gcg caa gaa ggt ctc att			739
Val Ile Ser Met Leu Glu Leu Ile Ala Ala Gln Glu Gly Leu Ile			
200	205	210	
gag aat ata aaa caa aga atc gac ttt ttg gca agc ctt gag gac gcc			787
Glu Asn Ile Lys Gln Arg Ile Asp Phe Leu Ala Ser Leu Glu Asp Ala			
215	220	225	
att aaa acg ctt cgg ggt acc aat tcc ttt aag aac cat cag atc aat			835
Ile Lys Thr Leu Arg Gly Thr Asn Ser Phe Lys Asn His Gln Ile Asn			
230	235	240	245
ctg ttg tac att ctc gcc cag att cag ctt ttc ggt aag gac gaa aca			883
Leu Leu Tyr Ile Leu Gly Gln Ile Gln Leu Phe Gly Lys Asp Glu Thr			
250	255	260	
ctt tca ctt gaa tcg gca gca aag ttt ctt aaa gtt tct aag gca act			931
Leu Ser Leu Glu Ser Ala Ala Lys Phe Leu Lys Val Ser Lys Ala Thr			
265	270	275	
gca acg agg tat ttt aga act ctc cga gaa atg gaa tta gtt cac gag			979
Ala Thr Arg Tyr Phe Arg Thr Leu Arg Glu Met Glu Leu Val His Glu			
280	285	290	
gtc agc aaa cgc cct ttg cgg ttt gcg ctc acg gat aaa ggt cgt gag			1027
Val Ser Lys Arg Pro Leu Arg Phe Ala Leu Thr Asp Lys Gly Arg Glu			
295	300	305	
ata gta ggt ctt gag gta aaa att tgactccata acgagaactt aat			1074
Ile Val Gly Leu Glu Val Lys Ile			
310	315		
<210> 896			
<211> 317			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 896			
Val Ile Ser Thr Asn Glu Ile Glu Asn Ile His Ser Thr Arg Arg Asp			
1 5 10 15			
Ile Glu Ile Ala Leu Asp Glu Ser Ser Thr Ser Glu Pro Lys Arg Phe			
20 25 30			
Ser Glu Ile Ser His Leu Tyr Leu Ala Leu Ala Glu Gly Lys Ile Ser			
35 40 45			
Phe Pro Glu Ser Pro Ser Glu Leu Arg Glu Leu Tyr Asp His Leu Met			
50 55 60			
His Gly Glu Leu Gly Lys Glu Asn Glu Leu Asp Gly Glu Ile Phe Arg			
65 70 75 80			
Gln Gly Pro Val Glu Ile Arg Asp Ser Arg Gln Lys Val Ile His Ser			
85 90 95			
Gly Phe Ser Pro Glu Ser Gln Ile Ile Glu Gly Ile Asn Ala Ile Ile			
100 105 110			

Lys Leu Ala His Ser Glu Glu Glu Ser Asn Leu Val Gly Ile Met Met
 115 120 125
 Ser His Phe Met Phe Glu Ser Ile His Pro Phe Tyr Asp Gly Asn Gly
 130 135 140
 Arg Thr Gly Arg Tyr Leu Leu Gly Ile Gln Leu Ser Lys Ile Leu Ser
 145 150 155 160
 Pro Ala Thr Ala Leu Thr Met Ser Ser Ala Ile Asn Gln Phe Arg Asn
 165 170 175
 Lys Tyr Tyr Lys Ala Phe His Ala Val Glu His Arg Leu Asn Arg Gly
 180 185 190
 Asp Gly Thr Pro Phe Val Ile Ser Met Leu Glu Leu Leu Ile Ala Ala
 195 200 205
 Gln Glu Gly Leu Ile Glu Asn Ile Lys Gln Arg Ile Asp Phe Leu Ala
 210 215 220
 Ser Leu Glu Asp Ala Ile Lys Thr Leu Arg Gly Thr Asn Ser Phe Lys
 225 230 235 240
 Asn His Gln Ile Asn Leu Leu Tyr Ile Leu Gly Gln Ile Gln Leu Phe
 245 250 255
 Gly Lys Asp Glu Thr Leu Ser Leu Glu Ser Ala Ala Lys Phe Leu Lys
 260 265 270
 Val Ser Lys Ala Thr Ala Thr Arg Tyr Phe Arg Thr Leu Arg Glu Met
 275 280 285
 Glu Leu Val His Glu Val Ser Lys Arg Pro Leu Arg Phe Ala Leu Thr
 290 295 300
 Asp Lys Gly Arg Glu Ile Val Gly Leu Glu Val Lys Ile
 305 310 315

<210> 897

<211> 1074

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1051)

<223> FRXA01930

<400> 897

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tgtcattcga cattattacc gctcactcac aatcgatgaa gtg att tca aca aat 115
 Val Ile Ser Thr Asn
 1 5

gag att gaa aat att cac tca act cgt cgg gat att gaa ata gcg ctt 163
 Glu Ile Glu Asn Ile His Ser Thr Arg Arg Asp Ile Glu Ile Ala Leu
 10 15 20

gat gaa tct tcc act agt gag cca aag aga ttt tgc gaa att tca cac 211
 Asp Glu Ser Ser Thr Ser Glu Pro Lys Arg Phe Ser Glu Ile Ser His
 25 30 35

ctt tac ctc gca ctt gcc gaa ggt aaa ata tcc ttt ccg gaa agc cca 259
 Leu Tyr Leu Ala Leu Ala Glu Gly Lys Ile Ser Phe Pro Glu Ser Pro
 40 45 50

agt gaa ctt cga gaa ctc tat gac cat tta atg cac ggc gag cta ggt 307
 Ser Glu Leu Arg Glu Leu Tyr Asp His Leu Met His Gly Glu Leu Gly
 55 60 65

aaa gaa aat gaa tta gat ggt gag att ttc cgc caa gga ccc gtg gaa 355
 Lys Glu Asn Glu Leu Asp Gly Glu Ile Phe Arg Gln Gly Pro Val Glu
 70 75 80 85

atc cgc gat agt cgg caa aaa gtg att cat tca ggt ttt tct cca gaa 403
 Ile Arg Asp Ser Arg Gln Lys Val Ile His Ser Gly Phe Ser Pro Glu
 90 95 100

tca cag atc atc gaa gga atc aac gca att att aag ctg gcg cac tca 451
 Ser Gln Ile Ile Glu Gly Ile Asn Ala Ile Ile Lys Leu Ala His Ser
 105 110 115

gaa gag gaa tcc aac ctt gtt ggc atc atg atg tca cac ttc atg ttt 499
 Glu Glu Glu Ser Asn Leu Val Gly Ile Met Met Ser His Phe Met Phe
 120 125 130

gaa tca att cac ccg ttt tat gat gga aac gga aga act ggg cgc tac 547
 Glu Ser Ile His Pro Phe Tyr Asp Gly Asn Gly Arg Thr Gly Arg Tyr
 135 140 145

ctt ctc ggg ata caa tta agc aaa att ctc tcc cct gct aca gca ctg 595
 Leu Leu Gly Ile Gln Leu Ser Lys Ile Leu Ser Pro Ala Thr Ala Leu
 150 155 160 165

aca atg tct tgc gca att aat caa ttt cga aac aag tac tac aaa gcg 643
 Thr Met Ser Ser Ala Ile Asn Gln Phe Arg Asn Lys Tyr Tyr Lys Ala
 170 175 180

ttt cat gcc gta gaa cac cga tta aat cgc gga gac gga aca ccg ttt 691
 Phe His Ala Val Glu His Arg Leu Asn Arg Gly Asp Gly Thr Pro Phe
 185 190 195

gtt att tcc atg ctt gag ctg tta att gca gcg caa gaa ggt ctc att 739
 Val Ile Ser Met Leu Glu Leu Leu Ile Ala Ala Gln Glu Gly Leu Ile
 200 205 210

gag aat ata aaa caa aga atc gac ttt ttg gca agc ctt gag gac gcc 787
 Glu Asn Ile Lys Gln Arg Ile Asp Phe Leu Ala Ser Leu Glu Asp Ala
 215 220 225

att aaa acg ctt ccg ggt acc aat tcc ttt aag aac cat cag atc aat 835
 Ile Lys Thr Leu Arg Gly Thr Asn Ser Phe Lys Asn His Gln Ile Asn
 230 235 240 245

ctg ttg tac att ctc ggc cag att cag ctt ttc ggt aag gac gaa aca 883
 Leu Leu Tyr Ile Leu Gly Gln Ile Gln Leu Phe Gly Lys Asp Glu Thr
 250 255 260

ctt tca ctt gaa tcg gca gca aag ttt ctt aaa gtt tct aag gca act 931
 Leu Ser Leu Glu Ser Ala Ala Lys Phe Leu Lys Val Ser Lys Ala Thr
 265 270 275

gca acg agg tat ttt aga act ctc cga gaa atg gaa tta gtt cac gag 979
 Ala Thr Arg Tyr Phe Arg Thr Leu Arg Glu Met Glu Leu Val His Glu
 280 285 290

gtc agc aaa cgc cct ttg cgg ttt gcg ctc acg gat aaa ggt cgt gag 1027
 Val Ser Lys Arg Pro Leu Arg Phe Ala Leu Thr Asp Lys Gly Arg Glu
 295 300 305

ata gta ggt ctt gag gta aaa att tgactccata acgagaactt aat 1074
 Ile Val Gly Leu Glu Val Lys Ile
 310 315

<210> 898

<211> 317

<212> PRT

<213> Corynebacterium glutamicum

<400> 898

Val Ile Ser Thr Asn Glu Ile Glu Asn Ile His Ser Thr Arg Arg Asp
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Ile Glu Ile Ala Leu Asp Glu Ser Ser Thr Ser Glu Pro Lys Arg Phe
 20 25 30

Ser Glu Ile Ser His Leu Tyr Leu Ala Leu Ala Glu Gly Lys Ile Ser
 35 40 45

Phe Pro Glu Ser Pro Ser Glu Leu Arg Glu Leu Tyr Asp His Leu Met
 50 55 60

His Gly Glu Leu Gly Lys Glu Asn Glu Leu Asp Gly Glu Ile Phe Arg
 65 70 75 80

Gln Gly Pro Val Glu Ile Arg Asp Ser Arg Gln Lys Val Ile His Ser
 85 90 95

Gly Phe Ser Pro Glu Ser Gln Ile Ile Glu Gly Ile Asn Ala Ile Ile
 100 105 110

Lys Leu Ala His Ser Glu Glu Glu Ser Asn Leu Val Gly Ile Met Met
 115 120 125

Ser His Phe Met Phe Glu Ser Ile His Pro Phe Tyr Asp Gly Asn Gly
 130 135 140

Arg Thr Gly Arg Tyr Leu Leu Gly Ile Gln Leu Ser Lys Ile Leu Ser
 145 150 155 160

Pro Ala Thr Ala Leu Thr Met Ser Ser Ala Ile Asn Gln Phe Arg Asn
 165 170 175

Lys Tyr Tyr Lys Ala Phe His Ala Val Glu His Arg Leu Asn Arg Gly
 180 185 190

Asp Gly Thr Pro Phe Val Ile Ser Met Leu Glu Leu Leu Ile Ala Ala
 195 200 205

Gln Glu Gly Leu Ile Glu Asn Ile Lys Gln Arg Ile Asp Phe Leu Ala
 210 215 220

Ser Leu Glu Asp Ala Ile Lys Thr Leu Arg Gly Thr Asn Ser Phe Lys
 225 230 235 240

Asn His Gln Ile Asn Leu Leu Tyr Ile Leu Gly Gln Ile Gln Leu Phe
 245 250 255

Gly Lys Asp Glu Thr Leu Ser Leu Glu Ser Ala Ala Lys Phe Leu Lys
 260 265 270

Val Ser Lys Ala Thr Ala Thr Arg Tyr Phe Arg Thr Leu Arg Glu Met
 275 280 285

Glu Leu Val His Glu Val Ser Lys Arg Pro Leu Arg Phe Ala Leu Thr
 290 295 300

Asp Lys Gly Arg Glu Ile Val Gly Leu Glu Val Lys Ile
 305 310 315

<210> 899
 <211> 1095
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1072)
 <223> RXN01944

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 ccggttacct tcgccttcaa atatcaccga tgaatgtccag gtg cgc acg gca aca 115
 Val Arg Thr Ala Thr
 1 5

ctg cat gtt act tcc agt gct ggc gaa gcc gcg aca acc atc aac ctc 163
 Leu His Val Thr Ser Ser Ala Gly Glu Ala Ala Thr Thr Ile Asn Leu
 10 15 20

acc gag gat gac ggc tct ttc aat tgg gct ctg cct gca gcg gat ctc 211
 Thr Glu Asp Asp Gly Ser Phe Asn Trp Ala Leu Pro Ala Ala Asp Leu
 25 30 35

acc gga aaa tcc tgg ttc gaa tac acc gta acc gcc acc gac gga ttc 259
 Thr Gly Lys Ser Trp Phe Glu Tyr Thr Val Thr Ala Thr Asp Gly Phe
 40 45 50

aac agc gtt acc acc gag ccg gta cgc gtc acc gtc gac ggc gcc aac 307
 Asn Ser Val Thr Thr Glu Pro Val Arg Val Thr Val Asp Gly Ala Asn
 55 60 65

acc gac ccg ctg cgc ctc aac ctg gaa gaa aac caa tgg gtc agt ggc 355
 Thr Asp Pro Leu Arg Leu Asn Leu Glu Glu Asn Gln Trp Val Ser Gly
 70 75 80 85

acc acc gat gtt atc ggt gct tca gat gtc ttc ggc gac aag ctt gaa 403

Thr	Thr	Asp	Val	Ile	Gly	Ala	Ser	Asp	Val	Phe	Gly	Asp	Lys	Leu	Glu	
				90					95					100		
ttg	ctt	atc	gac	gac	gcg	cct	gca	gtc	acc	aac	tcc	agc	ctg	tct	gcg	451
Leu	Leu	Ile	Asp	Asp	Ala	Pro	Ala	Val	Thr	Asn	Ser	Ser	Leu	Ser	Ala	
		105						110					115			
gcc	ccg	acg	ttt	gcg	atg	gaa	gta	acc	caa	act	gat	gtg	ttc	ttc	cgc	499
Ala	Pro	Thr	Phe	Ala	Met	Glu	Val	Thr	Gln	Thr	Asp	Val	Phe	Phe	Arg	
		120					125					130				
aac	ggc	atc	ctt	gcc	ggt	ggg	gaa	gaa	ctc	cgc	att	ttc	gat	caa	gga	547
Asn	Gly	Ile	Leu	Ala	Gly	Gly	Glu	Glu	Leu	Arg	ile	Phe	Asp	Gln	Gly	
		135				140					145					
act	tac	gcc	aac	acc	gaa	acc	atc	tcc	aca	cca	gtc	ccg	ctg	tat	cac	595
Thr	Tyr	Ala	Asn	Thr	Glu	Thr	Ile	Ser	Thr	Pro	Val	Pro	Leu	Tyr	His	
		150			155					160					165	
atc	aat	gag	gac	ggt	acc	ctc	aca	gtc	agt	gtg	tat	gcg	gga	act	aaa	643
Ile	Asn	Glu	Asp	Gly	Thr	Leu	Thr	Val	Ser	Val	Tyr	Ala	Gly	Thr	Lys	
				170					175					180		
gca	gca	cca	gaa	att	gac	ctc	aac	gag	aac	aat	gac	gat	ttc	cag	atc	691
Ala	Ala	Pro	Glu	Ile	Asp	Leu	Asn	Glu	Asn	Asn	Asp	Asp	Phe	Gln	Ile	
		185						190					195			
aga	aac	ctt	cga	cta	att	ctg	cct	gat	ggc	cgg	acc	ctc	acc	oct	gcc	739
Arg	Asn	Leu	Arg	Leu	Ile	Leu	Pro	Asp	Gly	Arg	Thr	Leu	Thr	Pro	Ala	
		200					205					210				
gga	att	tcc	gat	tct	aat	gcg	tgg	ctc	aac	atg	gga	gac	agc	gct	gga	787
Gly	Ile	Ser	Asp	Ser	Asn	Ala	Trp	Leu	Asn	Met	Gly	Asp	Ser	Ala	Gly	
		215				220					225					
aaa	ctc	gat	ttc	ttc	gat	gcc	acc	ttc	gcc	ctc	cct	gag	gat	gct	ttc	835
Lys	Leu	Asp	Phe	Phe	Asp	Ala	Thr	Phe	Ala	Leu	Pro	Glu	Asp	Ala	Phe	
		230			235					240				245		
acc	ggt	gtg	gca	cac	gca	tgg	gat	acc	acc	caa	agc	aca	gat	gga	gaa	883
Thr	Gly	Val	Ala	His	Ala	Trp	Asp	Thr	Thr	Gln	Ser	Thr	Asp	Gly	Glu	
				250					255					260		
cac	cac	atc	acc	att	tcc	cgc	gaa	gac	ggc	ggg	gaa	atc	agc	cgc	acc	931
His	His	Ile	Thr	Ile	Ser	Arg	Glu	Asp	Gly	Gly	Glu	Ile	Ser	Arg	Thr	
		265						270					275			
atc	cgg	ggt	gat	aat	act	gcc	cca	gaa	ctc	acc	ggt	tct	gga	ggt	gaa	979
Ile	Arg	Val	Asp	Asn	Thr	Ala	Pro	Glu	Leu	Thr	Val	Ser	Gly	Val	Glu	
		280				285						290				
gaa	gga	caa	gaa	ctg	cgc	ggc	acc	gta	gaa	att	gat	gcc	cag	gca	acc	1027
Glu	Gly	Gln	Glu	Leu	Arg	Gly	Thr	Val								

<210> 900

<211> 324

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 900

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 20 25 30

Pro Ala Ala Asp Leu Thr Gly Lys Ser Trp Phe Glu Tyr Thr Val Thr
 35 40 45

Ala Thr Asp Gly Phe Asn Ser Val Thr Thr Glu Pro Val Arg Val Thr
 50 55 60

Val Asp Gly Ala Asn Thr Asp Pro Leu Arg Leu Asn Leu Glu Glu Asn
 65 70 75 80

Gln Trp Val Ser Gly Thr Thr Asp Val Ile Gly Ala Ser Asp Val Phe
 85 90 95

Gly Asp Lys Leu Glu Leu Leu Ile Asp Asp Ala Pro Ala Val Thr Asn
 100 105 110

Ser Ser Leu Ser Ala Ala Pro Thr Phe Ala Met Glu Val Thr Gln Thr
 115 120 125

Asp Val Phe Phe Arg Asn Gly Ile Leu Ala Gly Gly Glu Glu Leu Arg
 130 135 140

Ile Phe Asp Gln Gly Thr Tyr Ala Asn Thr Glu Thr Ile Ser Thr Pro
 145 150 155 160

Val Pro Leu Tyr His Ile Asn Glu Asp Gly Thr Leu Thr Val Ser Val
 165 170 175

Tyr Ala Gly Thr Lys Ala Ala Pro Glu Ile Asp Leu Asn Glu Asn Asn
 180 185 190

Asp Asp Phe Gln Ile Arg Asn Leu Arg Leu Ile Leu Pro Asp Gly Arg
 195 200 205

Thr Leu Thr Pro Ala Gly Ile Ser Asp Ser Asn Ala Trp Leu Asn Met
 210 215 220

Gly Asp Ser Ala Gly Lys Leu Asp Phe Phe Asp Ala Thr Phe Ala Leu
 225 230 235 240

Pro Glu Asp Ala Phe Thr Gly Val Ala His Ala Trp Asp Thr Thr Gln
 245 250 255

Ser Thr Asp Gly Glu His His Ile Thr Ile Ser Arg Glu Asp Gly Gly
 260 265 270

Glu Ile Ser Arg Thr Ile Arg Val Asp Asn Thr Ala Pro Glu Leu Thr
 275 280 285

Val Ser Gly Val Glu Glu Gly Gln Glu Leu Arg Gly Thr Val Glu Ile
 290 295 300

Asp Ala Gln Ala Thr Asp Ala Gly Ala Gly Val Lys Ser Val Glu Thr
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Leu Leu Asp Gly

<210> 901
 <211> 407
 <212> DNA
 <213> *Corynebacterium glutamicum*

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 <222> (1)..(384)
 <223> FRXA01944

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gcc gga att tcc gat tct aat gcg tgg ctc aac atg gga gac agc gct 96
 Ala Gly Ile Ser Asp Ser Asn Ala Trp Leu Asn Met Gly Asp Ser Ala
 20 25 30

gga aaa ctc gat ttc ttc gat gcc acc ttc gcc ctc cct gag gat gct 144
 Gly Lys Leu Asp Phe Phe Asp Ala Thr Phe Ala Leu Pro Glu Asp Ala
 35 40 45

ttc acc ggt gtg gca cac gca tgg gat acc acc caa agc aca gat gga 192
 Phe Thr Gly Val Ala His Ala Trp Asp Thr Thr Gln Ser Thr Asp Gly
 50 55 60

gaa cac cac atc acc att tcc cgc gaa gac ggc ggg gaa atc agc cgc 240
 Glu His His Ile Thr Ile Ser Arg Glu Asp Gly Gly Glu Ile Ser Arg
 65 70 75 80

acc atc cgg gtt gat aat act gcc cca gaa ctc acc gtt tct gga gtt 288
 Thr Ile Arg Val Asp Asn Thr Ala Pro Glu Leu Thr Val Ser Gly Val
 85 90 95

gaa gaa gga caa gaa ctg cgc gcc acc gta gaa att gat gcc cag gca 336
 Glu Glu Gly Gln Glu Leu Arg Gly Thr Val Glu Ile Asp Ala Gln Ala
 100 105 110

acc gat gcg ggt gcg gcc gtg aag agc gtc gag acg ctt ctc gac gcc 384
 Thr Asp Ala Gly Ala Gly Val Lys Ser Val Glu Thr Leu Leu Asp Gly
 115 120 125

taacgcgtgc aactccact aac 407

<210> 902
 <211> 128
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 902

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 1 5 10 15

Ala Gly Ile Ser Asp Ser Asn Ala Trp Leu Asn Met Gly Asp Ser Ala
 20 25 30

Gly Lys Leu Asp Phe Phe Asp Ala Thr Phe Ala Leu Pro Glu Asp Ala
 35 40 45

Phe Thr Gly Val Ala His Ala Trp Asp Thr Thr Gln Ser Thr Asp Gly
 50 55 60

Glu His His Ile Thr Ile Ser Arg Glu Asp Gly Gly Glu Ile Ser Arg
 65 70 75 80

Thr Ile Arg Val Asp Asn Thr Ala Pro Glu Leu Thr Val Ser Gly Val
 85 90 95

Glu Glu Gly Gln Glu Leu Arg Gly Thr Val Glu Ile Asp Ala Gln Ala
 100 105 110

Thr Asp Ala Gly Ala Gly Val Lys Ser Val Glu Thr Leu Leu Asp Gly
 115 120 125

<210> 903

<211> 673

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(673)

<223> FRXA01636

<400> 903

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ccgtttacct tcgcttccaa atatcaccga tgatgtccag gtg cgc acg gca aca 115
 Val Arg Thr Ala Thr 5
 1

ctg cat gtt act tcc agt gct ggc gaa gcc gcg aca acc atc aac ctc 163
 Leu His Val Thr Ser Ser Ala Gly Glu Ala Ala Thr Thr Ile Asn Leu 20
 10 15

acc gag gat gac ggc tct ttc aat tgg gct ctg cct gca gcg gat ctc 211
 Thr Glu Asp Asp Gly Ser Phe Asn Trp Ala Leu Pro Ala Ala Asp Leu 35
 25 30

acc gga aaa tcc tgg ttc gaa tac acc gta acc gcc acc gac gga ttc 259
 Thr Gly Lys Ser Trp Phe Glu Tyr Thr Val Thr Ala Thr Asp Gly Phe 40
 45 50

aac agc gtt acc acc gag cgg gta cgc gtc acc gtc gac ggc gcc aac 307
 Asn Ser Val Thr Thr Glu Pro Val Arg Val Thr Val Asp Gly Ala Asn 55
 60 65

acc gac ccg ctg cgc ctc aac ctg gaa gaa aac caa tgg gtc agt ggc 355
 Thr Asp Pro Leu Arg Leu Asn Leu Glu Glu Asn Gln Trp Val Ser Gly
 70 75 80 85

acc acc gat gtt atc ggt gct tca gat gtc ttc ggc gac aag ctt gaa 403
 Thr Thr Asp Val Ile Gly Ala Ser Asp Val Phe Gly Asp Lys Leu Glu
 90 95 100

ttg ctt atc gac gac gcg cct gca gtc acc aac tcc agc ctg tct gcg 451
 Leu Leu Ile Asp Asp Ala Pro Ala Val Thr Asn Ser Ser Leu Ser Ala
 105 110 115

gcc ccg acg ttt gcg atg gaa gta acc caa act gat gtg ttc ttc cgc 499
 Ala Pro Thr Phe Ala Met Glu Val Thr Gln Thr Asp Val Phe Phe Arg
 120 125 130

aac ggc atc ctt gcc ggt ggg gaa gaa ctc cgc att ttc gat caa gga 547
 Asn Gly Ile Leu Ala Gly Gly Glu Glu Leu Arg Ile Phe Asp Gln Gly
 135 140 145

act tac gcc aac acc gaa acc atc tcc aca cca gtc ccg ctg tat cac 595
 Thr Tyr Ala Asn Thr Glu Thr Ile Ser Thr Pro Val Pro Leu Tyr His
 150 155 160 165

atc aat gag gac ggt acc ctc aca gtc agt gtg tat gcg gga act aaa 643
 Ile Asn Glu Asp Gly Thr Leu Thr Val Ser Val Tyr Ala Gly Thr Lys
 170 175 180

gca gca cca gaa att gac ctc aac gag aac 673
 Ala Ala Pro Glu Ile Asp Leu Asn Glu Asn
 185 190

<210> 904

<211> 191

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 904

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 1 5 10 15

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 20 25 30

Pro Ala Ala Asp Leu Thr Gly Lys Ser Trp Phe Glu Tyr Thr Val Thr
 35 40 45

Ala Thr Asp Gly Phe Asn Ser Val Thr Thr Glu Pro Val Arg Val Thr
 50 55 60

Val Asp Gly Ala Asn Thr Asp Pro Leu Arg Leu Asn Leu Glu Glu Asn
 65 70 75 80

Gln Trp Val Ser Gly Thr Thr Asp Val Ile Gly Ala Ser Asp Val Phe
 85 90 95

Gly Asp Lys Leu Glu Leu Leu Ile Asp Asp Ala Pro Ala Val Thr Asn
 100 105 110

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Ser Ser Leu Ser Ala Ala Pro Thr Phe Ala Met Glu Val Thr Gln Thr
   115                               120
Asp Val Phe Phe Arg Asn Gly Ile Leu Ala Gly Gly Glu Glu Leu Arg
   130                               135                               140
Ile Phe Asp Gln Gly Thr Tyr Ala Asn Thr Glu Thr Ile Ser Thr Pro
   145                               150                               155                               160
Val Pro Leu Tyr His Ile Asn Glu Asp Gly Thr Leu Thr Val Ser Val
   165                               170                               175
Tyr Ala Gly Thr Lys Ala Ala Pro Glu Ile Asp Leu Asn Glu Asn
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<210> 905

<211> 2115

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(2092)

<223> RXN01945

<400> 905

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                               Val Gln Leu Pro Leu
                               1                               5
acc acc ggt tcc atc gct ttg gat aaa ggt gaa cac acc ttg gtt atc 163
Thr Thr Gly Ser Ile Ala Leu Asp Lys Gly Glu His Thr Leu Val Ile
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cgt gca gaa gat gaa gta gga aac cgc acc gag aaa acc atc acg ttt 211
Arg Ala Glu Asp Glu Val Gly Asn Arg Thr Glu Lys Thr Ile Thr Phe
                               25                               30                               35
agc act ccg gat gaa aac ccc atc agt ggt gac tac gct cca agc aat 259
Ser Thr Pro Asp Glu Asn Pro Ile Ser Gly Asp Tyr Ala Pro Ser Asn
                               40                               45                               50
ggg gcc acc gtg ggc gtc ggt gac gtt aag tta tct gca cga gca agt 307
Gly Ala Thr Val Gly Val Gly Asp Val Lys Leu Ser Ala Arg Ala Ser
                               55                               60                               65
gat cca agt ggc gat act gtc aag atg acg ttc ctg gaa gcc gat tca 355
Asp Pro Ser Gly Asp Thr Val Lys Met Thr Phe Leu Glu Ala Asp Ser
                               70                               75                               80                               85
cca aaa tta gat agt ggt cgc gtc cga atg tca tca gga acg gta gaa 403
Pro Lys Leu Asp Ser Gly Arg Val Arg Met Ser Ser Gly Thr Val Glu
                               90                               95                               100
gat gcc gga agt gtc tcg cgc gcc gag gcg aaa atg ttg gag agg gga 451
Asp Ala Gly Ser Val Ser Arg Ala Glu Ala Lys Met Leu Glu Arg Gly
                               105                               110                               115

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gac gtc gag aag cta tcc agc ctg gat ggg ctg ggc atg gaa gtt acc	499
Asp Val Glu Lys Leu Ser Ser Leu Asp Gly Leu Gly Met Glu Val Thr	
120 125 130	
tcc gac gcc gca ctg ccg tac cag ctt ttt gaa gtc gat gcg gcg gat	547
Ser Asp Ala Ala Leu Pro Tyr Gln Leu Phe Glu Val Asp Ala Ala Asp	
135 140 145	
gca ctc gcg gcc gac act gaa gtg cgc ctg aat tgg gcg gga tcc gcc	595
Ala Leu Ala Ala Asp Thr Glu Val Arg Leu Asn Trp Ala Gly Ser Ala	
150 155 160 165	
gat ggt cgc gcg cag gtg atc atg tat gtt ttc gat ggc gag gcg tgg	643
Asp Gly Arg Ala Gln Val Ile Met Tyr Val Phe Asp Gly Glu Ala Trp	
170 175 180	
gtt gag gtg gat cgt cac ttg acc gcc gat gag ctg gaa gag ttt acg	691
Val Glu Val Asp Arg His Leu Thr Gly Asp Glu Leu Glu Glu Phe Thr	
185 190 195	
ctg cag gcc gtc gtc aat gcg gaa aaa ttt gca atc gcc gcc act gtc	739
Leu Gln Gly Val Val Asn Ala Glu Lys Phe Ala Ile Gly Gly Thr Val	
200 205 210	
acc gta ttg att cag cac tcc gaa gcc ttc gcc ggt gcg gat cat tca	787
Thr Val Leu Ile Gln His Ser Glu Gly Phe Ala Gly Ala Asp His Ser	
215 220 225	
act aga aat tcc gac gtg acc gca gcg cac ccg gat gat gtg gct cgc	835
Thr Arg Asn Ser Asp Val Thr Ala Ala His Pro Asp Asp Val Ala Arg	
230 235 240 245	
tct gag tac gat ttc acc ctc gcg tgg gaa tct gac acc cag tac tac	883
Ser Glu Tyr Asp Phe Thr Leu Ala Trp Glu Ser Asp Thr Gln Tyr Tyr	
250 255 260	
aac gag gaa ttc cac gag cac caa acc aac atc cat gac tac gtg ctc	931
Asn Glu Glu Phe His Glu His Gln Thr Asn Ile His Asp Tyr Val Leu	
265 270 275	
gcc gaa cgg gag aac aag aat att cag ttc atg ttc cac act gcc gat	979
Ala Glu Arg Glu Asn Lys Asn Ile Gln Phe Met Phe His Thr Gly Asp	
280 285 290	
gtt gtc gac gac tgg gat cag ccc gcg cag tgg gcc aca gcc aac ccc	1027
Val Val Asp Asp Trp Asp Gln Pro Ala Gln Trp Ala Thr Ala Asn Pro	
295 300 305	
gaa tac cag cgc ctc gac gac gcc gcc ctg cca tat tct gtc ctt gcc	1075
Glu Tyr Gln Arg Leu Asp Asp Ala Gly Leu Pro Tyr Ser Val Leu Ala	
310 315 320 325	
gga aac cac gat gtt ggc cac acc agc aat gac tac acc gaa ttc agc	1123
Gly Asn His Asp Val Gly His Thr Ser Asn Asp Tyr Thr Glu Phe Ser	
330 335 340	
cga cac ttc gcc gaa cag gcg tac gta gac aac ccg tgg tac gcc gaa	1171
Arg His Phe Gly Glu Gln Arg Tyr Val Asp Asn Pro Trp Tyr Gly Glu	
345 350 355	
tcc tac caa gac aac cga ggg cac tac gat cta ttt tct gcc gcc gga	1219

Ser	Tyr	Gln	Asp	Asn	Arg	Gly	His	Tyr	Asp	Leu	Phe	Ser	Ala	Gly	Gly	
		360					365					370				
att Ile	gac Asp	ttc Phe	att Ile	aac Asn	gta Val	gcg Ala	atg Met	ggc Gly	tgg Trp	ggt Gly	cca Pro	gac Asp	gac Asp	gaa Glu	gaa Glu	1267
		375				380					385					
atc Ile	gcg Ala	tgg Trp	atg Met	aac Asn	gag Glu	gtc Val	ctg Leu	gcc Ala	aag Lys	cat His	ccc Pro	gag Glu	cgt Arg	gtg Val	gcg Ala	1315
		390				395				400					405	
atc Ile	ctc Leu	aac Asn	ctc Leu	cac His	gaa Glu	ttc Phe	atg Met	ctc Leu	acc Thr	acc Thr	ggc Gly	gga Gly	ctt Leu	ggc Gly	ccg Pro	1363
					410				415					420		
atc Ile	ccg Pro	cag Gln	cgc Arg	att Ile	ctc Leu	gac Asp	gag Glu	gtc Val	gca Ala	gcc Ala	acc Thr	aac Asn	cca Pro	aat Asn	gtc Val	1411
					425				430				435			
agc Ser	atg Met	atc Ile	atg Met	tcc Ser	ggc Gly	cac His	tac Tyr	cac His	gac Asp	gca Ala	ttc Phe	caa Arg	cgc Arg	acc Thr	gac Asp	1459
				440			445					450				
tcc Ser	ttt Phe	gac Asp	gac Asp	gat Asp	ggt Gly	gat Asp	gga Gly	gta Val	gat Asp	gac Asp	cgc Thr	acc Thr	gtc Val	acc Thr	tct Ser	1507
				455		460					465					
atg Met	ctt Leu	ttc Phe	gat Asp	tac Tyr	caa Gln	ggc Gly	cta Leu	ccg Pro	gag Glu	ggc Gly	gga Gly	cag Gln	ggg Gly	tac Tyr	ctc Leu	1555
					475					480				485		
cga Arg	ctt Leu	ctc Leu	cac His	ttt Phe	gat Asp	aac Asn	caa Gln	ggc Gly	caa Gln	aag Lys	atg Met	atg Met	gtg Val	cgc Thr	acc Thr	1603
					490				495					500		
tat Tyr	tca Ser	cca Pro	tcc Ser	ctg Leu	aag Lys	gat Asp	tac Tyr	aac Asn	tct Ser	gat Asp	gaa Glu	ccc Pro	tca Ser	ctg Leu	ttg Leu	1651
					505				510				515			
ggg Gly	cct Pro	gca Ala	gac Glu	ccc Asp	aac Pro	atg Asn	tat Met	caa Gln	gaa Glu	ttc Phe	gaa Glu	gtg Val	tcc Ser	tac Tyr		1699
				520			525				530					
gag Glu	cag Gln	ctc Leu	ggc Gly	atc Ile	aaa Lys	cca Pro	gag Glu	ggc Gly	cgc Arg	acc Thr	ctg Leu	atc Ile	ggc Gly	gat Asp	tcc Ser	1747
					535		540				545					
ttc Phe	agc Ser	gcc Ala	gat Asp	ttc Phe	ttg Leu	acc Thr	tcc Ser	aat Asn	gaa Glu	att Ile	gga Gly	ata Ile	gtt Val	gat Asp	gag Glu	1795
					555					560					565	
gtt Val	cct Pro	tct Ser	gga Gly	acg Thr	atc Ile	gct Ala	ttc Phe	acg Thr	aac Asn	tgg Trp	aag Lys	gac Asp	gta Val	acc Thr	gaa Glu	1843
					570					575				580		
ggt Gly	cgc Arg	cac His	agt Ser	tgg Tyr	tat Tyr	gtt Val	cgc Arg	tcc Ser	gag Glu	gat Asp	cct Thr	ttc Phe	ggc Gly	ggc Gly	gtc Val	1891
				585				590					595			
gag Glu	att Ile	tca Ser	ccc Val	gtg Val	cag Gln	ttc Ser	ttc Phe	att Ala	gcc Gly	ggg Gly	gaa Glu	gag Glu	gct Val	ggc Gly	ggg Gly	1939

600	605	610	
aac gcg ccc ggc act gga agc tcc aat ggc ggt tca tcc cac gga tta			1987
Asn Ala Pro Gly Thr Gly	Ser Ser Asn Gly Gly	Ser Ser His Gly Leu	
615	620	625	
tgg ggt gcg ctt gcg gaa ttc ttt gcc gga gcg gca gcc ctg gct gga			2035
Trp Gly Ala Leu Ala Glu Phe Phe Ala Gly	Ala Ala Ala Leu Ala Gly		
630	635	640	645
gct gcg atc gca ttt gtc ccc gga att tgg gac tat gtg acc aac gca			2083
Ala Ala Ile Ala Phe Val Pro Gly Ile Trp	Asp Tyr Val Thr Asn Ala		
650	655	660	
ttc aag cga taattatgga taggtaaacg ctc			2115
Phe Lys Arg			

<210> 906

<211> 664

<212> PRT

<213> Corynebacterium glutamicum

<400> 906

Val Gln Leu Pro Leu Thr Thr Gly Ser Ile Ala Leu Asp Lys Gly Glu
1 5 10 15

His Thr Leu Val Ile Arg Ala Glu Asp Glu Val Gly Asn Arg Thr Glu
20 25 30

Lys Thr Ile Thr Phe Ser Thr Pro Asp Glu Asn Pro Ile Ser Gly Asp
35 40 45

Tyr Ala Pro Ser Asn Gly Ala Thr Val Gly Val Gly Asp Val Lys Leu
50 55 60

Ser Ala Arg Ala Ser Asp Pro Ser Gly Asp Thr Val Lys Met Thr Phe
65 70 75 80

Leu Glu Ala Asp Ser Pro Lys Leu Asp Ser Gly Arg Val Arg Met Ser
85 90 95

Ser Gly Thr Val Glu Asp Ala Gly Ser Val Ser Arg Ala Glu Ala Lys
100 105 110

Met Leu Glu Arg Gly Asp Val Glu Lys Leu Ser Ser Leu Asp Gly Leu
115 120 125

Gly Met Glu Val Thr Ser Asp Ala Ala Leu Pro Tyr Gln Leu Phe Glu
130 135 140

Val Asp Ala Ala Asp Ala Leu Ala Ala Asp Thr Glu Val Arg Leu Asn
145 150 155 160

Trp Ala Gly Ser Ala Asp Gly Arg Ala Gln Val Ile Met Tyr Val Phe
165 170 175

Asp Gly Glu Ala Trp Val Glu Val Asp Arg His Leu Thr Gly Asp Glu
180 185 190

Leu Glu Glu Phe Thr Leu Gln Gly Val Val Asn Ala Glu Lys Phe Ala
 195 200 205
 Ile Gly Gly Thr Val Thr Val Leu Ile Gln His Ser Glu Gly Phe Ala
 210 215 220
 Gly Ala Asp His Ser Thr Arg Asn Ser Asp Val Thr Ala Ala His Pro
 225 230 235 240
 Asp Asp Val Ala Arg Ser Glu Tyr Asp Phe Thr Leu Ala Trp Glu Ser
 245 250 255
 Asp Thr Gln Tyr Tyr Asn Glu Glu Phe His Glu His Gln Thr Asn Ile
 260 265 270
 His Asp Tyr Val Leu Ala Glu Arg Glu Asn Lys Asn Ile Gln Phe Met
 275 280 285
 Phe His Thr Gly Asp Val Val Asp Asp Trp Asp Gln Pro Ala Gln Trp
 290 295 300
 Ala Thr Ala Asn Pro Glu Tyr Gln Arg Leu Asp Asp Ala Gly Leu Pro
 305 310 315 320
 Tyr Ser Val Leu Ala Gly Asn His Asp Val Gly His Thr Ser Asn Asp
 325 330 335
 Tyr Thr Glu Phe Ser Arg His Phe Gly Glu Gln Arg Tyr Val Asp Asn
 340 345 350
 Pro Trp Tyr Gly Glu Ser Tyr Gln Asp Asn Arg Gly His Tyr Asp Leu
 355 360 365
 Phe Ser Ala Gly Gly Ile Asp Phe Ile Asn Val Ala Met Gly Trp Gly
 370 375 380
 Pro Asp Asp Glu Glu Ile Ala Trp Met Asn Glu Val Leu Ala Lys His
 385 390 395 400
 Pro Glu Arg Val Ala Ile Leu Asn Leu His Glu Phe Met Leu Thr Thr
 405 410 415
 Gly Gly Leu Gly Pro Ile Pro Gln Arg Ile Leu Asp Glu Val Ala Ala
 420 425 430
 Thr Asn Pro Asn Val Ser Met Ile Met Ser Gly His Tyr His Asp Ala
 435 440 445
 Phe Gln Arg Thr Asp Ser Phe Asp Asp Asp Gly Asp Gly Val Asp Asp
 450 455 460
 Arg Thr Val Thr Ser Met Leu Phe Asp Tyr Gln Gly Leu Pro Glu Gly
 465 470 475 480
 Gly Gln Gly Tyr Leu Arg Leu Leu His Phe Asp Asn Gln Gly Gln Lys
 485 490 495
 Met Met Val Arg Thr Tyr Ser Pro Ser Leu Lys Asp Tyr Asn Ser Asp
 500 505 510
 Glu Pro Ser Leu Leu Gly Pro Ala Glu Asp Pro Asn Met Tyr Gln Glu

515										520										525										
Phe	Glu	Val	Ser	Tyr	Glu	Gln	Leu	Gly	Ile	Lys	Pro	Glu	Gly	Arg	Thr															
					530						535						540													
Leu	Ile	Gly	Asp	Ser	Phe	Ser	Ala	Asp	Phe	Leu	Thr	Ser	Asn	Glu	Ile															
					545						550						555													
Gly	Ile	Val	Asp	Glu	Val	Pro	Ser	Gly	Thr	Ile	Ala	Phe	Thr	Asn	Trp															
					565						570						575													
Lys	Asp	Val	Thr	Glu	Gly	Arg	His	Ser	Trp	Tyr	Val	Arg	Ser	Glu	Asp															
					580						585						590													
Pro	Phe	Gly	Gly	Val	Glu	Ile	Ser	Pro	Val	Gln	Ser	Phe	Ile	Ala	Gly															
					595						600						605													
Glu	Glu	Ala	Gly	Gly	Asn	Ala	Pro	Gly	Thr	Gly	Ser	Ser	Asn	Gly	Gly															
					610						615						620													
Ser	Ser	His	Gly	Leu	Trp	Gly	Ala	Leu	Ala	Glu	Phe	Phe	Ala	Gly	Ala															
					625						630						635													
Ala	Ala	Leu	Ala	Gly	Ala	Ala	Ile	Ala	Phe	Val	Pro	Gly	Ile	Trp	Asp															
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Tyr	Val	Thr	Asn	Ala	Phe	Lys	Arg																							
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<210> 907																														
<211> 1342																														
<212> DNA																														
<213> Corynebacterium glutamicum																														
<220>																														
<221> CDS																														
<222> (101)..(1342)																														
<223> FRXA01945																														
<400> 907																														
agaagggacaa gaactgcgcg gcaccgtaga aattgatgcc caggcaaccg atgcgggtgc 60																														
gggcgtgaag agcgtcgaga cgctttctcga cggctaaccg																				gtg	caa	ctt	cca	cta						
																				Val	Gln	Leu	Pro	Leu						
																				1					5					
acc acc ggt tcc atc gct ttg gat aaa ggt gaa cac acc ttg gtt atc																														
Thr Thr Gly Ser Ile Ala Leu Asp Lys Gly Glu His Thr Leu Val Ile																														
					10						15						20													
cgt gca gaa gat gaa gta gga aac cgc acc gag aaa acc atc acg ttt																														
Arg Ala Glu Asp Glu Val Gly Asn Arg Thr Glu Lys Thr Ile Thr Phe																														
					25						30						35													
agc act ccg gat gaa aac ccc atc agt ggt gac tac gct cca agc aat																														
Ser Thr Pro Asp Glu Asn Pro Ile Ser Gly Asp Tyr Ala Pro Ser Asn																														
					40						45						50													
ggg gcc acc gtg ggc gtc ggt gad gtt aag tta tct gca cga gca agt																														
Gly Ala Thr Val Glv Val Glv Asp Val Lvs Leu Ser Ala Arg Ala Ser																														

55	60	65	
gat cca agt ggc gat act gtc aag atg acg ttc ctg gaa gcc gat tca Asp Pro Ser Gly Asp Thr Val Lys Met Thr Phe Leu Glu Ala Asp Ser	70	75	80
cca aaa tta gat agt ggt cgc gtc cga atg tca tca gga acg gta gaa Pro Lys Leu Asp Ser Gly Arg Val Arg Met Ser Ser Gly Thr Val Glu	90	95	100
gat gcc gga agt gtc tgc cgc gcc gag gcg aaa atg ttg gag agg gga Asp Ala Gly Ser Val Ser Arg Ala Glu Ala Lys Met Leu Glu Arg Gly	105	110	115
gac gtc gag aag cta tcc agc ctg gat ggc ctg ggc atg gaa gtt acc Asp Val Glu Lys Leu Ser Ser Leu Asp Gly Leu Gly Met Glu Val Thr	120	125	130
tcc gac gcc gca ctg ccg tac cag ctt ttt gaa gtc gat gcg gcg gat Ser Asp Ala Ala Leu Pro Tyr Gln Leu Phe Glu Val Asp Ala Ala Asp	135	140	145
gca ctc gcg gcc gac act gaa gtg cgc ctg aat tgg gcg gga tcc gcc Ala Leu Ala Ala Asp Thr Glu Val Arg Leu Asn Trp Ala Gly Ser Ala	150	155	160
gat ggt cgc gcg cag gtg atc atg tat gtt ttc gat gcc gag gcg tgg Asp Gly Arg Ala Gln Val Ile Met Tyr Val Phe Asp Gly Glu Ala Trp	170	175	180
gtt gag gtg gat cgt cac ttg acc gcc gat gag ctg gaa gag ttt acg Val Glu Val Asp Arg His Leu Thr Thr Gly Asp Glu Leu Glu Phe Thr	185	190	195
ctg cag gcc gtc gtc aat gcg gaa aaa ttt gca atc gcc gcc act gtc Leu Gln Gly Val Val Asn Ala Glu Lys Phe Ala Ile Gly Gly Thr Val	200	205	210
acc gta ttg att cag cac tcc gaa gcc ttc gcc ggt gcg gat cat tca Thr Val Leu Ile Gln His Ser Glu Gly Phe Ala Gly Ala Asp His Ser	215	220	225
act aga aat tcc gac gtg acc gca gcg cac ccg gat gat gtg gct cgc Thr Arg Asn Ser Asp Val Thr Ala Ala His Pro Asp Asp Val Ala Arg	230	235	240
tct gag tac gat ttc acc ctc gcg tgg gaa tct gac acc cag tac tac Ser Glu Tyr Asp Phe Thr Leu Ala Trp Glu Ser Asp Thr Gln Tyr Tyr	250	255	260
aac gag gaa ttc cac gag cac caa acc aac atc cat gac tac gtg ctc Asn Glu Glu Phe His Glu His Gln Thr Asn Ile His Asp Tyr Val Leu	265	270	275
gcc gaa cgg gag aac aag aat att cag ttc atg ttc cac act gcc gat Ala Glu Arg Glu Asn Lys Asn Ile Gln Phe Met Phe His Thr Gly Asp	280	285	290
gtt gtc gac gac tgg gat cag ccc gcg cag tgg gcc aca gcc aac ccc Val Val Asp Asp Trp Asp Gln Pro Ala Gln Trp Ala Thr Ala Asn Pro	295	300	305

355

403

451

499

547

595

643

691

739

787

835

883

931

979

1027

gaa tac cag cgc ctc gac gac gcc ggc ctg cca tat tct gtc ctt gcc 1075
 Glu Tyr Gln Arg Leu Asp Asp Ala Gly Leu Pro Tyr Ser Val Leu Ala
 310 315 320 325

gga aac cac gat gtt ggc cac acc agc aat gac tac acc gaa ttc agc 1123
 Gly Asn His Asp Val Gly His Thr Ser Asn Asp Tyr Thr Glu Phe Ser
 330 335 340

cga cac ttc ggc gaa cag cgc tac gta gac aac ccg tgg tac ggc gaa 1171
 Arg His Phe Gly Glu Gln Arg Tyr Val Asp Asn Pro Trp Tyr Gly Glu
 345 350 355

tcc tac caa gac aac cga ggg cac tac gat cta ttt tct gcc ggc gga 1219
 Ser Tyr Gln Asp Asn Arg Gly His Tyr Asp Leu Phe Ser Ala Gly Gly
 360 365 370

att gac ttc att aac gta gcg atg ggc tgg ggt cca gac gac gaa gaa 1267
 Ile Asp Phe Ile Asn Val Ala Met Gly Trp Gly Pro Asp Asp Glu Glu
 375 380 385

atc gcg tgg atg aac gag gtc ctg gcc aag cat ccc gag cgt gtg gcg 1315
 Ile Ala Trp Met Asn Glu Val Leu Ala Lys His Pro Glu Arg Val Ala
 390 395 400 405

atc ctc aac ctc cac gaa ttc atg ctc 1342
 Ile Leu Asn Leu His Glu Phe Met Leu
 410

<210> 908
 <211> 414
 <212> FRT
 <213> Corynebacterium glutamicum

<400> 908
 Val Gln Leu Pro Leu Thr Thr Gly Ser Ile Ala Leu Asp Lys Gly Glu
 1 5 10 15
 His Thr Leu Val Ile Arg Ala Glu Asp Glu Val Gly Asn Arg Thr Glu
 20 25 30
 Lys Thr Ile Thr Phe Ser Thr Pro Asp Glu Asn Pro Ile Ser Gly Asp
 35 40 45
 Tyr Ala Pro Ser Asn Gly Ala Thr Val Gly Val Gly Asp Val Lys Leu
 50 55 60
 Ser Ala Arg Ala Ser Asp Pro Ser Gly Asp Thr Val Lys Met Thr Phe
 65 70 75 80
 Leu Glu Ala Asp Ser Pro Lys Leu Asp Ser Gly Arg Val Arg Met Ser
 85 90 95
 Ser Gly Thr Val Glu Asp Ala Gly Ser Val Ser Arg Ala Glu Ala Lys
 100 105 110
 Met Leu Glu Arg Gly Asp Val Glu Lys Leu Ser Ser Leu Asp Gly Leu
 115 120 125
 Gly Met Glu Val Thr Ser Asp Ala Ala Leu Pro Tyr Gln Leu Phe Glu

130	135	140
Val Asp Ala Ala Asp	Ala Leu Ala Ala Asp	Thr Glu Val Arg Leu Asn
145	150	155
Trp Ala Gly Ser Ala Asp	Gly Arg Ala Gln Val Ile Met Tyr Val Phe	
	165	170
Asp Gly Glu Ala Trp Val Glu Val Asp Arg His Leu Thr Gly Asp Glu		
	180	185
Leu Glu Glu Phe Thr Leu Gln Gly Val Val Asn Ala Glu Lys Phe Ala		
	195	200
Ile Gly Gly Thr Val Thr Val Leu Ile Gln His Ser Glu Gly Phe Ala		
	210	215
Gly Ala Asp His Ser Thr Arg Asn Ser Asp Val Thr Ala Ala His Pro		
225	230	235
Asp Asp Val Ala Arg Ser Glu Tyr Asp Phe Thr Leu Ala Trp Glu Ser		
	245	250
Asp Thr Gln Tyr Tyr Asn Glu Glu Phe His Glu His Gln Thr Asn Ile		
	260	265
His Asp Tyr Val Leu Ala Glu Arg Glu Asn Lys Asn Ile Gln Phe Met		
	275	280
Phe His Thr Gly Asp Val Val Asp Asp Trp Asp Gln Pro Ala Gln Trp		
	290	295
Ala Thr Ala Asn Pro Glu Tyr Gln Arg Leu Asp Asp Ala Gly Leu Pro		
305	310	315
Tyr Ser Val Leu Ala Gly Asn His Asp Val Gly His Thr Ser Asn Asp		
	325	330
Tyr Thr Glu Phe Ser Arg His Phe Gly Glu Gln Arg Tyr Val Asp Asn		
	340	345
Pro Trp Tyr Gly Glu Ser Tyr Gln Asp Asn Arg Gly His Tyr Asp Leu		
	355	360
Phe Ser Ala Gly Gly Ile Asp Phe Ile Asn Val Ala Met Gly Trp Gly		
	370	375
Pro Asp Asp Glu Glu Ile Ala Trp Met Asn Glu Val Leu Ala Lys His		
385	390	395
Pro Glu Arg Val Ala Ile Leu Asn Leu His Glu Phe Met Leu		
	405	410

<210> 909

<211> 518

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(495)

<223> FRXA01627

<400> 909

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 Arg Thr Tyr Ser Pro Ser Leu Lys Asp Tyr Asn Ser Asp Glu Pro Ser
 1 5 10 15

ctg ttg ggg cct gca gaa gac ccc aac atg tat caa gaa ttc gaa gtg 96
 Leu Leu Gly Pro Ala Glu Asp Pro Asn Met Tyr Gln Glu Phe Glu Val
 20 25 30

tcc tac gag cag ctg ggc atc aaa cca gag ggc cgc acc ctg atc ggc 144
 Ser Tyr Glu Gln Leu Gly Ile Lys Pro Glu Gly Arg Thr Leu Ile Gly
 35 40 45

gat tcc ttc agc gcc gat ttc ttg acc tcc aat gaa att gga ata gtt 192
 Asp Ser Phe Ser Ala Asp Phe Leu Thr Ser Asn Glu Ile Gly Ile Val
 50 55 60

gat gag gtt cct tct gga acg atc gct ttc acg aac tgg aag gac gta 240
 Asp Glu Val Pro Ser Gly Thr Ile Ala Phe Thr Asn Trp Lys Asp Val
 65 70 75 80

acc gaa ggt cgc cac agt tgg tat gtt cgc tcc gag gat cct ttc ggc 288
 Thr Glu Gly Arg His Ser Trp Tyr Val Arg Ser Glu Asp Pro Phe Gly
 85 90 95

ggc gtc gag att tca ccc gtg cag tcc ttc att gcc ggg gaa gag gct 336
 Gly Val Glu Ile Ser Pro Val Gln Ser Phe Ile Ala Gly Glu Glu Ala
 100 105 110

ggc ggg aac gcg ccc ggc act gga agc tcc aat ggc ggt tca tcc cac 384
 Gly Gly Asn Ala Pro Gly Thr Gly Ser Ser Asn Gly Gly Ser Ser His
 115 120 125

gga tta tgg ggt gcg ctt gcg gaa ttc ttt gcc gga gcg gca gcc ctg 432
 Gly Leu Trp Gly Ala Leu Ala Glu Phe Phe Ala Gly Ala Ala Ala Leu
 130 135 140

gct gga gct gcg atc gca ttt gtc ccc gga att tgg gac tat gtg acc 480
 Ala Gly Ala Ala Ile Ala Phe Val Pro Gly Ile Trp Asp Tyr Val Thr
 145 150 155 160

aac gca ttc aag cga taattatgga taggtaaacg ctc 518
 Asn Ala Phe Lys Arg
 165

<210> 910

<211> 165

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 910

Arg Thr Tyr Ser Pro Ser Leu Lys Asp Tyr Asn Ser Asp Glu Pro Ser
 1 5 10 15

Leu Leu Gly Pro Ala Glu Asp Pro Asn Met Tyr Gln Glu Phe Glu Val
 20 25 30

[illegible][illegible][illegible]

ggt ggt cac ggg ctc acc gag att gcc aac acc cag cta gtg cct gtg 355
 Gly Gly His Gly Leu Thr Glu Ile Ala Asn Thr Gln Leu Val Pro Val
 70 75 80 85

ctt gag cta cca aag ttc aat cct ttt gag gca ctt gct atc cac ctt 403
 Leu Glu Leu Pro Lys Phe Asn Pro Phe Glu Ala Leu Ala Ile His Leu
 90 95 100

gaa gcc gcc aac aac taagaaagca tccttcacga ctg 441
 Glu Ala Ala Asn Asn
 105

<210> 912

<211> 106

<212> PRT

<213> Corynebacterium glutamicum

<400> 912

Met Pro Gln His Phe Ser Gln Glu Asn Tyr Arg Lys Ala Pro Val Ile
 1 5 10 15

Met Ser Ala Pro Leu Thr Ile His Asp Leu Leu Ser Thr Asn Ser Lys
 20 25 30

Leu Asn Leu Lys Trp Leu Thr Cys Thr Val Leu Asn Ser Pro Asn Leu
 35 40 45

Thr Glu Pro Cys Ile Thr Val Ser Val Asn His Thr Glu Gly Met Ser
 50 55 60

Leu Val Ser Phe Glu Gly Gly His Gly Leu Thr Glu Ile Ala Asn Thr
 65 70 75 80

Gln Leu Val Pro Val Leu Glu Leu Pro Lys Phe Asn Pro Phe Glu Ala
 85 90 95

Leu Ala Ile His Leu Glu Ala Ala Asn Asn
 100 105

<210> 913

<211> 441

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(418)

<223> FRXA01960

<400> 913
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caacacccca tgaggcatct gcttcacatggg gtgtttttgct atg ccg caa cac ttt 115
 Met Pro Gln His Phe
 1 5

tct caa gaa aac tac aga aag gcc ccc gtc att atg tct gca ccg ctc 163
 Ser Gln Glu Asn Tyr Arg Lys Ala Pro Val Ile Met Ser Ala Pro Leu
 10 15 20

acc att cat gat ctg ctg tcc acc aat tgc aag ctt aac ctc aag tgg 211
 Thr Ile His Asp Leu Leu Ser Thr Asn Ser Lys Leu Asn Leu Lys Trp
 25 30 35

ctg acc tgc act gtc ttg aac agc cca aat ctc ccc gaa ccc tgc atc 259
 Leu Thr Cys Thr Val Leu Asn Ser Pro Asn Leu Pro Glu Pro Cys Ile
 40 45 50

acg gtt tct gtg aac cac acc gaa ggc atg tcc ctg gtc tct ttc gaa 307
 Thr Val Ser Val Asn His Thr Glu Gly Met Ser Leu Val Ser Phe Glu
 55 60 65

ggg ggt cac ggg ctc acc gag att gcc aac acc cag cta gtg cct gtg 355
 Gly Gly His Gly Leu Thr Glu Ile Ala Asn Thr Gln Leu Val Pro Val
 70 75 80 85

ctt gag cta cca aag ttc aat cct ttt gag gca ctt gct atc cac ctt 403
 Leu Glu Leu Pro Lys Phe Asn Pro Phe Glu Ala Leu Ala Ile His Leu
 90 95 100

gaa gcc gcc aac aac taagaaagca tccttcacga ctg 441
 Glu Ala Ala Asn Asn
 105

<210> 914

<211> 106

<212> PRT

<213> Corynebacterium glutamicum

<400> 914

Met Pro Gln His Phe Ser Gln Glu Asn Tyr Arg Lys Ala Pro Val Ile
 1 5 10 15

Met Ser Ala Pro Leu Thr Ile His Asp Leu Leu Ser Thr Asn Ser Lys
 20 25 30

Leu Asn Leu Lys Trp Leu Thr Cys Thr Val Leu Asn Ser Pro Asn Leu
 35 40 45

Pro Glu Pro Cys Ile Thr Val Ser Val Asn His Thr Glu Gly Met Ser
 50 55 60

Leu Val Ser Phe Glu Gly Gly His Gly Leu Thr Glu Ile Ala Asn Thr
 65 70 75 80

Gln Leu Val Pro Val Leu Glu Leu Pro Lys Phe Asn Pro Phe Glu Ala
 85 90 95

Leu Ala Ile His Leu Glu Ala Ala Asn Asn
 100 105

<210> 915

<211> 1173

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1150)

<223> RXN01985

<400> 915

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gttattccgt tgtgtttcga gaaagagaga gaaacttttc atg cgt acg tct cgc 115
Met Arg Thr Ser Arg
1 5

gtt cta gcc ggc att ctt gcc gca acc ctc aag gtg tcc ctc gcg gcc 163
Val Leu Ala Gly Ile Leu Ala Ala Thr Leu Thr Val Ser Leu Ala Ala
10 15 20

tgc tcc cag gat tct tca gaa acg tcc tcc aat tcg tct tca gca gca 211
Cys Ser Gln Asp Ser Ser Glu Thr Ser Ser Asn Ser Ser Ser Ala Ala
25 30 35

tcc caa agc tct gac gtt tcc aac gag gcg ttc cct gtc acc att gag 259
Ser Gln Ser Ser Asp Val Ser Asn Glu Ala Phe Pro Val Thr Ile Glu
40 45 50

cac gct ttc ggc gag acc acc att gag tcc aag cca gaa cgc atc gca 307
His Ala Phe Gly Glu Thr Thr Ile Glu Ser Lys Pro Glu Arg Ile Ala
55 60 65

act gtt ggc tgg tcc aac cat gaa gtc cct ctc gca ttg ggt gtg act 355
Thr Val Gly Trp Ser Asn His Glu Val Pro Leu Ala Leu Gly Val Thr
70 75 80 85

cct gtc ggc ttt gag aag gtc acg tgg ggc gac gat gac aac aac ggc 403
Pro Val Gly Phe Glu Lys Val Thr Trp Gly Asp Asp Asp Asn Asn Gly
90 95 100

atc ttg cca tgg gtg gaa gaa acc ttg agc aag ctc ggc tcc gat gag 451
Ile Leu Pro Trp Val Glu Glu Thr Leu Ser Lys Leu Gly Ser Asp Glu
105 110 115

cct gtg ctt ttc gat gcc acc gat tcc att cct ttt gag gag atc gcc 499
Pro Val Leu Phe Asp Ala Thr Asp Ser Ile Pro Phe Glu Glu Ile Ala
120 125 130

aac act gct ccg gat gtc att ttg gcg tcc tac tct ggc atc acc cag 547
Asn Thr Ala Pro Asp Val Ile Leu Ala Ser Tyr Ser Gly Ile Thr Gln
135 140 145

gaa gac tac gat cag ctg tcc cag atc gca cct gtg gtt gcc tac cca 595
Glu Asp Tyr Asp Gln Leu Ser Gln Ile Ala Pro Val Val Ala Tyr Pro
150 155 160 165

gaa atc gca tgg ggc acc tcc ctg gat gaa atg att gag atg aac tot 643
Glu Ile Ala Trp Gly Thr Ser Leu Asp Glu Met Ile Glu Met Asn Ser
170 175 180

aag gcg att ggc ttg gag caa gaa ggc aag gat ctc atc gca gat ctg 691
Lys Ala Ile Gly Leu Glu Gln Glu Gly Lys Asp Leu Ile Ala Asp Leu
185 190 195

gat gca gag gtt gct tcc gcc atc gat gcc aac cca gag ttg aag gat 739
Asp Ala Glu Val Ala Ser Ala Ile Asp Ala Asn Pro Glu Leu Lys Asp
200 205 210

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gcg aag cct gta ttc gcg ttc ttc gat gag agc gat ttc tcg cag att 787
Ala Lys Pro Val Phe Ala Phe Phe Asp Glu Ser Asp Phe Ser Gln Ile
215 220 225

ggc gtg tac acc agc att gat cct cgc atg agc ttc ttg ctt gat gcg 835
Gly Val Tyr Thr Ser Ile Asp Pro Arg Met Ser Phe Leu Leu Asp Ala
230 235 240 245

ggc gtc cag gaa gct tca gtc ctc aag gag cac tcc agc cca gat agc 883
Gly Val Gln Glu Ala Ser Val Leu Lys Glu His Ser Ser Pro Asp Ser
250 255 260

ttc tac gag cag gtt tct gca gaa aac cct gaa acc ttc gac gat gtt 931
Phe Tyr Glu Gln Val Ser Ala Glu Asn Pro Glu Thr Phe Asp Asp Val
265 270 275

gat gtg atc atc acc tac gcc acc gaa gat gat gct gca aac gct gag 979
Asp Val Ile Ile Thr Tyr Gly Thr Glu Asp Asp Ala Ala Asn Ala Glu
280 285 290

ctg ttg tcc aag atg cag gct gat cca ctg ctg tct cga atc cca gct 1027
Leu Leu Ser Lys Met Gln Ala Asp Pro Leu Leu Ser Arg Ile Pro Ala
295 300 305

atc gcc gag gcc aag gtt gtg ttc ttg ggt gct aac cca ctg gct gct 1075
Ile Ala Glu Gly Lys Val Val Phe Leu Gly Ala Asn Pro Leu Ala Ala
310 315 320 325

tca gcg aat gaa tcc cca cta tct att cct tgg ggt atc aac gat tac 1123
Ser Ala Asn Glu Ser Pro Leu Ser Ile Pro Trp Gly Ile Asn Asp Tyr
330 335 340

ttt gca aaa ctc gcc gaa cct ctg aag taaaactgct tgatgtcaac 1170
Phe Ala Lys Leu Ala Glu Pro Leu Lys
345 350

aac 1173

<210> 916
<211> 350
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 916
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Val Ser Leu Ala Ala Cys Ser Gln Asp Ser Ser Glu Thr Ser Ser Asn
20 25 30
Ser Ser Ser Ala Ala Ser Gln Ser Ser Asp Val Ser Asn Glu Ala Phe
35 40 45
Pro Val Thr Ile Glu His Ala Phe Gly Glu Thr Thr Ile Glu Ser Lys
50 55 60
Pro Glu Arg Ile Ala Thr Val Gly Trp Ser Asn His Glu Val Pro Leu
65 70 75 80

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Ala Leu Gly Val Thr Pro Val Gly Phe Glu Lys Val Thr Trp Gly Asp
      85                      90                      95
Asp Asp Asn Asn Gly Ile Leu Pro Trp Val Glu Glu Thr Leu Ser Lys
      100                    105                    110
Leu Gly Ser Asp Glu Pro Val Leu Phe Asp Ala Thr Asp Ser Ile Pro
      115                    120                    125
Phe Glu Glu Ile Ala Asn Thr Ala Pro Asp Val Ile Leu Ala Ser Tyr
      130                    135                    140
Ser Gly Ile Thr Gln Glu Asp Tyr Asp Gln Leu Ser Gln Ile Ala Pro
      145                    150                    155                    160
Val Val Ala Tyr Pro Glu Ile Ala Trp Gly Thr Ser Leu Asp Glu Met
      165                    170                    175
Ile Glu Met Asn Ser Lys Ala Ile Gly Leu Glu Gln Glu Gly Lys Asp
      180                    185                    190
Leu Ile Ala Asp Leu Asp Ala Glu Val Ala Ser Ala Ile Asp Ala Asn
      195                    200                    205
Pro Glu Leu Lys Asp Ala Lys Pro Val Phe Ala Phe Phe Asp Glu Ser
      210                    215                    220
Asp Phe Ser Gln Ile Gly Val Tyr Thr Ser Ile Asp Pro Arg Met Ser
      225                    230                    235                    240
Phe Leu Leu Asp Ala Gly Val Gln Glu Ala Ser Val Leu Lys Glu His
      245                    250                    255
Ser Ser Pro Asp Ser Phe Tyr Glu Gln Val Ser Ala Glu Asn Pro Glu
      260                    265                    270
Thr Phe Asp Asp Val Asp Val Ile Ile Thr Tyr Gly Thr Glu Asp Asp
      275                    280                    285
Ala Ala Asn Ala Glu Leu Leu Ser Lys Met Gln Ala Asp Pro Leu Leu
      290                    295                    300
Ser Arg Ile Pro Ala Ile Ala Glu Gly Lys Val Val Phe Leu Gly Ala
      305                    310                    315                    320
Asn Pro Leu Ala Ala Ser Ala Asn Glu Ser Pro Leu Ser Ile Pro Trp
      325                    330                    335
Gly Ile Asn Asp Tyr Phe Ala Lys Leu Ala Glu Pro Leu Lys
      340                    345                    350

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<210> 917

<211> 336

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(313)

<223> RXN01987

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gaaagaaaaa ctcaatcagc cataaaggag cttgatcccg atg act ttc cca gca 115
                                         Met Thr Phe Pro Ala
                                         1                               5

caa tct cga cga ctc gcc cga agc acc acc gac aaa tgg atc ggc ggc 163
Gln Ser Arg Arg      Leu Ala Arg Ser Thr Asp Lys Trp Ile Gly Gly
                        10                               15                20

gtc gct ggt ggc ctc gca gag acc tac ggt tgg aat ccg gcc tat gtg 211
Val Ala Gly Gly Leu Ala Glu Thr Tyr Gly Trp Asn Pro Ala Tyr Val
                        25                               30                35

cgt ctc gcg ttc gtg gcg tcg gtt ctg ttt cca ctg cca ggt tca cag 259
Arg Leu Ala Phe Val Ala Ser Val Leu Phe Pro Leu Pro Gly Ser Gln
                        40                               45                50

atc ctg ttc tac gcc cta gcg tgg ctg atc atc cca tcc cga gaa aat 307
Ile Leu Phe Tyr Ala Leu Ala Trp Leu Ile Ile Pro Ser Arg Glu Asn
                        55                               60                65

cgc ttc taacgtgcgt tgcataacgc aga 336
Arg Phe
70

<210> 918
<211> 71
<212> PRT
<213> Corynebacterium glutamicum

<400> 918
Met Thr Phe Pro Ala Gln Ser Arg Arg Leu Ala Arg Ser Thr Thr Asp
  1          5          10          15
Lys Trp Ile Gly Gly Val Ala Gly Gly Leu Ala Glu Thr Tyr Gly Trp
      20          25          30
Asn Pro Ala Tyr Val Arg Leu Ala Phe Val Ala Ser Val Leu Phe Pro
      35          40          45
Leu Pro Gly Ser Gln Ile Leu Phe Tyr Ala Leu Ala Trp Leu Ile Ile
      50          55          60
Pro Ser Arg Glu Asn Arg Phe
65          70

<210> 919
<211> 336
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(313)
<223> FRXA01987

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gaaagaaaaa ctcaatcagc cataaaggag ctgatacccg atg act ttc cca gca 115
                                   Met Thr Phe Pro Ala
                                   1           5

caa tct cga cga ctc gcc cga agc acc acc gac aaa tgg atc ggc ggc 163
Gln Ser Arg Arg Leu Ala Arg Ser Thr Thr Asp Lys Trp Ile Gly Gly
                10                15                20

gtc gct ggt ggc ctc gca gag acc tac ggt tgg aat ccg gcc tat gtg 211
Val Ala Gly Gly Leu Ala Glu Thr Tyr Gly Trp Asn Pro Ala Tyr Val
                25                30                35

cgt ctc gcg ttc gtg gcg tcg gtt ctg ttt cca ctg cca ggt tca cag 259
Arg Leu Ala Phe Val Ala Ser Val Leu Phe Pro Leu Pro Gly Ser Gln
                40                45                50

atc ctg ttc tac gcc cta gcg tgg ctg atc atc cca tcc cga gaa aat 307
Ile Leu Phe Tyr Ala Leu Ala Trp Leu Ile Ile Ile Ser Arg Glu Asn
                55                60                65

cgc ttc taacgtgcgt tgacataacgc aga 336
Arg Phe
70

<210> 920
<211> 71
<212> PRT
<213> Corynebacterium glutamicum

<400> 920
Met Thr Phe Pro Ala Gln Ser Arg Arg Leu Ala Arg Ser Thr Thr Asp
1           5           10           15

Lys Trp Ile Gly Gly Val Ala Gly Gly Leu Ala Glu Thr Tyr Gly Trp
20           25           30

Asn Pro Ala Tyr Val Arg Leu Ala Phe Val Ala Ser Val Leu Phe Pro
35           40           45

Leu Pro Gly Ser Gln Ile Leu Phe Tyr Ala Leu Ala Trp Leu Ile Ile
50           55           60

Pro Ser Arg Glu Asn Arg Phe
65           70

<210> 921
<211> 549
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(526)
<223> RXN01988

<400> 921

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65	70	75	80	
Leu Thr Leu Ser	Val Val Ala Leu Gly Asn Glu Glu Val Asp Ala Leu			
	85	90	95	
Gly His Ser Glu Gly Gln Ala Val His Ser Leu Leu Glu Ile His Thr				
100	105	110		
Pro Lys Arg Ser Trp Pro Leu Ser Glu Leu Tyr Ile Asp Asp Asn Glu				
115	120	125		
Gly Leu Ala Gln Val Ser Arg Cys Phe Ala Arg Leu Val Gly				
130	135	140		

<210> 923

<211> 341

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(318)

<223> FRXA01988

<400> 923

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1	5 10 15

gtt gcc gag ctt tat gct gac gcc cgc gag cac ctc gac aat ggt gca	96
Val Ala Glu Leu Tyr Ala Asp Ala Arg Glu His Leu Asp Asn Gly Ala	
	20 25 30

acc cag gtg atg atc ccc gtc att tca cct tcc aac ctg acc ttg tca	144
Thr Gln Val Met Ile Pro Val Ile Ser Pro Ser Asn Leu Thr Leu Ser	
	35 40 45

gta gtt gcc ctg gcc aat caa gag gtt gac gca ctg gcc cat tcc gaa	192
Val Val Ala Leu Gly Asn Gln Glu Val Asp Ala Leu Gly His Ser Glu	
	50 55 60

gga caa gca gtt cac tcc ctt ctg gaa att cat acc cgg aag cgc agc	240
Gly Gln Ala Val His Ser Leu Leu Glu Ile His Thr Pro Lys Arg Ser	
	65 70 75 80

tgg cct ctt tcc gag ctt tat att gat gac aat gag ggt ttg gct cag	288
Trp Pro Leu Ser Glu Leu Tyr Ile Asp Asp Asn Glu Gly Leu Ala Gln	
	85 90 95

gtg tog cgc tgc ttc gcc cgc ctt gtt ggc tagtcccacc ccaccaattg	338
Val Ser Arg Cys Phe Ala Arg Leu Val Gly	
	100 105

cat

341

<210> 924

<211> 106

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 924

Met Ile Asp Pro Leu Thr Pro Val Val Pro Ile Thr Thr Gly Thr Ser
 1 5 10 15

Val Ala Glu Leu Tyr Ala Asp Ala Arg Glu His Leu Asp Asn Gly Ala
 20 25 30

Thr Gln Val Met Ile Pro Val Ile Ser Pro Ser Asn Leu Thr Leu Ser
 35 40 45

Val Val Ala Leu Gly Asn Gln Glu Val Asp Ala Leu Gly His Ser Glu
 50 55 60

Gly Gln Ala Val His Ser Leu Leu Glu Ile His Thr Pro Lys Arg Ser
 65 70 75 80

Trp Pro Leu Ser Glu Leu Tyr Ile Asp Asp Asn Glu Gly Leu Ala Gln
 85 90 95

Val Ser Arg Cys Phe Ala Arg Leu Val Gly
 100 105

<210> 925

<211> 996

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> {101}..{973}

<223> RXN01991

<400> 925

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tcgacgagga tcagctattc ttacaaaaat tcatttgaat atg acg aat ttg ttg 115
 Met Thr Asn Leu Leu
 1 5

cgg cat ttc ccg agt acc gac gta gct gcg tgg gaa cca acc gtt gtg 163
 Pro His Phe Pro Ser Thr Asp Val Ala Ala Trp Glu Pro Thr Val Val
 10 15 20

tat tca gcg gat aag acc aca gca aca gcg acg ttt aag aat att cct 211
 Tyr Ser Ala Asp Lys Thr Thr Ala Thr Ala Thr Phe Lys Asn Ile Pro
 25 30 35

tgc gat att tcc ttt agt tgg act ggt att gaa gca cta gag cca ttt 259
 Ser Asp Ile Ser Phe Ser Trp Thr Gly Ile Glu Ala Leu Glu Pro Phe
 40 45 50

agc cct ggt aaa acc ttc gaa cat aag gtg caa ggt tct gtt ggt gaa 307
 Ser Pro Gly Lys Thr Phe Glu His Lys Val Gln Gly Ser Val Gly Glu
 55 60 65

cca gcg ggg gcg ttc act agg gat aac tat ttc act gag ggt gag ctc 355

Pro Ala Gly Ala Phe Thr Arg Asp Asn Tyr Phe Thr Glu Gly Glu Leu
70 75 80 85

tac aaa cat cgc cac gca gac gat ctg ctt tcc ggt gat ggc ttg ttt 403
Tyr Lys His Arg His Ala Asp Asp Leu Leu Ser Gly Asp Gly Leu Phe
90 95 100

ggc ccc aac atc acc gat ggc gat ggc aac ctc ccc tct gtt gat gac 451
Gly Pro Asn Ile Thr Asp Gly Asp Gly Asn Leu Pro Ser Val Asp Asp
105 110 115

ggc aag gac ggt gac gat ggg tct gat ggc tca gac ggc cga gac ggt 499
Gly Lys Asp Gly Asp Asp Gly Ser Asp Gly Ser Asp Gly Arg Asp Gly
120 125 130

gtt gtc gcc att gat gtt gtt gac aat gct gac ggc acg gtg act gtc 547
Val Val Ala Ile Asp Val Val Asp Asn Ala Asp Gly Thr Val Thr Val
135 140 145

acc ttg tcc gat ggc act acg ttt act ctt gat gct ggt caa gac ggc 595
Thr Leu Ser Asp Gly Thr Thr Phe Thr Leu Asp Ala Gly Gln Asp Gly
150 155 160 165

aaa gat ggt ctt gac ggg ctt gat ggt act ggc cta acg ctg gaa tct 643
Lys Asp Gly Leu Asp Gly Leu Asp Gly Thr Gly Leu Thr Leu Glu Ser
170 175 180

gct acc cct gat gag gac ggc aac atc acc tat gtt ctt tct gac ggt 691
Ala Thr Pro Asp Glu Asp Gly Asn Ile Thr Tyr Val Leu Ser Asp Gly
185 190 195

act gag ttc act gtg cgc aac ggt gtt gat ggg tca gac ggt aag gac 739
Thr Glu Phe Thr Val Arg Asn Gly Val Asp Gly Ser Asp Gly Lys Asp
200 205 210

ggc aaa gat gga gtc aat ggc aca gat ggc gta gac ggg tca gac ggt 787
Gly Lys Asp Gly Val Asn Gly Thr Asp Gly Val Asp Gly Ser Asp Gly
215 220 225

aaa ggt ctg gta gag gtg tcc cga gtt acc aac gac aac ggc tca gtg 835
Lys Gly Leu Val Glu Val Ser Arg Val Thr Asn Asp Asn Gly Ser Val
230 235 240 245

acc att acc tac gag gac ggt tca cag atc acc acg aag cca acg ccg 883
Thr Ile Thr Tyr Glu Asp Gly Ser Gln Ile Thr Thr Lys Pro Thr Pro
250 255 260

aca aac tgg ctg tcc aag ctg ctt gat ttg ctt ctc ccg ctg ttt aat 931
Thr Asn Trp Leu Ser Lys Leu Leu Asp Leu Leu Pro Leu Phe Asn
265 270 275

ctg ttc ggt ctt ggt ggc ggc tcc gtc att agt tcc agt aag 973
Leu Phe Gly Leu Gly Gly Ser Val Ile Ser Ser Ser Lys
280 285 290

tagttttttt actccctgtt ttg 996

<210> 926
<211> 291
<212> PRT

<213> *Corynebacterium glutamicum*

<400> 926

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Met Thr Asn Leu Leu Pro His Phe Pro Ser Thr Asp Val Ala Ala Trp
 1          5          10          15

Glu Pro Thr Val Val Tyr Ser Ala Asp Lys Thr Thr Ala Thr Ala Thr
 20          25          30

Phe Lys Asn Ile Pro Ser Asp Ile Ser Phe Ser Trp Thr Gly Ile Glu
 35          40          45

Ala Leu Glu Pro Phe Ser Pro Gly Lys Thr Phe Glu His Lys Val Gln
 50          55          60

Gly Ser Val Gly Glu Pro Ala Gly Ala Phe Thr Arg Asp Asn Tyr Phe
 65          70          75          80

Thr Glu Gly Glu Leu Tyr Lys His Arg His Ala Asp Asp Leu Leu Ser
 85          90          95

Gly Asp Gly Leu Phe Gly Pro Asn Ile Thr Asp Gly Asp Gly Asn Leu
100          105          110

Pro Ser Val Asp Asp Gly Lys Asp Gly Asp Asp Gly Ser Asp Gly Ser
115          120          125

Asp Gly Arg Asp Gly Val Val Ala Ile Asp Val Val Asp Asn Ala Asp
130          135          140

Gly Thr Val Thr Val Thr Leu Ser Asp Gly Thr Thr Phe Thr Leu Asp
145          150          155          160

Ala Gly Gln Asp Gly Lys Asp Gly Leu Asp Gly Leu Asp Gly Thr Gly
165          170          175

Leu Thr Leu Glu Ser Ala Thr Pro Asp Glu Asp Gly Asn Ile Thr Tyr
180          185          190

Val Leu Ser Asp Gly Thr Glu Phe Thr Val Arg Asn Gly Val Asp Gly
195          200          205

Ser Asp Gly Lys Asp Gly Lys Asp Gly Val Asn Gly Thr Asp Gly Val
210          215          220

Asp Gly Ser Asp Gly Lys Gly Leu Val Glu Val Ser Arg Val Thr Asn
225          230          235          240

Asp Asn Gly Ser Val Thr Ile Thr Tyr Glu Asp Gly Ser Gln Ile Thr
245          250          255

Thr Lys Pro Thr Pro Thr Asn Trp Leu Ser Lys Leu Leu Asp Leu Leu
260          265          270

Leu Pro Leu Phe Asn Leu Phe Gly Leu Gly Gly Gly Ser Val Ile Ser
275          280          285

Ser Ser Lys
290

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aaa gat ggt ctt gac ggg ctt gat ggt act ggc cta acg ctg gaa tct 643
Lys Asp Gly Leu Asp Gly Leu Asp Gly Thr Gly Leu Thr Leu Glu Ser
170 175 180

gct acc cct gat gag gac ggc aac atc acc tat gtt ctt tct gac ggt 691
 Ala Thr Pro Asp Glu Asp Gly Asn Ile Thr Tyr Val Leu Ser Asp Gly
 185 190 195

act gag ttc act gtg cgc aac ggt gtt gat ggg tca gac ggt aag gac 739
 Thr Glu Phe Thr Val Arg Asn Gly Val Asp Gly Ser Asp Gly Lys Asp
 200 205 210

ggc aaa gat gga gtc aat ggc aca gat ggc gta gac ggg tca gac ggt 787
 Gly Lys Asp Gly Val Asn Gly Thr Asp Gly Val Asp Gly Ser Asp Gly
 215 220 225

aaa ggt ctg gta gag gtg tcc cga gtt acc aac gac aac ggc tca gtg 835
 Lys Gly Leu Val Glu Val Ser Arg Val Thr Asn Asp Asn Gly Ser Val
 230 235 240 245

acc att acc tac gag gac ggt tca cag atc acc acg aag cca acg ccg 883
 Thr Ile Thr Tyr Glu Asp Gly Ser Gln Ile Thr Thr Lys Pro Thr Pro
 250 255 260

aca aac tgg ctg 895
 Thr Asn Trp Leu
 265

<210> 928
 <211> 265
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 928
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Glu Pro Thr Val Val Tyr Ser Ala Asp Lys Thr Thr Ala Thr Ala Thr
 20 25 30

Phe Lys Asn Ile Pro Ser Asp Ile Ser Phe Ser Trp Thr Gly Ile Glu
 35 40 45

Ala Leu Glu Pro Phe Ser Pro Gly Lys Thr Phe Glu His Lys Val Gln
 50 55 60

Gly Ser Val Gly Glu Pro Ala Gly Ala Phe Thr Arg Asp Asn Tyr Phe
 65 70 75 80

Thr Glu Gly Glu Leu Tyr Lys His Arg His Ala Asp Asp Leu Leu Ser
 85 90 95

Gly Asp Gly Leu Phe Gly Pro Asn Ile Thr Asp Gly Asp Gly Asn Leu
 100 105 110

Pro Ser Val Asp Asp Gly Lys Asp Gly Asp Asp Gly Ser Asp Gly Ser
 115 120 125

Asp Gly Arg Asp Gly Val Val Ala Ile Asp Val Val Asp Asn Ala Asp
 130 135 140

Gly Thr Val Thr Val Thr Leu Ser Asp Gly Thr Thr Phe Thr Leu Asp
 145 150 155 160

Ala Gly Gln Asp Gly Lys Asp Gly Leu Asp Gly Leu Asp Gly Thr Gly
 165 170 175

Leu Thr Leu Glu Ser Ala Thr Pro Asp Glu Asp Gly Asn Ile Thr Tyr
 180 185 190

Val Leu Ser Asp Gly Thr Glu Phe Thr Val Arg Asn Gly Val Asp Gly
 195 200 205

Ser Asp Gly Lys Asp Gly Lys Asp Gly Val Asn Gly Thr Asp Gly Val
 210 215 220

Asp Gly Ser Asp Gly Lys Gly Leu Val Glu Val Ser Arg Val Thr Asn
 225 230 235 240

Asp Asn Gly Ser Val Thr Ile Thr Tyr Glu Asp Gly Ser Gln Ile Thr
 245 250 255

Thr Lys Pro Thr Pro Thr Asn Trp Leu
 260 265

<210> 929

<211> 660

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(637)

<223> RXN01996

<400> 929

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gttaaaaaacg aaacacactt tcaccgaaaa ggacttccca atg agc aag ttg act 115
 Met Ser Lys Leu Thr 5

ggc acc tgg acc ctc gac cct gca cac acc gaa atc aag ttc gtg gct 163
 Gly Thr Trp Thr Leu Asp Pro Ala His Thr Glu Ile Lys Phe Val Ala 20

cgc cac gca atg gtt acc aag gtt cgc ggt gaa ttc acc gag tac acc 211
 Arg His Ala Met Val Thr Lys Val Arg Gly Glu Phe Thr Glu Tyr Thr 35

gac tcc att gtc gta gat gct gaa aac cca gag aac tcc tct gca aag 259
 Asp Ser Ile Val Val Asp Ala Glu Asn Pro Glu Asn Ser Ser Ala Lys 40 45 50

gtt gtt atc aag acc gct tcc gtt acc acc ggc aac gca gac cgc gat 307
 Val Val Ile Lys Thr Ala Ser Val Thr Thr Gly Asn Ala Asp Arg Asp 55 60 65

gca cac gtt aag ggc gac gac ttc ttc gca gta gac aag ttc oct gaa 355
 Ala His Val Lys Gly Asp Asp Phe Phe Ala Val Asp Lys Phe Pro Glu 70 75 80 85

atg act ttc gaa gct act tcc ttt gtt atc aag aac gaa aac gaa ggc 403
 Met Thr Phe Glu Ala Thr Ser Phe Val Ile Lys Asn Glu Asn Glu Gly

90	95	100	
acc gtt acc ggc gac ctc aca att cgt gac acc acc aag tcc gtc acc			451
Thr Val Thr Gly Asp Leu Thr Ile Arg Asp Thr Thr Lys Ser Val Thr			
105	110	115	
ctg gac gtt gag gtt ggt ggc gtt gct gag gat cca ttc ggc aac acc			499
Leu Asp Val Glu Val Gly Gly Val Ala Glu Asp Pro Phe Gly Asn Thr			
120	125	130	
cgc ctt ggc ttc gaa gcc tcc acc gaa atc aac cgc aag gac ttc ggc			547
Arg Leu Gly Phe Glu Ala Ser Thr Glu Ile Asn Arg Lys Asp Phe Gly			
135	140	145	
gta gat ttc cag gct cca ctc tcc acc ggt ggc gtt ctg gtt tct gag			595
Val Asp Phe Gln Ala Pro Leu Ser Thr Gly Gly Val Leu Val Ser Glu			
150	155	160	
aag atc aag atc gag atc gac ggc tcc gca atc aag gct gct			637
Lys Ile Lys Ile Glu Ile Asp Gly Ser Ala Ile Lys Ala Ala			
170	175		
taagcgccca caaacaacaaa gcc			660
<210> 930			
<211> 179			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 930			
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1	5	10	15
Ile Lys Phe Val Ala Arg His Ala Met Val Thr Lys Val Arg Gly Glu			
20	25	30	
Phe Thr Glu Tyr Thr Asp Ser Ile Val Val Asp Ala Glu Asn Pro Glu			
35	40	45	
Asn Ser Ser Ala Lys Val Val Ile Lys Thr Ala Ser Val Thr Thr Gly			
50	55	60	
Asn Ala Asp Arg Asp Ala His Val Lys Gly Asp Asp Phe Phe Ala Val			
65	70	75	80
Asp Lys Phe Pro Glu Met Thr Phe Glu Ala Thr Ser Phe Val Ile Lys			
85	90	95	
Asn Glu Asn Glu Gly Thr Val Thr Gly Asp Leu Thr Ile Arg Asp Thr			
100	105	110	
Thr Lys Ser Val Thr Leu Asp Val Glu Val Gly Gly Val Ala Glu Asp			
115	120	125	
Pro Phe Gly Asn Thr Arg Leu Gly Phe Glu Ala Ser Thr Glu Ile Asn			
130	135	140	
Arg Lys Asp Phe Gly Val Asp Phe Gln Ala Pro Leu Ser Thr Gly Gly			
145	150	155	160

Val Leu Val Ser Glu Lys Ile Lys Ile Glu Ile Asp Gly Ser Ala Ile
 165 170 175

Lys Ala Ala

<210> 931

<211> 647

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (88)..(624)

<223> FRXA01996

<400> 931

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cacactttca ccgaaaagga cttcccaatg agc aag ttg act ggc acc tgg acc 114
 Met Ser Lys Leu Thr Gly Thr Trp Thr
 1 5

ctc gac cct gca cac acc gaa atc aag ttc gtg gct cgc cac gca atg 162
 Leu Asp Pro Ala His Thr Glu Ile Lys Phe Val Ala Arg His Ala Met
 10 15 20 25

gtt acc aag gtt cgc ggt gaa ttc acc gag tac acc gac tcc att gtc 210
 Val Thr Lys Val Arg Gly Glu Phe Thr Glu Tyr Thr Asp Ser Ile Val
 30 35 40

gta gat gct gaa aac cca gag aac tcc tct gca aag gtt gtt atc aag 258
 Val Asp Ala Glu Asn Pro Glu Asn Ser Ser Ala Lys Val Val Ile Lys
 45 50 55

acc gct tcc gtt acc acc ggc aac gca gac cgc gat gca cac gtt aag 306
 Thr Ala Ser Val Thr Thr Gly Asn Ala Asp Arg Asp Ala His Val Lys
 60 65 70

ggc gac gac ttc ttc gca gta gac aag ttc cct gaa atg act ttc gaa 354
 Gly Asp Asp Phe Phe Ala Val Asp Lys Phe Pro Glu Met Thr Phe Glu
 75 80 85

gct act tcc ttt gtt atc aag aac gaa aac gaa ggc acc gtt acc ggc 402
 Ala Thr Ser Phe Val Ile Lys Asn Glu Asn Glu Gly Thr Val Thr Gly
 90 95 100 105

gac ctc aca att cgt gac acc acc aag tcc gtc acc ctg gac gtt gag 450
 Asp Leu Thr Ile Arg Asp Thr Thr Lys Val Thr Leu Asp Val Glu
 110 115 120

gtt ggt ggc gtt gct gag gat cca ttc ggc aac acc cgc ctt ggc ttc 498
 Val Gly Gly Val Ala Glu Asp Pro Phe Gly Asn Thr Arg Leu Gly Phe
 125 130 135

gaa gcc tcc acc gaa atc aac cgc aag gac ttc ggc gta gat ttc cag 546
 Glu Ala Ser Thr Glu Ile Asn Arg Lys Asp Phe Gly Val Asp Phe Gln
 140 145 150

gct cca ctc tcc acc ggt ggc gtt ctg gtt tct gag aag atc aag atc 594

Ala Pro Leu Ser Thr Gly Gly Val Leu Val Ser Glu Lys Ile Lys Ile
 155 160 165

gag atc gac ggc tcc gca atc aag gct gct taagcgccca caaacaaaaa 644
 Glu Ile Asp Gly Ser Ala Ile Lys Ala Ala
 170 175

gcc 647

<210> 932
 <211> 179
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 932
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Ile Lys Phe Val Ala Arg His Ala Met Val Thr Lys Val Arg Gly Glu
 20 25 30

Phe Thr Glu Tyr Thr Asp Ser Ile Val Val Asp Ala Glu Asn Pro Glu
 35 40 45

Asn Ser Ser Ala Lys Val Val Ile Lys Thr Ala Ser Val Thr Thr Gly
 50 55 60

Asn Ala Asp Arg Asp Ala His Val Lys Gly Asp Asp Phe Phe Ala Val
 65 70 75 80

Asp Lys Phe Pro Glu Met Thr Phe Glu Ala Thr Ser Phe Val Ile Lys
 85 90 95

Asn Glu Asn Glu Gly Thr Val Thr Gly Asp Leu Thr Ile Arg Asp Thr
 100 105 110

Thr Lys Ser Val Thr Leu Asp Val Glu Val Gly Gly Val Ala Glu Asp
 115 120 125

Pro Phe Gly Asn Thr Arg Leu Gly Phe Glu Ala Ser Thr Glu Ile Asn
 130 135 140

Arg Lys Asp Phe Gly Val Asp Phe Gln Ala Pro Leu Ser Thr Gly Gly
 145 150 155 160

Val Leu Val Ser Glu Lys Ile Lys Ile Glu Ile Asp Gly Ser Ala Ile
 165 170 175

Lys Ala Ala

<210> 933
 <211> 756
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 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(733)

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tggaagcccc agccgcggtc caagagacag ttgcgccgac gtccaccctt taggacgctg 60

gaa aag gca tcc gtg gag ctt tcc gaa aaa ttt cac cca gaa cgc acc 163
Glu Lys Ala Ser Val Glu Leu Ser Glu Lys Phe His Pro Glu Arg Thr
10 15 20

ggc gca gcc cct cag tac ctg ttt tgg ctg ctc gcg ctc cct gtc atc 259
Gly Ala Ala Pro Gln Tyr Leu Phe Trp Leu Leu Ala Leu Pro Val Ile
40 45 50

atc acc gca aac tac gcc ttc aag ggc aaa aag gtt gtg gcc tgg gaa 355
Ile Thr Ala Asn Tyr Ala Phe Lys Gly Lys Lys Val Val Ala Trp Glu
70 75 80 85

gac ctc gca gga atc gga ttc aag ggt gcc cgc act ttc gct cgc acc 403
Asp Leu Ala Gly Ile Gly Phe Lys Gly Ala Arg Thr Phe Ala Arg Thr
90 95 100

acc tcc gat gca gaa gtc acc ctc ccg ggc gtc acc ttc aac tcc ctt 451
Thr Ser Asp Ala Glu Val Thr Leu Pro Gly Val Thr Phe Asn Ser Leu
105 110 115

ccc cgc ctt gaa gct gct tcc cac ggc cgc atc ccc gat gcg atc acc 499
Pro Arg Leu Glu Ala Ala Ser His Gly Arg Ile Pro Asp Ala Ile Thr
120 125 130

gca agc aag gaa gca gcc gac ggC aag gtt gta gtc gtt caa gaa gac 547
Ala Ser Lys Glu Ala Ala Asp Gly Lys Val Val Val Val Gln Glu Asp
135 140 145

ggc tac tcc gtg atg atg tcc aag gaa gag tac ttg gag cgc caa aag 595
Gly Tyr Ser Val Met Met Ser Lys Glu Glu Tyr Leu Glu Arg Gln Lys
150 155 160 165

gca ctg ggc aag cca gtt cag ttg aac ttc gat gac gac acc gat ggg 643
Ala Leu Gly Lys Pro Val Gln Leu Asn Phe Asp Asp Asp Thr Asp Gly
170 175 180

aat aca aca caa aca gaa agc gtt gaa tcc caa gag acc gga caa gcc 691
Asn Thr Thr Gln Thr Glu Ser Val Glu Ser Gln Glu Thr Gly Gln Ala
185 190 195

gcg tct gaa acc tca cat cgt gat aac cct gcg tca cag cac 733
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756

<210> 934

<211> 211

<212> PRT

<213> Corynebacterium glutamicum

<400> 934

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His	Pro	Glu	Arg	Thr	His	Ile	Leu	Gly	Ala	Val	Val	Phe	Gly	Leu	Ile
			20					25					30		

Ser	Leu	Leu	Val	Ile	Gly	Ala	Ala	Pro	Gln	Tyr	Leu	Phe	Trp	Leu	Leu
	35					40						45			

Ala	Leu	Pro	Val	Ile	Phe	Gly	Tyr	Trp	Val	Leu	Lys	Ser	Ser	Thr	Ile
	50				55						60				

Val	Asp	Glu	Gln	Gly	Ile	Thr	Ala	Asn	Tyr	Ala	Phe	Lys	Gly	Lys	Lys
	65				70					75				80	

Val	Val	Ala	Trp	Glu	Asp	Leu	Ala	Gly	Ile	Gly	Phe	Lys	Gly	Ala	Arg
				85					90					95	

Thr	Phe	Ala	Arg	Thr	Thr	Ser	Asp	Ala	Glu	Val	Thr	Leu	Pro	Gly	Val
			100					105					110		

Thr	Phe	Asn	Ser	Leu	Pro	Arg	Leu	Glu	Ala	Ala	Ser	His	Gly	Arg	Ile
				115			120					125			

Pro	Asp	Ala	Ile	Thr	Ala	Ser	Lys	Glu	Ala	Ala	Asp	Gly	Lys	Val	Val
	130				135						140				

Val	Val	Gln	Glu	Asp	Gly	Tyr	Ser	Val	Met	Met	Ser	Lys	Glu	Glu	Tyr
	145				150					155				160	

Leu	Glu	Arg	Gln	Lys	Ala	Leu	Gly	Lys	Pro	Val	Gln	Leu	Asn	Phe	Asp
				165					170					175	

Asp	Asp	Thr	Asp	Gly	Asn	Thr	Thr	Gln	Thr	Glu	Ser	Val	Glu	Ser	Gln
			180				185						190		

Glu	Thr	Gly	Gln	Ala	Ala	Ser	Glu	Thr	Ser	His	Arg	Asp	Asn	Pro	Ala
		195					200					205			

Ser	Gln	His
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<210> 935

<211> 452

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(429)

<223> FRXA02007

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Gly Ile Thr Ala Asn Tyr Ala Phe Lys Gly Lys Lys Val Val Ala Trp
  1           5           10           15

aaa gac ctc gca gga atc gga ttc aag ggt gcc cgc act ttc gct cgc 96
Lys Asp Leu Ala Gly Ile Gly Phe Lys Gly Ala Arg Thr Phe Ala Arg
          20           25           30

ccc acc tcc gat gca gaa gtc acc ctc ccg ggc gtc acc ttc aac tcc 144
Pro Thr Ser Asp Ala Glu Val Thr Leu Pro Gly Val Thr Phe Asn Ser
      35           40           45

ctt ccc cgc ctt gaa gct gct tcc cac ggc cgc atc ccc gat gcg atc 192
Leu Pro Arg Leu Glu Ala Ala Ser His Gly Arg Ile Pro Asp Ala Ile
      50           55           60

acc gca agc aag gaa gca gcc gac ggc aag gtt gta gtc gtt caa gaa 240
Thr Ala Ser Lys Glu Ala Ala Asp Gly Lys Val Val Val Val Gln Glu
      65           70           75

gac ggc tac tcc gtg atg atg tcc aag gaa gag tac ttg gag cgc caa 288
Asp Gly Tyr Ser Val Met Met Ser Lys Glu Glu Tyr Leu Glu Arg Gln
          85           90           95

aag gca ctg ggc aag cca gtt cag ttg aac ttc gat gac gac acc gat 336
Lys Ala Leu Gly Lys Pro Val Gln Leu Asn Phe Asp Asp Asp Thr Asp
      100           105           110

ggg aat aca aca caa aca gaa agc gtt gaa tcc caa gag acc gga caa 384
Gly Asn Thr Thr Gln Thr Glu Ser Val Glu Ser Gln Glu Thr Gly Gln
      115           120           125

gcc gcg tct gaa acc tca cat cgt gat aac cct gcg tca cag cac 429
Ala Ala Ser Glu Thr Ser His Arg Asp Asn Pro Ala Ser Gln His
      130           135           140

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<210> 936
<211> 143
<212> PRT
<213> Corynebacterium glutamicum

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Lys Asp Leu Ala Gly Ile Gly Phe Lys Gly Ala Arg Thr Phe Ala Arg
      20           25           30

Pro Thr Ser Asp Ala Glu Val Thr Leu Pro Gly Val Thr Phe Asn Ser
      35           40           45

Leu Pro Arg Leu Glu Ala Ala Ser His Gly Arg Ile Pro Asp Ala Ile
      50           55           60

Thr Ala Ser Lys Glu Ala Ala Asp Gly Lys Val Val Val Val Gln Glu
      65           70           75           80

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Asp Gly Tyr Ser Val Met Met Ser Lys Glu Glu Tyr Leu Glu Arg Gln
85 90 95

Lys Ala Leu Gly Lys Pro Val Gln Leu Asn Phe Asp Asp Asp Thr Asp
100 105 110

Gly Asn Thr Thr Gln Thr Glu Ser Val Glu Ser Gln Glu Thr Gly Gln
115 120 125

Ala Ala Ser Glu Thr Ser His Arg Asp Asn Pro Ala Ser Gln His
130 135 140

<210> 937

<211> 630

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> {101}..(607)

<223> RXN02014

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ctgcaatctc taccgcacac accatcacga ttcgctcacc atg gaa aac att gca 115
Met Glu Asn Ile Ala
1 5

gaa cag gca gga gtg ggt gtt gca act tta tac cga aac ttc ccc gat 163
Glu Gln Ala Gly Val Gly Val Ala Thr Leu Tyr Arg Asn Phe Pro Asp
10 15 20

cgc ttc aca ctg gac atg gca tgc gcc caa tac ctt ttc aac gtg gtg 211
Arg Phe Thr Leu Asp Met Ala Cys Ala Gln Tyr Leu Phe Asn Val Val
25 30 35

atc tcc ctg caa ctg caa gcc atc agc acc ttc ccc acc gac cca gaa 259
Ile Ser Leu Gln Leu Gln Ala Ile Ser Thr Phe Pro Thr Asp Pro Glu
40 45 50

ggc gtg tgg acc tcc ttc aac caa cta ctt ttc gac cgc ggc cta ggc 307
Gly Val Trp Thr Ser Phe Asn Gln Leu Leu Phe Asp Arg Gly Leu Gly
55 60 65

tcc ctg gtc cca gca ctt gcc cca gaa tcc tta gac gac ctg ccc gac 355
Ser Leu Val Pro Ala Leu Ala Pro Glu Ser Leu Asp Asp Leu Pro Asp
70 75 80 85

gag gtc tcc gcc ctg cgt cgc acc aca gag aaa aac acc aca aca ctg 403
Glu Val Ser Ala Leu Arg Arg Thr Thr Glu Lys Asn Thr Thr Thr Leu
90 95 100

atc aac cta gcc aag cag cac gga ctg gta cac cac gac atc gcg ccg 451
Ile Asn Leu Ala Lys Gln His Gly Leu Val His His Asp Ile Ala Pro
105 110 115

ggc acc tac atc gtc ggt ttg atc acc att tcc cgc cca cct atc acc 499
Gly Thr Tyr Ile Val Gly Leu Ile Thr Ile Ser Arg Pro Pro Ile Thr

120	125	130	
gcg ctg gcg aca att tca gaa aac tcc cac aaa gca ctg ctt ggc ctt			547
Ala Leu Ala Thr Ile Ser Glu Asn Ser His Lys Ala Leu Leu Gly Leu			
135	140	145	
tat ttg tcc ggt ctt aaa cac ggc atg atg gct aac atc gga gaa cat			595
Tyr Leu Ser Gly Leu Lys His Gly Met Met Ala Asn Ile Gly Glu His			
150	155	160	165
gac gga aag tcc tgaatagca gtttcotttt tag			630
Asp Gly Lys Ser			

<210> 938

<211> 169

<212> PRT

<213> Corynebacterium glutamicum

<400> 938

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Leu Phe Asn Val Val Ile Ser Leu Gln Leu Gln Ala Ile Ser Thr Phe			
35	40	45	
Pro Thr Asp Pro Glu Gly Val Trp Thr Ser Phe Asn Gln Leu Leu Phe			
50	55	60	
Asp Arg Gly Leu Gly Ser Leu Val Pro Ala Leu Ala Pro Glu Ser Leu			
65	70	75	80
Asp Asp Leu Pro Asp Glu Val Ser Ala Leu Arg Arg Thr Thr Glu Lys			
85	90	95	
Asn Thr Thr Thr Leu Ile Asn Leu Ala Lys Gln His Gly Leu Val His			
100	105	110	
His Asp Ile Ala Pro Gly Thr Tyr Ile Val Gly Leu Ile Thr Ile Ser			
115	120	125	
Arg Pro Pro Ile Thr Ala Leu Ala Thr Ile Ser Glu Asn Ser His Lys			
130	135	140	
Ala Leu Leu Gly Leu Tyr Leu Ser Gly Leu Lys His Gly Met Met Ala			
145	150	155	160
Asn Ile Gly Glu His Asp Gly Lys Ser			
165			

<210> 939

<211> 419

<212> DNA

<213> Corynebacterium glutamicum

<220>

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 <222> (1)..(396)
 <223> FRXA02014

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 ggc gtg tgg acc tcc ttc aac caa cta ctt ttc gac cgc ggc cta ggc 96
 Gly Val Trp Thr Ser Phe Asn Gln Leu Leu Phe Asp Arg Gly Leu Gly
 20 25 30
 tcc ctc gtc cca gca ctt gcc cca gaa tcc tta gac gac ctc ccc gac 144
 Ser Leu Val Pro Ala Leu Ala Pro Glu Ser Leu Asp Asp Leu Pro Asp
 35 40 45
 gag gtc tcc gcc ctg cgt cgc acc aca gag aaa aac acc aca aca ctc 192
 Glu Val Ser Ala Leu Arg Arg Thr Thr Glu Lys Asn Thr Thr Thr Leu
 50 55 60
 atc aac cta gcc aag cag cac gga ctc gta cac cac gac atc gcg ccg 240
 Ile Asn Leu Ala Lys Gln His Gly Leu Val His His Asp Ile Ala Pro
 65 70 75 80
 ggc acc tac atc gtc ggt ttg atc acc att tcc cgc cca cct atc acc 288
 Gly Thr Tyr Ile Val Gly Leu Ile Thr Ile Ser Arg Pro Pro Ile Thr
 85 90 95
 gcg ctg gcg aca att tca gaa aac tcc cac aaa gca ctg ctt ggc ctt 336
 Ala Leu Ala Thr Ile Ser Glu Asn Ser His Lys Ala Leu Leu Gly Leu
 100 105 110
 tat ttg tcc ggt ctt aaa cac ggc atg atg gct aac atc gga gaa cat 384
 Tyr Leu Ser Gly Leu Lys His Gly Met Met Ala Asn Ile Gly Glu His
 115 120 125
 gac gga aag tcc tgatctagca gtttcctttt tag 419
 Asp Gly Lys Ser
 130

<210> 940
 <211> 132
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 940
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 Gly Val Trp Thr Ser Phe Asn Gln Leu Leu Phe Asp Arg Gly Leu Gly
 20 25 30
 Ser Leu Val Pro Ala Leu Ala Pro Glu Ser Leu Asp Asp Leu Pro Asp
 35 40 45
 Glu Val Ser Ala Leu Arg Arg Thr Thr Glu Lys Asn Thr Thr Thr Leu
 50 55 60
 Ile Asn Leu Ala Lys Gln His Gly Leu Val His His Asp Ile Ala Pro


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65              70              75              80
Gly Thr Tyr Ile Val Gly Leu Ile Thr Ile Ser Arg Pro Pro Ile Thr
      85              90              95
Ala Leu Ala Thr Ile Ser Glu Asn Ser His Lys Ala Leu Leu Gly Leu
      100             105             110
Tyr Leu Ser Gly Leu Lys His Gly Met Met Ala Asn Ile Gly Glu His
      115             120             125
Asp Gly Lys Ser
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<210> 941

<211> 524

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(501)

<223> RXN02019

<400> 941

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gca atc cct act tcc cta ctg ccc agc acc tcc tac gat tgg att gac 96
Ala Ile Pro Thr Ser Leu Leu Pro Ser Thr Ser Tyr Asp Ser Ile Asp
      20              25              30

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gat gta gtt ggg ctc gtt gcg gcc tcc aca tta agt tcc ggg gaa ata 144
Asp Val Val Gly Leu Val Ala Ala Ser Thr Leu Ser Ser Gly Glu Ile
      35              40              45

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gcc aca aag cct cga ttc gtg ggc acc gaa ttg ata aac tcc att gcg 192
Ala Thr Lys Pro Arg Phe Val Gly Thr Glu Leu Ile Asn Ser Ile Ala
      50              55              60

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aca aac gtc act gat agc tct ttg gtg gaa gaa att aac atg gtt cca 240
Thr Asn Val Thr Asp Ser Ser Leu Val Glu Glu Ile Asn Met Val Pro
      65              70              75              80

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ctc agt ttg gct gaa cct tcc gtc atc ccc cta ctg cag cat ggg gac 288
Leu Ser Leu Ala Glu Pro Ser Val Ile Pro Leu Leu Gln His Gly Asp
      85              90              95

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acc att tgg gtt gtt tcc caa gac cca gac acc ggt ctc cca gag aac 336
Thr Ile Ser Val Val Ser Gln Asp Pro Asp Thr Gly Leu Pro Glu Asn
      100             105             110

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att gct gca ggt gga aca gta att ctg gcg ggt ggt aca gac ccc tca 384
Ile Ala Ala Gly Gly Thr Val Ile Leu Ala Gly Gly Thr Asp Pro Ser
      115             120             125

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acc atc ttg att gcg ctt cca caa tca atc gct gaa aag gtt gca gca 432
Thr Ile Leu Ile Ala Leu Pro Gln Ser Ile Ala Glu Lys Val Ala Ala
      130             135             140

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caa tgc ctc aat acc cct ctg gcg gta gtc ctg acc gga gac aga gca 480
 Gln Ser Leu Asn Thr Pro Leu Ala Val Val Leu Thr Gly Asp Arg Ala
 145 150 155 160

gat aat tac aca acc gaa gaa tagttcccta ttcaaaaaaa agg 524
 Asp Asn Tyr Thr Thr Glu Glu
 165

<210> 942

<211> 167

<212> PRT

<213> Corynebacterium glutamicum

<400> 942

Glu Ile Pro Ala Gly Thr Lys Val Glu Ala Ser Asp Leu Gly Leu Gln
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Ala Ile Pro Thr Ser Leu Leu Pro Ser Thr Ser Tyr Asp Ser Ile Asp
 20 25 30

Asp Val Val Gly Leu Val Ala Ala Ser Thr Leu Ser Ser Gly Glu Ile
 35 40 45

Ala Thr Lys Pro Arg Phe Val Gly Thr Glu Leu Ile Asn Ser Ile Ala
 50 55 60

Thr Asn Val Thr Asp Ser Ser Leu Val Glu Glu Ile Asn Met Val Pro
 65 70 75 80

Leu Ser Leu Ala Glu Pro Ser Val Ile Pro Leu Leu Gln His Gly Asp
 85 90 95

Thr Ile Ser Val Val Ser Gln Asp Pro Asp Thr Gly Leu Pro Glu Asn
 100 105 110

Ile Ala Ala Gly Gly Thr Val Ile Leu Ala Gly Gly Thr Asp Pro Ser
 115 120 125

Thr Ile Leu Ile Ala Leu Pro Gln Ser Ile Ala Glu Lys Val Ala Ala
 130 135 140

Gln Ser Leu Asn Thr Pro Leu Ala Val Val Leu Thr Gly Asp Arg Ala
 145 150 155 160

Asp Asn Tyr Thr Thr Glu Glu
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<210> 943

<211> 515

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(492)

<223> FRXA02019

<400> 943

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Ala Gly Thr Lys Val Glu Ala Ser Asp Leu Gly Leu Gln Ala Ile Pro
1 5 10 15

act tcc cta ctg ccc agc acc tcc tac gat tcg att gac gat gta gtt 96
Thr Ser Leu Leu Pro Ser Thr Ser Tyr Asp Ser Ile Asp Asp Val Val
20 25 30

ggg ctc gtt gcg gcc tcc aca tta agt tcc ggg gaa ata gcc aca aag 144
Gly Leu Val Ala Ala Ser Thr Leu Ser Ser Gly Glu Ile Ala Thr Lys
35 40 45

cct cga ttc gtg ggc acc gaa ttg ata aac tcc att gcg aca aac gtc 192
Pro Arg Phe Val Gly Thr Glu Leu Ile Asn Ser Ile Ala Thr Asn Val
50 55 60

act gat agc tct ttg gtg gaa gaa att aac atg gtt cca ctc agt ttg 240
Thr Asp Ser Ser Leu Val Glu Glu Ile Asn Met Val Pro Leu Ser Leu
65 70 75 80

gct gaa cct tcc gtc atc ccc cta ctg cag cat ggg gac acc att tcg 288
Ala Glu Pro Ser Val Ile Pro Leu Leu Gln His Gly Asp Thr Ile Ser
85 90 95

gtt gtt tcc caa gac cca gac acc ggt ctc cca gag aac att gct gca 336
Val Val Ser Gln Asp Pro Asp Thr Gly Leu Pro Glu Asn Ile Ala Ala
100 105 110

ggg gga aca gta att ctg gcg ggt ggt aca gac ccc tca acc atc ttg 384
Gly Gly Thr Val Ile Leu Ala Gly Gly Thr Asp Pro Ser Thr Ile Leu
115 120 125

att gcg ctt cca caa tca atc gct gaa aag gtt gca gca caa tcg ctc 432
Ile Ala Leu Pro Gln Ser Ile Ala Glu Lys Val Ala Ala Gln Ser Leu
130 135 140

aat acc cct ctg gcg gta gtc ctg acc gga gac aga gca aat aat tac 480
Asn Thr Pro Leu Ala Val Val Leu Thr Gly Asp Arg Ala Asn Asn Tyr
145 150 155 160

aca acc gaa gaa tagttcccta ttcaaaaaaa agg 515
Thr Thr Glu Glu

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<210> 944

<211> 164

<212> PRT

<213> Corynebacterium glutamicum

<400> 944

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Ala Gly Thr Lys Val Glu Ala Ser Asp Leu Gly Leu Gln Ala Ile Pro
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Thr Ser Leu Leu Pro Ser Thr Ser Tyr Asp Ser Ile Asp Asp Val Val
20 25 30

Gly Leu Val Ala Ala Ser Thr Leu Ser Ser Gly Glu Ile Ala Thr Lys
35 40 45

Pro Arg Phe Val Gly Thr Glu Leu Ile Asn Ser Ile Ala Thr Asn Val

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      50              55              60
Thr Asp Ser Ser Leu Val Glu Glu Ile Asn Met Val Pro Leu Ser Leu
65              70              75              80
Ala Glu Pro Ser Val Ile Pro Leu Leu Gln His Gly Asp Thr Ile Ser
      85              90              95
Val Val Ser Gln Asp Pro Asp Thr Gly Leu Pro Glu Asn Ile Ala Ala
      100             105             110
Gly Gly Thr Val Ile Leu Ala Gly Gly Thr Asp Pro Ser Thr Ile Leu
      115             120             125
Ile Ala Leu Pro Gln Ser Ile Ala Glu Lys Val Ala Ala Gln Ser Leu
      130             135             140
Asn Thr Pro Leu Ala Val Val Leu Thr Gly Asp Arg Ala Asn Asn Tyr
      145             150             155             160

Thr Thr Glu Glu

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<210> 945
<211> 891
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(868)
<223> RXN02023

<400> 945
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gacttcgcga atgtaactag agactagagg aggaaacacg atg gct cct aaa caa 115
Met Ala Pro Lys Gln
1
act ccc agc cca gag aag aat cga aac ctg gtg gga cca gtt ctg caa 163
Thr Pro Ser Pro Glu Lys Asn Arg Asn Leu Val Gly Pro Val Leu Gln
10 15 20
cgt cgg cag aca gag ggt act ttt gat caa cgc ttg cta gaa atg cgc 211
Arg Arg Gln Thr Glu Gly Thr Phe Asp Gln Arg Leu Leu Glu Met Arg
25 30 35
gct gat cac aat tgg aag cac gcc gat cca tgg cgt gta ctg cgt att 259
Ala Asp His Asn Trp Lys His Ala Asp Pro Trp Arg Val Leu Arg Ile
40 45 50
cag tct gag ttt gtg gcg ggt ttt gat gcc ctc cac gag atg cca aag 307
Gln Ser Glu Phe Val Ala Gly Phe Asp Ala Leu His Glu Met Pro Lys
55 60 65
gcc gta acc gtc ttt ggt tcc gca cgc att aaa gag gat cac ccg tac 355
Ala Val Thr Val Phe Gly Ser Ala Arg Ile Lys Glu Asp His Pro Tyr
70 75 80 85

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tac aag gcg ggt gta gaa ctt ggt gaa aag ctc gtt gca gcg gac tac 403
 Tyr Lys Ala Gly Val Glu Leu Gly Glu Lys Leu Val Ala Ala Asp Tyr
 90 95 100

gca gtt gtc acc ggt ggc ggt cca ggt ctg atg gaa gcc ccc aat aag 451
 Ala Val Val Thr Gly Gly Gly Pro Gly Leu Met Glu Ala Pro Asn Lys
 105 110 115

ggg gca agc gag gcc aat ggt tta tca gtt ggt ctg ggc att gag ttg 499
 Gly Ala Ser Glu Ala Asn Gly Leu Ser Val Gly Leu Gly Ile Glu Leu
 120 125 130

cca cat gaa cag cat ctg aac cct tat gtg gat ttg ggt ctg aac ttc 547
 Pro His Glu Gln His Leu Asn Pro Tyr Val Asp Leu Gly Leu Asn Phe
 135 140 145

cgg tac ttc ttc gca cgc aag acc atg ttc ctg aaa tac tcc cag gct 595
 Arg Tyr Phe Phe Ala Arg Lys Thr Met Phe Leu Lys Tyr Ser Gln Ala
 150 155 160 165

ttt gtg tgt ctg cct ggt ggt ttc ggc acg ctc gat gag ctt ttc gag 643
 Phe Val Cys Leu Pro Gly Gly Phe Gly Thr Leu Asp Glu Leu Phe Glu
 170 175 180

gtc ctc tgc atg gta caa acc ggc aag gta ccc aac ttt ccc atc gtg 691
 Val Leu Cys Met Val Gln Thr Gly Lys Val Pro Asn Phe Pro Ile Val
 185 190 195

ctg atc ggc act gag ttc tgg gca ggt ttg gtg gat tgg atc cgt cac 739
 Leu Ile Gly Thr Glu Phe Trp Ala Gly Leu Val Asp Trp Ile Arg His
 200 205 210

cgc ctg gta gag gaa ggc atg atc gat gag aag gat gtt gac cgg atg 787
 Arg Leu Val Glu Glu Gly Met Ile Asp Glu Lys Asp Val Asp Arg Met
 215 220 225

ttg gtc act gat gac ctg gat cag gcc gtc aaa ttc atc gtc gat gca 835
 Leu Val Thr Asp Asp Leu Asp Gln Ala Val Lys Phe Ile Val Asp Ala
 230 235 240 245

cac gct gga ttg gac gta gcg cgt ctc cac aat taagcagtgg ctacattagg 888
 His Ala Gly Leu Asp Val Ala Arg Leu His Asn
 250 255

tgt 891

<210> 946
 <211> 256
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 946
 Met Ala Pro Lys Gln Thr Pro Ser Pro Glu Lys Asn Arg Asn Leu Val
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 Gly Pro Val Leu Gln Arg Arg Gln Thr Glu Gly Thr Phe Asp Gln Arg
 20 25 30
 Leu Leu Glu Met Arg Ala Asp His Asn Trp Lys His Ala Asp Pro Trp
 35 40 45

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Arg Val Leu Arg Ile Gln Ser Glu Phe Val Ala Gly Phe Asp Ala Leu
  50                      55                      60

His Glu Met Pro Lys Ala Val Thr Val Phe Gly Ser Ala Arg Ile Lys
  65                      70                      75                      80

Glu Asp His Pro Tyr Tyr Lys Ala Gly Val Glu Leu Gly Glu Lys Leu
                      85                      90                      95

Val Ala Ala Asp Tyr Ala Val Val Thr Gly Gly Gly Pro Gly Leu Met
  100                      105                      110

Glu Ala Pro Asn Lys Gly Ala Ser Glu Ala Asn Gly Leu Ser Val Gly
  115                      120                      125

Leu Gly Ile Glu Leu Pro His Glu Gln His Leu Asn Pro Tyr Val Asp
  130                      135                      140

Leu Gly Leu Asn Phe Arg Tyr Phe Phe Ala Arg Lys Thr Met Phe Leu
  145                      150                      155                      160

Lys Tyr Ser Gln Ala Phe Val Cys Leu Pro Gly Gly Phe Gly Thr Leu
                      165                      170                      175

Asp Glu Leu Phe Glu Val Leu Cys Met Val Gln Thr Gly Lys Val Pro
  180                      185                      190

Asn Phe Pro Ile Val Leu Ile Gly Thr Glu Phe Trp Ala Gly Leu Val
  195                      200                      205

Asp Trp Ile Arg His Arg Leu Val Glu Glu Gly Met Ile Asp Glu Lys
  210                      215                      220

Asp Val Asp Arg Met Leu Val Thr Asp Asp Leu Asp Gln Ala Val Lys
  225                      230                      235                      240

Phe Ile Val Asp Ala His Ala Gly Leu Asp Val Ala Arg Leu His Asn
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<210> 947

<211> 891

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(868)

<223> FRXA02023

<400> 947

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gacttccgaa atgtaactag agactagagg aggaaacacg atg gct cct aaa caa 115

Met Ala Pro Lys Gln
1 5

act ccc agc cca gag aag aat cga aac ctg gtg gga cca gtt ctg caa 163
 Thr Pro Ser Pro Glu Lys Asn Arg Asn Leu Val Gly Pro Val Leu Gln
 10 15 20

cgt cgg cag aca gag ggt act ttt gat caa cgc ttg cta gaa atg cgc 211
 Arg Arg Gln Thr Glu Gly Thr Phe Asp Gln Arg Leu Leu Glu Met Arg
 25 30 35

gct gat cac aat tgg aag cac gcc gat cca tgg cgt gta ctg cgt att 259
 Ala Asp His Asn Trp Lys His Ala Asp Pro Trp Arg Val Leu Arg Ile
 40 45 50

cag tct gag ttt gtg gcg ggt ttt gat gcc ctc cac gag atg cca aag 307
 Gln Ser Glu Phe Val Ala Gly Phe Asp Ala Leu His Glu Met Pro Lys
 55 60 65

gcc gta acc gtc ttt ggt tcc gca cgc att aaa gag gat cac cgc tac 355
 Ala Val Thr Val Phe Gly Ser Ala Arg Ile Lys Glu Asp His Pro Tyr
 70 75 80 85

tac aag gcg ggt gta gaa ctt ggt gaa aag ctc gtt gct gct gac tac 403
 Tyr Lys Ala Gly Val Glu Leu Gly Glu Lys Leu Val Ala Ala Asp Tyr
 90 95 100

gca gtt gtc acc ggt ggc ggt cca ggt ctg atg gaa gcc ccc aat aag 451
 Ala Val Val Thr Gly Gly Gly Pro Gly Leu Met Glu Ala Pro Asn Lys
 105 110 115

ggg gca agc gag gcc aat ggt tta tca gtt ggt ctg gcc att gag ttg 499
 Gly Ala Ser Glu Ala Asn Gly Leu Ser Val Gly Leu Gly Ile Glu Leu
 120 125 130

cca cat gaa cag cac ctg aac cct tat gtg gat ttg ggt ctg aac ttc 547
 Pro His Glu Gln His Leu Asn Pro Tyr Val Asp Leu Gly Leu Asn Phe
 135 140 145

cgg tac ttc ttc gca cgc aag acc atg ttc ctg aaa tac tcc cag gct 595
 Arg Tyr Phe Phe Ala Arg Lys Thr Met Phe Leu Lys Tyr Ser Gln Ala
 150 155 160 165

ttt gtg tgt ctg cct ggc ggt ttc ggc acg ctc gat gag ctt ttc gag 643
 Phe Val Cys Leu Pro Gly Gly Phe Gly Thr Leu Asp Glu Leu Phe Glu
 170 175 180

gtc ctc tgc atg gta caa acc ggc aag gta acc aac ttt ccc atc gtg 691
 Val Leu Cys Met Val Gln Thr Gly Lys Val Thr Asn Phe Pro Ile Val
 185 190 195

ctg atc ggc act gag ttc tgg gca ggt ttg gtg gat tgg atc cgt cac 739
 Leu Ile Gly Thr Glu Phe Trp Ala Gly Leu Val Asp Trp Ile Arg His
 200 205 210

cgc ctg gta gag gaa ggc atg atc gat gag aag gat gtt gac cgg atg 787
 Arg Leu Val Glu Glu Gly Met Ile Asp Glu Lys Asp Val Asp Arg Met
 215 220 225

ttg gtc act gat gac ctg gat cag gcc gtc aaa ttc atc gtc gat gca 835
 Leu Val Thr Asp Asp Leu Asp Gln Ala Val Lys Phe Ile Val Asp Ala
 230 235 240 245

cac gct gga ttg gac gta gcg cgt ctc cac aat taagcagtgg ctacattagg 888

His Ala Gly Leu Asp Val Ala Arg Leu His Asn
250 255

tgt

891

<210> 948

<211> 256

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 948

Met Ala Pro Lys Gln Thr Pro Ser Pro Glu Lys Asn Arg Asn Leu Val
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Gly Pro Val Leu Gln Arg Arg Gln Thr Glu Gly Thr Phe Asp Gln Arg
20 25 30

Leu Leu Glu Met Arg Ala Asp His Asn Trp Lys His Ala Asp Pro Trp
35 40 45

Arg Val Leu Arg Ile Gln Ser Glu Phe Val Ala Gly Phe Asp Ala Leu
50 55 60

His Glu Met Pro Lys Ala Val Thr Val Phe Gly Ser Ala Arg Ile Lys
65 70 75 80

Glu Asp His Pro Tyr Lys Ala Gly Val Glu Leu Gly Glu Lys Leu
85 90 95

Val Ala Ala Asp Tyr Ala Val Val Thr Gly Gly Gly Pro Gly Leu Met
100 105 110

Glu Ala Pro Asn Lys Gly Ala Ser Glu Ala Asn Gly Leu Ser Val Gly
115 120 125

Leu Gly Ile Glu Leu Pro His Glu Gln His Leu Asn Pro Tyr Val Asp
130 135 140

Leu Gly Leu Asn Phe Arg Tyr Phe Phe Ala Arg Lys Thr Met Phe Leu
145 150 155 160

Lys Tyr Ser Gln Ala Phe Val Cys Leu Pro Gly Gly Phe Gly Thr Leu
165 170 175

Asp Glu Leu Phe Glu Val Leu Cys Met Val Gln Thr Gly Lys Val Thr
180 185 190

Asn Phe Pro Ile Val Leu Ile Gly Thr Glu Phe Trp Ala Gly Leu Val
195 200 205

Asp Trp Ile Arg His Arg Leu Val Glu Glu Gly Met Ile Asp Glu Lys
210 215 220

Asp Val Asp Arg Met Leu Val Thr Asp Asp Leu Asp Gln Ala Val Lys
225 230 235 240

Phe Ile Val Asp Ala His Ala Gly Leu Asp Val Ala Arg Leu His Asn
245 250 255


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<222> (101)..(670)  
<223> RXN02032
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Met Pro Phe Leu Gln																	115
atc tct ctg ctt tcc atc ggt gtc gcc ggc gat cgc ttt gct tgt tcc																	
Ile Ser Leu Leu Ser 10 Ile Gly Val Ala 15 Asp Ala Phe Ala Cys Ser 20																	163
gtt gtc cgc ggc acc gcc att caa gtc aac ctt ttc aaa cgc gca ctt																	
Val Val Arg Gly 25 Thr Ala Ile Gln Val 30 Asn Leu Phe Lys Arg 35 Ala Leu																	211
gtt ctc gcg ggc atc ttt ggt gtc ttc caa gcg gca atg cct tta atc																	
Val Leu Ala Gly 40 Ile Phe Gly Val Phe Gln Ala Ala Met 50 Pro Leu Ile																	259
ggc tgg ttc att ggc cgt ttc ttt gct gga atc acc ttc atc gct gaa																	
Gly Trp Phe Ile Gly Arg Phe 60 Phe Ala Gly Ile Thr Phe Ile Ala Glu																	307
att gat cac tgg atc gct ttt gca cta ttg ggt att gtc ggc acc aaa																	
Ile Asp His Trp Ile Ala 75 Phe Ala Leu Leu Gly 80 Ile Val Gly Thr Lys 85																	355
atg atc tgg gat gcc caa cct gaa gat gaa acc att gtc gat																	
Met Ile Trp Asp Ala 90 Phe Gln Pro Glu Asp 95 Asp Glu Thr Ile Val Asp 100																	403
gac ggc cgc gtt caa ttt aga cca gca att atc ctg ggc cta gcc acc																	
Asp Gly Arg Val Gln 105 Phe Arg Pro Ala 110 Ile Ile Leu Gly Leu Ala Thr 115																	451
agc att gac gca tta gcc gta ggc atg ggc ctg gca ttc gtg gaa gtt																	
Ser Ile Asp Ala Leu Ala Val Gly 120 Met Gly Leu Ala Phe Val Glu Val 130																	499
tcc atc ctc aaa gtg gca ctg tcc atg ggc agc atc acc ttc gca ctt																	
Ser Ile Leu Lys Val Ala Leu 140 Ser Met Gly Ser Ile Thr Phe Ala Leu 145																	547
tcg ctt gct ggc gcc tgg atc gga cac cat ggt gga gga aag ttt ggc																	
Ser Leu Ala Gly Ala Trp 155 Ile Gly His His Gly 160 Gly Gly Lys Phe Gly 165																	595
aag tqg gct acg att ctt ggc gga ata atc ttg atc gga atc ggc gca																	
																	643

Lys Trp Ala Thr Ile Leu Gly Gly Ile Ile Leu Ile Gly Ile Gly Ala
170 175 180

aac atc gtc tac gaa cac ctc agc gcg taaccctcgg cgcattatcc 690
Asn Ile Val Tyr Glu His Leu Ser Ala
185 190

tca 693

<210> 950

<211> 190

<212> PRT

<213> Corynebacterium glutamicum

<400> 950

Met Pro Phe Leu Gln Ile Ser Leu Leu Ser Ile Gly Val Ala Ala Asp
1 5 10 15

Ala Phe Ala Cys Ser Val Val Arg Gly Thr Ala Ile Gln Val Asn Leu
20 25 30

Phe Lys Arg Ala Leu Val Leu Ala Gly Ile Phe Gly Val Phe Gln Ala
35 40 45

Ala Met Pro Leu Ile Gly Trp Phe Ile Gly Arg Phe Phe Ala Gly Ile
50 55 60

Thr Phe Ile Ala Glu Ile Asp His Trp Ile Ala Phe Ala Leu Leu Gly
65 70 75 80

Ile Val Gly Thr Lys Met Ile Trp Asp Ala Phe Gln Pro Glu Asp Asp
85 90 95

Glu Thr Ile Val Asp Asp Gly Arg Val Gln Phe Arg Pro Ala Ile Ile
100 105 110

Leu Gly Leu Ala Thr Ser Ile Asp Ala Leu Ala Val Gly Met Gly Leu
115 120 125

Ala Phe Val Glu Val Ser Ile Leu Lys Val Ala Leu Ser Met Gly Ser
130 135 140

Ile Thr Phe Ala Leu Ser Leu Ala Gly Ala Trp Ile Gly His His Gly
145 150 155 160

Gly Gly Lys Phe Gly Lys Trp Ala Thr Ile Leu Gly Gly Ile Ile Leu
165 170 175

Ile Gly Ile Gly Ala Asn Ile Val Tyr Glu His Leu Ser Ala
180 185 190

<210> 951

<211> 693

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(670)

<400> 951

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               Met Pro Phe Leu Gln
                1             5

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atc tct ctg ctt tcc atc ggt gtc gcc gcc gat gcg ttt gct tgt tcc 163
Ile Ser Leu Leu Ser Ile Gly Val Ala Ala Asp Ala Phe Ala Cys Ser
10 15 20

ggt gtc cgc ggc acc gcc att caa gtc aac ctt ttc aaa cgc gca ctt 211
Val Val Arg Gly Thr Ala Ile Gln Val Asn Leu Phe Lys Arg Ala Leu
25 30 35

ggt ctc gcg ggc atc ttt ggt gtc ttc caa gcg gca atg cct tta atc 259
Val Leu Ala Gly Ile Phe Gly Val Phe Gln Ala Ala Met Pro Leu Ile
40 45 50

ggc tgg ttc att ggc cgt ttc ttt gct gga atc acc ttc atc gct gaa 307
Gly Trp Phe Ile Gly Arg Phe Phe Ala Gly Ile Thr Phe Ile Ala Glu
55 60 65

att gat cac tgg atc gct ttt gca cta ttg ggt att gtc ggc acc aaa 355
Ile Asp His Trp Ile Ala Phe Ala Leu Leu Gly Ile Val Gly Thr Lys
70 75 80 85

atg atc tgg gat gcc ttc caa cct gaa gat gat gaa acc att gtc gat 403
Met Ile Trp Asp Ala Phe Gln Pro Glu Asp Asp Glu Thr Ile Val Asp
90 95 100

gac ggc cgc gtt caa ttt aga cca gca att atc ctg ggg cta gcc acc 451
Asp Gly Arg Val Gln Phe Arg Pro Ala Ile Ile Leu Gly Leu Ala Thr
105 110 115

agc att gac gca tta gcc gta ggc atg ggc ctg gca ttc gtg gaa gtt 499
 Ser Ile Asp Ala Leu Ala Val Gly Met Gly Leu Ala Phe Val Glu Val
 120 125 130

tcc atc ctc aaa gtg gca ctg tcc atg ggc agc atc acc ttc gca ctt 547
Ser Ile Leu Lys Val Ala Leu Ser Met Gly Ser Ile Thr Phe Ala Leu
135 140 145

tgc ctt gct ggc gcc tgg atc gga cac cat ggt gga gga aag ttt ggc 595
Ser Leu Ala Gly Ala Trp Ile Gly His His Gly Gly Gly Lys Phe Gly
150 155 160 165

aag tgg gct acg att ctt ggc gga ata atc ttg atc gga atc ggc gca 643
Lys Trp Ala Thr Ile Leu Gly Gly Ile Ile Leu Ile Gly Ile Gly Ala
170 175 180

aac atc gtc tac gaa cac ctc agc gcg taacctcgg cgcattatcc 690
Asn Ile Val Tyr Glu His Leu Ser Ala
185 190

tca 693

<210> 952

<211> 190

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 952

Met Pro Phe Leu Gln Ile Ser Leu Leu Ser Ile Gly Val Ala Ala Asp
 1 5 10 15

Ala Phe Ala Cys Ser Val Val Arg Gly Thr Ala Ile Gln Val Asn Leu
 20 25 30

Phe Lys Arg Ala Leu Val Leu Ala Gly Ile Phe Gly Val Phe Gln Ala
 35 40 45

Ala Met Pro Leu Ile Gly Trp Phe Ile Gly Arg Phe Phe Ala Gly Ile
 50 55 60

Thr Phe Ile Ala Glu Ile Asp His Trp Ile Ala Phe Ala Leu Leu Gly
 65 70 75 80

Ile Val Gly Thr Lys Met Ile Trp Asp Ala Phe Gln Pro Glu Asp Asp
 85 90 95

Glu Thr Ile Val Asp Asp Gly Arg Val Gln Phe Arg Pro Ala Ile Ile
 100 105 110

Leu Gly Leu Ala Thr Ser Ile Asp Ala Leu Ala Val Gly Met Gly Leu
 115 120 125

Ala Phe Val Glu Val Ser Ile Leu Lys Val Ala Leu Ser Met Gly Ser
 130 135 140

Ile Thr Phe Ala Leu Ser Leu Ala Gly Ala Trp Ile Gly His His Gly
 145 150 155 160

Gly Gly Lys Phe Gly Lys Trp Ala Thr Ile Leu Gly Gly Ile Ile Leu
 165 170 175

Ile Gly Ile Gly Ala Asn Ile Val Tyr Glu His Leu Ser Ala
 180 185 190

<210> 953

<211> 863

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(840)

<223> RXN02039

<400> 953

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 Lys Ala Ser Ile Ser Asn Leu Ser Phe Trp Thr Ser Thr Ser Thr Thr
 1 5 10 15

gca ccc ctt tgg ctc gtg ggc acg ctt gtg tgg ctg gcg gtg cag gcg 96
 Ala Pro Leu Trp Leu Val Gly Thr Leu Val Trp Leu Ala Val Gln Ala
 20 25 30

gtg atg cat gac ggc gag ctt tac cat gtg gaa gtt ccc acg att gcg 144
Val Met His Asp Gly Glu Leu Tyr His Val Glu Val Pro Thr Ile Ala
35 40 45

ctg gtc atc ggc ttt ggc gcg cag ctt ctg atc ggt gtg atg agt tat 192
Leu Val Ile Gly Phe Gly Ala Gln Leu Leu Ile Gly Val Met Ser Tyr
50 55 60

cta ctg ccg tcg acg atg ggt ggc ggc gcg agc gcg gtg cgg act gga 240
Leu Leu Pro Ser Thr Met Gly Gly Gly Ala Ser Ala Val Arg Thr Gly
65 70 75 80

acg cac att tta aac act gcg ggg ctg ttt agg tgg acg ctg atc aac 288
Thr His Ile Leu Asn Thr Ala Gly Leu Phe Arg Trp Thr Leu Ile Asn
85 90 95

ggc ggc ctg gcg att tgg ctg ctc acc gac aat tgg tgg ctg cgc gtc 336
Gly Gly Leu Ala Ile Trp Leu Leu Thr Asp Asn Ser Trp Leu Arg Val
100 105 110

gtg gtg tct ctg ctg agt atc gga gcg ttg gca gtt ttt gtc att ctg 384
Val Val Ser Leu Leu Ser Ile Gly Ala Leu Ala Val Phe Val Ile Leu
115 120 125

ctg ccc aag gct gtg cgg gcg cag cgc gga gtg atc acc aaa aag cgc 432
Leu Pro Lys Ala Val Arg Ala Gln Arg Gly Val Ile Thr Lys Lys Arg
130 135 140

gaa cca att act ccg ccg gag gag cct cga ctc aat caa att acc gcg 480
Glu Pro Ile Thr Pro Pro Glu Glu Pro Arg Leu Asn Gln Ile Thr Ala
145 150 155 160

gga atc tct gtg ctt gcc ctg att ttg gca gca ttc ggt ggg ctc aac 528
Gly Ile Ser Val Leu Ala Leu Ile Leu Ala Ala Phe Gly Gly Leu Asn
165 170 175

ccc ggt gtt gcg ccg gtg gca agc tca aat gaa gac gtc tat gct gtg 576
Pro Gly Val Ala Pro Val Ala Ser Ser Asn Glu Asp Val Tyr Ala Val
180 185 190

acc att acc gca ggt gac atg gtg ttt atc cct gat gtg att gaa gtg 624
Thr Ile Thr Ala Gly Asp Met Val Phe Ile Pro Asp Val Ile Glu Val
195 200 205

cct gct ggt aaa tca ctc gaa gtc acg atg ctc aac gaa gac gac atg 672
Pro Ala Gly Lys Ser Leu Glu Val Thr Met Leu Asn Glu Asp Asp Met
210 215 220

gtg cac gat ctg aaa ttt gcc aac ggt gtg caa acc gga cgt gtg gcg 720
Val His Asp Leu Lys Phe Ala Asn Gly Val Gln Thr Gly Arg Val Ala
225 230 235 240

cca ggt gat gaa att acg gtg acc gtc ggc gat att tcc gaa gac atg 768
Pro Gly Asp Glu Ile Thr Val Thr Val Gly Asp Ile Ser Glu Asp Met
245 250 255

gac ggc tgg tgc acc atc gct ggg cac cgc gcg caa gga atg gat ctg 816
Asp Gly Trp Cys Thr Ile Ala Gly His Arg Ala Gln Gly Met Asp Leu
260 265 270

gaa gta aag gtt gcg gct ccg aat taaccaagggt ctgctgaaaa act 863

Glu Val Lys Val Ala Ala Pro Asn
275 280

<210> 954

<211> 280

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 954

Lys Ala Ser Ile Ser Asn Leu Ser Phe Trp Thr Ser Thr Ser Thr Thr
1 5 10 15

Ala Pro Leu Trp Leu Val Gly Thr Leu Val Trp Leu Ala Val Gln Ala
20 25 30

Val Met His Asp Gly Glu Leu Tyr His Val Glu Val Pro Thr Ile Ala
35 40 45

Leu Val Ile Gly Phe Gly Ala Gln Leu Leu Ile Gly Val Met Ser Tyr
50 55 60

Leu Leu Pro Ser Thr Met Gly Gly Gly Ala Ser Ala Val Arg Thr Gly
65 70 75 80

Thr His Ile Leu Asn Thr Ala Gly Leu Phe Arg Trp Thr Leu Ile Asn
85 90 95

Gly Gly Leu Ala Ile Trp Leu Leu Thr Asp Asn Ser Trp Leu Arg Val
100 105 110

Val Val Ser Leu Leu Ser Ile Gly Ala Leu Ala Val Phe Val Ile Leu
115 120 125

Leu Pro Lys Ala Val Arg Ala Gln Arg Gly Val Ile Thr Lys Lys Arg
130 135 140

Glu Pro Ile Thr Pro Pro Glu Glu Pro Arg Leu Asn Gln Ile Thr Ala
145 150 155 160

Gly Ile Ser Val Leu Ala Leu Ile Leu Ala Ala Phe Gly Gly Leu Asn
165 170 175

Pro Gly Val Ala Pro Val Ala Ser Ser Asn Glu Asp Val Tyr Ala Val
180 185 190

Thr Ile Thr Ala Gly Asp Met Val Phe Ile Pro Asp Val Ile Glu Val
195 200 205

Pro Ala Gly Lys Ser Leu Glu Val Thr Met Leu Asn Glu Asp Asp Met
210 215 220

Val His Asp Leu Lys Phe Ala Asn Gly Val Gln Thr Gly Arg Val Ala
225 230 235 240

Pro Gly Asp Glu Ile Thr Val Thr Val Gly Asp Ile Ser Glu Asp Met
245 250 255

Asp Gly Trp Cys Thr Ile Ala Gly His Arg Ala Gln Gly Met Asp Leu
260 265 270

Glu Val Lys Val Ala Ala Pro Asn
275 280

<210> 955

<211> 833

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(810)

<223> FRXA02039

<400> 955

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Thr Ser Thr Ser Thr Ala Pro Leu Trp Leu Val Gly Thr Leu Val
1 5 10 15

tgg ctg gcg gtg cag gcg gtg atg cat gac ggc gag ctt tac cat gtg 96
Trp Leu Ala Val Gln Ala Val Met His Asp Gly Glu Leu Tyr His Val
20 25 30

gaa gtt ccc acg att gcg ctg gtc atc ggc ttt ggc gcg cag ctt ctg 144
Glu Val Pro Thr Ile Ala Leu Val Ile Gly Phe Gly Ala Gln Leu Leu
35 40 45

atc ggt gtg atg agt tat cta ctg ccg tgc acg atg ggt ggc ggc gcg 192
Ile Gly Val Met Ser Tyr Leu Leu Pro Ser Thr Met Gly Gly Gly Ala
50 55 60

agc gcg gtg cgg act gga acg cac att tta aac act gcg ggg ctg ttt 240
Ser Ala Val Arg Thr Gly Thr His Ile Leu Asn Thr Ala Gly Leu Phe
65 70 75 80

agg tgg acg ctg atc aac ggt ggc ctg gcg att tgg ctg ctc acc gac 288
Arg Trp Thr Leu Ile Asn Gly Gly Leu Ala Ile Trp Leu Leu Thr Asp
85 90 95

aat tgc tgg ctg cgc gtc gtg gtg tct ctg ctg agt atc gga gcg ttg 336
Asn Ser Trp Leu Arg Val Val Val Ser Leu Leu Ser Ile Gly Ala Leu
100 105 110

gca gtt ttt gtc att ctg ctg ccc aag gct gtg cgg gcg cag cgc gga 384
Ala Val Phe Val Ile Leu Leu Pro Lys Ala Val Arg Ala Gln Arg Gly
115 120 125

gtg atc acc aaa aag cgc gaa cca att act ccg ccg gag gag cct cga 432
Val Ile Thr Lys Lys Arg Glu Pro Ile Thr Pro Pro Glu Glu Pro Arg
130 135 140

ctc aat caa att acc gcg gga atc tct gtg ctt gcc ctg att ttg gca 480
Leu Asn Gln Ile Thr Ala Gly Ile Ser Val Leu Ala Leu Ile Leu Ala
145 150 155 160

gca ttc ggt ggg ctc aac ccc ggt gtt gcg ccg gtg gca agc tca aat 528
Ala Phe Gly Gly Leu Asn Pro Gly Val Ala Pro Val Ala Ser Ser Asn
165 170 175

gaa gac gtc tat gct gtg acc att acc gca ggt gac atg gtg ttt atc 576
Glu Asp Val Tyr Ala Val Thr Ile Thr Ala Gly Asp Met Val Phe Ile

180	185	190	
cct gat gtg att gaa gtg cct gct ggt aaa tca ctc gaa gtc acg atg			624
Pro Asp Val Ile Glu Val Pro Ala Gly Lys Ser Leu Glu Val Thr Met			
195	200	205	
ctc aac gaa gac gac atg gtg cac gat ctg aaa ttt gcc aac ggt gtg			672
Leu Asn Glu Asp Asp Met Val His Asp Leu Lys Phe Ala Asn Gly Val			
210	215	220	
caa acc gga cgt gtg gcg cca ggt gat gaa att acg gtg acc gtc ggc			720
Gln Thr Gly Arg Val Ala Pro Gly Asp Glu Ile Thr Val Thr Val Gly			
225	230	235	240
gat att tcc gaa gac atg gac ggc tgg tgc acc atc gct ggg cac cgc			768
Asp Ile Ser Glu Asp Met Asp Gly Trp Cys Thr Ile Ala Gly His Arg			
245	250	255	
gcg caa gga atg gat ctg gaa gta aag gtt gcg gct ccg aat			810
Ala Gln Gly Met Asp Leu Glu Val Lys Val Ala Ala Pro Asn			
260	265	270	
taaccaagggtctgtgaaaa act			833
<210> 956			
<211> 270			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 956			
Thr Ser Thr Ser Thr Thr Ala Pro Leu Trp Leu Val Gly Thr Leu Val			
1	5	10	15
Trp Leu Ala Val Gln Ala Val Met His Asp Gly Glu Leu Tyr His Val			
20	25	30	
Glu Val Pro Thr Ile Ala Leu Val Ile Gly Phe Gly Ala Gln Leu Leu			
35	40	45	
Ile Gly Val Met Ser Tyr Leu Leu Pro Ser Thr Met Gly Gly Gly Ala			
50	55	60	
Ser Ala Val Arg Thr Gly Thr His Ile Leu Asn Thr Ala Gly Leu Phe			
65	70	75	80
Arg Trp Thr Leu Ile Asn Gly Gly Leu Ala Ile Trp Leu Leu Thr Asp			
85	90	95	
Asn Ser Trp Leu Arg Val Val Val Ser Leu Leu Ser Ile Gly Ala Leu			
100	105	110	
Ala Val Phe Val Ile Leu Leu Pro Lys Ala Val Arg Ala Gln Arg Gly			
115	120	125	
Val Ile Thr Lys Lys Arg Glu Pro Ile Thr Pro Pro Glu Glu Pro Arg			
130	135	140	
Leu Asn Gln Ile Thr Ala Gly Ile Ser Val Leu Ala Leu Ile Leu Ala			
145	150	155	160

Ala Phe Gly Gly Leu Asn Pro Gly Val Ala Pro Val Ala Ser Ser Asn
 165 170 175

Glu Asp Val Tyr Ala Val Thr Ile Thr Ala Gly Asp Met Val Phe Ile
 180 185 190

Pro Asp Val Ile Glu Val Pro Ala Gly Lys Ser Leu Glu Val Thr Met
 195 200 205

Leu Asn Glu Asp Asp Met Val His Asp Leu Lys Phe Ala Asn Gly Val
 210 215 220

Gln Thr Gly Arg Val Ala Pro Gly Asp Glu Ile Thr Val Thr Val Gly
 225 230 235 240

Asp Ile Ser Glu Asp Met Asp Gly Trp Cys Thr Ile Ala Gly His Arg
 245 250 255

Ala Gln Gly Met Asp Leu Glu Val Lys Val Ala Ala Pro Asn
 260 265 270

<210> 957

<211> 1506

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1483)

<223> RXN02044

<400> 957

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tagttggtgc aaaccaataa tagctatagc cccaatacaa atg gtc acc cca atc 115
 Met Val Thr Pro Ile 5

atg ggg aat tcg aac tct atc ctg ggc att tac cgt cag aaa atc caa 163
 Met Gly Asn Ser Asn Ser Ile Leu Gly Ile Tyr Arg Gln Lys Ile Gln 10 15 20

aat cga cat ttg gtt tct acg ctt ttt agg gca tac ttc cca atc gtg 211
 Asn Arg His Leu Val Ser Thr Leu Phe Arg Ala Tyr Phe Pro Ile Val 25 30 35

acc gag ctg att att tta ttg att gtt atc gtg acg gcg ctc gcc ttc 259
 Thr Glu Leu Ile Ile Leu Leu Ile Val Ile Val Thr Ala Leu Ala Phe 40 45 50

gat ttc aca aac gga ttc cac gac acc ggc aat gcg atg gcc aca tcc 307
 Asp Phe Thr Asn Gly Phe His Asp Thr Gly Asn Ala Met Ala Thr Ser 55 60 65

att gcc aca ggc gct cta aaa cct aaa gtc gcc gtg gca cta tcc gcc 355
 Ile Ala Thr Gly Ala Leu Lys Pro Lys Val Ala Val Ala Leu Ser Ala 70 75 80 85

tca ctg aac ctt gtt ggc gca ttc ctc tct gta gaa gtt gcg aca act 403
 Ser Leu Asn Leu Val Gly Ala Phe Leu Ser Val Glu Val Ala Thr Thr

	90	95	100	
	gtt gcc aaa ggc gtt gtt gac ctc gac caa ttc gac cta agc aat gcc			451
	Val Ala Lys Gly Val Val Asp Leu Asp Gln Phe Asp Leu Ser Asn Ala			
	105	110	115	
	tgg gat tcc cac cag ctc ctg ctt gtc gtc ttc gcc ggc ctc att ggc			499
	Trp Asp Ser Ser His Gln Leu Leu Leu Val Val Phe Ala Gly Leu Ile Gly			
	120	125	130	
	gcc atc gtc tgg aac ctt ctg acc tgg ctg cta ggc att cct tcc agc			547
	Ala Ile Val Trp Asn Leu Leu Thr Trp Leu Leu Gly Ile Pro Ser Ser			
	135	140	145	
	tcc tct cac gca ctt ttc ggt ggc ctc att ggc gcc gca att gct tca			595
	Ser Ser His Ala Leu Phe Gly Gly Leu Ile Gly Ala Ala Ile Ala Ser			
	150	155	160	165
	ctc ggt ttc ggc gga gtg gtg tgg gaa ggt gtc ttg tcc aag atg atc			643
	Leu Gly Phe Gly Gly Val Val Trp Glu Gly Val Leu Ser Lys Met Ile			
	170	175	180	
	atc cca gca ttg gct gca cca gtt gtt gca ggt ctc gtg gcc gcc atc			691
	Ile Pro Ala Leu Ala Ala Pro Val Val Ala Gly Leu Val Ala Ala Ile			
	185	190	195	
	ggc act ttc gcc gtg tac agc atc aca aag gca gtt gga gac aac gag			739
	Gly Thr Phe Ala Val Tyr Ser Ile Thr Lys Ala Val Gly Asp Asn Glu			
	200	205	210	
	aag aac cgt tac ttc cgc tgg ggt cag atc ggc tcc gct tcc ttg gtt			787
	Lys Asn Arg Tyr Phe Arg Trp Gly Gln Ile Gly Ser Ala Ser Leu Val			
	215	220	225	
	tcc ctg gca cac ggc acc aac gat gcc cag aag acc atg ggc gtt atc			835
	Ser Leu Ala His Gly Thr Asn Asp Ala Gln Lys Thr Met Gly Val Ile			
	230	235	240	245
	ttc ctt tcc ctg gtt gcc acc ggt cac ctg gga act gac gct gac atc			883
	Phe Leu Ser Leu Val Ala Thr Gly His Leu Gly Thr Asp Ala Asp Ile			
	250	255	260	
	cca ttc tgg gtc aag gct aca tgt gca ttg gca atc gca atc ggt acc			931
	Pro Phe Trp Val Lys Ala Thr Cys Ala Leu Ala Ile Ala Ile Gly Thr			
	265	270	275	
	tac ttg ggt ggt tgg cgc gtt atc cgc aca ctg ggc aaa ggc ttg gtt			979
	Tyr Leu Gly Gly Trp Arg Val Ile Arg Thr Leu Gly Lys Gly Leu Val			
	280	285	290	
	gag att gat tcc cct cag ggc atg gca gca gaa act tct tct gca gca			1027
	Glu Ile Asp Ser Pro Gln Gly Met Ala Ala Glu Thr Ser Ser Ala Ala			
	295	300	305	
	atc att ttg act tct tcc cac ttc ggt atg gca ctg tcc acc act cac			1075
	Ile Ile Leu Thr Ser Ser His Phe Gly Met Ala Leu Ser Thr Thr His			
	310	315	320	325
	gtt gct act ggc tcc atc atg ggt acc ggc att gga cgt aaa ggg gcg			1123
	Val Ala Thr Gly Ser Ile Met Gly Thr Gly Ile Gly Arg Lys Gly Ala			
	330	335	340	

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aag gtt cgt tgg tcc gtc gca gga cgc atg gca atg gcc tgg gtt atc 1171
Lys Val Arg Trp Ser Val Ala Gly Arg Met Ala Met Ala Trp Val Ile
345 350 355

acc ctc cct gcc tcc gcg atc gtt ggc gtt ttc tgc tgg tgg gta gct 1219
Thr Leu Pro Ala Ser Ala Ile Val Gly Val Phe Cys Trp Trp Val Ala
360 365 370

cac gga att ggt ctt atc agc tca gac ctc ctc gga gtc ctc gtt gca 1267
His Gly Ile Gly Leu Ile Ser Ser Asp Leu Leu Gly Val Leu Val Ala
375 380 385

ttc gcc att ctg gtc att ctg tct ggc tac att tac gcc cgt tcc cgt 1315
Phe Ala Ile Leu Val Ile Leu Ser Gly Tyr Ile Tyr Ala Arg Ser Arg
390 395 400 405

cgc gtg cct gtt gat cca agc aac gtc aac gct gac tgg aat gaa gaa 1363
Arg Val Pro Val Asp Pro Ser Asn Val Asn Ala Asp Trp Asn Glu Glu
410 415 420

tca aac agc gtg gaa cct gca aca cct tcc gcc ccg gct gct tct gag 1411
Ser Asn Ser Val Glu Pro Ala Thr Pro Ser Ala Pro Ala Ala Ser Glu
425 430 435

att aca gaa gct cct gcc gct cca gcc gct caa gcc gtt caa gat ctc 1459
Ile Thr Glu Ala Pro Ala Ala Pro Ala Ala Gln Ala Val Gln Asp Leu
440 445 450

aac aac gag aat gag gta acc aag taatgaactt cgctactatt ttc 1506
Asn Asn Glu Asn Glu Val Thr Lys
455 460

<210> 958
<211> 461
<212> PRT
<213> Corynebacterium glutamicum

<400> 958
Met Val Thr Pro Ile Met Gly Asn Ser Asn Ser Ile Leu Gly Ile Tyr
1 5 10 15

Arg Gln Lys Ile Gln Asn Arg His Leu Val Ser Thr Leu Phe Arg Ala
20 25 30

Tyr Phe Pro Ile Val Thr Glu Leu Ile Ile Leu Leu Ile Val Ile Val
35 40 45

Thr Ala Leu Ala Phe Asp Phe Thr Asn Gly Phe His Asp Thr Gly Asn
50 55 60

Ala Met Ala Thr Ser Ile Ala Thr Gly Ala Leu Lys Pro Lys Val Ala
65 70 75 80

Val Ala Leu Ser Ala Ser Leu Asn Leu Val Gly Ala Phe Leu Ser Val
85 90 95

Glu Val Ala Thr Thr Val Ala Lys Gly Val Val Asp Leu Asp Gln Phe
100 105 110

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Asp Leu Ser Asn Ala Trp Asp Ser His Gln Leu Leu Val Val Phe
 115 120 125
 Ala Gly Leu Ile Gly Ala Ile Val Trp Asn Leu Leu Thr Trp Leu Leu
 130 135 140
 Gly Ile Pro Ser Ser Ser Ser His Ala Leu Phe Gly Gly Leu Ile Gly
 145 150 155 160
 Ala Ala Ile Ala Ser Leu Gly Phe Gly Gly Val Val Trp Glu Gly Val
 165 170 175
 Leu Ser Lys Met Ile Ile Pro Ala Leu Ala Ala Pro Val Val Ala Gly
 180 185 190
 Leu Val Ala Ala Ile Gly Thr Phe Ala Val Tyr Ser Ile Thr Lys Ala
 195 200 205
 Val Gly Asp Asn Glu Lys Asn Arg Tyr Phe Arg Trp Gly Gln Ile Gly
 210 215 220
 Ser Ala Ser Leu Val Ser Leu Ala His Gly Thr Asn Asp Ala Gln Lys
 225 230 235 240
 Thr Met Gly Val Ile Phe Leu Ser Leu Val Ala Thr Gly His Leu Gly
 245 250 255
 Thr Asp Ala Asp Ile Pro Phe Trp Val Lys Ala Thr Cys Ala Leu Ala
 260 265 270
 Ile Ala Ile Gly Thr Tyr Leu Gly Gly Trp Arg Val Ile Arg Thr Leu
 275 280 285
 Gly Lys Gly Leu Val Glu Ile Asp Ser Pro Gln Gly Met Ala Ala Glu
 290 295 300
 Thr Ser Ser Ala Ala Ile Ile Leu Thr Ser Ser His Phe Gly Met Ala
 305 310 315 320
 Leu Ser Thr Thr His Val Ala Thr Gly Ser Ile Met Gly Thr Gly Ile
 325 330 335
 Gly Arg Lys Gly Ala Lys Val Arg Trp Ser Val Ala Gly Arg Met Ala
 340 345 350
 Met Ala Trp Val Ile Thr Leu Pro Ala Ser Ala Ile Val Gly Val Phe
 355 360 365
 Cys Trp Trp Val Ala His Gly Ile Gly Leu Ile Ser Ser Asp Leu Leu
 370 375 380
 Gly Val Leu Val Ala Phe Ala Ile Leu Val Ile Leu Ser Gly Tyr Ile
 385 390 395 400
 Tyr Ala Arg Ser Arg Arg Val Pro Val Asp Pro Ser Asn Val Asn Ala
 405 410 415
 Asp Trp Asn Glu Glu Ser Asn Ser Val Glu Pro Ala Thr Pro Ser Ala
 420 425 430
 Pro Ala Ala Ser Glu Ile Thr Glu Ala Pro Ala Ala Pro Ala Ala Gln

435

440

445

Ala Val Gln Asp Leu Asn Asn Glu Asn Glu Val Thr Lys
 450 455 460

<210> 959

<211> 384

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(361)

<223> RXN02045

<400> 959

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ccgttcaaga tctcaacaac gagaatgagg taaccaagta atg aac ttc gct act 115
 Met Asn Phe Ala Thr
 1 5

att ttc gga agc atc ttt gag gtc acc ctc gtg ggc att ttg ctc ggc 163
 Ile Phe Gly Ser Ile Phe Glu Val Thr Leu Val Gly Ile Leu Leu Gly
 10 15 20

gca ggc ctt cca gcc ctt ttt gca tta gga atc cgc ttt gct cac agc 211
 Ala Gly Leu Pro Ala Leu Phe Ala Leu Gly Ile Arg Phe Ala His Ser
 25 30 35

cct tct tcc aac ggc acc aac gct ctt gga aaa att gct tca acc atc 259
 Pro Ser Ser Asn Gly Thr Asn Ala Leu Gly Lys Ile Ala Ser Thr Ile
 40 45 50

tgc ttt gcc atc att gcg gtt gct atc atc gct ggc att ctc tgg gtc 307
 Cys Phe Ala Ile Ile Ala Val Ala Ile Ile Ala Gly Ile Leu Trp Val
 55 60 65

acc aaa gca acg atc tac cag tac tct ggt ttc gac att ttc ggc act 355
 Thr Lys Ala Thr Ile Tyr Gln Tyr Ser Gly Phe Asp Ile Phe Gly Thr
 70 75 80 85

gaa ggc taaaagcacc agctgcgaat aac 384
 Glu Gly

<210> 960

<211> 87

<212> PRT

<213> Corynebacterium glutamicum

<400> 960

Met Asn Phe Ala Thr Ile Phe Gly Ser Ile Phe Glu Val Thr Leu Val
 1 5 10 15

Gly Ile Leu Leu Gly Ala Gly Leu Pro Ala Leu Phe Ala Leu Gly Ile
 20 25 30

Arg Phe Ala His Ser Pro Ser Ser Asn Gly Thr Asn Ala Leu Gly Lys

```

          35              40              45
Ile Ala Ser Thr Ile Cys Phe Ala Ile Ile Ala Val Ala Ile Ile Ala
   50              55              60
Gly Ile Leu Trp Val Thr Lys Ala Thr Ile Tyr Gln Tyr Ser Gly Phe
   65              70              75              80
Asp Ile Phe Gly Thr Glu Gly
          85

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<210> 961
 <211> 384
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(361)
 <223> FRXA02045

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cogttcaaga tctcaacaac gagaatgagg taaccaagta atg aac ttc gct act 115
          Met Asn Phe Ala Thr
          1              5
att ttc gga agc atc ttt gag gtc acc ctc gtg ggc att ttg ctc ggc 163
Ile Phe Gly Ser Ile Phe Glu Val Thr Leu Val Gly Ile Leu Leu Gly
          10              15              20
gca ggc ctt cca gcc ctt ttt gca tta gga atc cgc ttt gct cac agc 211
Ala Gly Leu Pro Ala Leu Phe Ala Leu Gly Ile Arg Phe Ala His Ser
          25              30              35
cct tct tcc aac ggc acc aac gct ctt gga aaa att gct tca acc atc 259
Pro Ser Ser Asn Gly Thr Asn Ala Leu Gly Lys Ile Ala Ser Thr Ile
          40              45              50
tgc ttt gcc atc att gcg gtt gct atc atc gct ggc att ctc tgg gtc 307
Cys Phe Ala Ile Ile Ala Val Ala Ile Ile Ala Gly Ile Leu Trp Val
          55              60              65
acc aaa gca acg atc tac cag tac tct ggt ttc gac att ttc gcc act 355
Thr Lys Ala Thr Ile Tyr Gln Tyr Ser Gly Phe Asp Ile Phe Gly Thr
          70              75              80              85
gaa ggc taaaagcacc agctgcgaat aac 384
Glu Gly

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<210> 962
 <211> 87
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 962
 Met Asn Phe Ala Thr Ile Phe Gly Ser Ile Phe Glu Val Thr Leu Val

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      1               5               10               15
Gly Ile Leu Leu Gly Ala Gly Leu Pro Ala Leu Phe Ala Leu Gly Ile
      20               25               30
Arg Phe Ala His Ser Pro Ser Ser Asn Gly Thr Asn Ala Leu Gly Lys
      35               40               45
Ile Ala Ser Thr Ile Cys Phe Ala Ile Ile Ala Val Ala Ile Ile Ala
      50               55               60
Gly Ile Leu Trp Val Thr Lys Ala Thr Ile Tyr Gln Tyr Ser Gly Phe
      65               70               75               80
Asp Ile Phe Gly Thr Glu Gly
      85

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<210> 963

<211> 732

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(709)

<223> RXN02049

<400> 963

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atctggagtt gccggagttt ccttctggtg gtttggacta  gtg cgc tat ctg acg  115
                                     Val Arg Tyr Leu Thr
                                     1               5

```

```

ctg gcc aca atc atc gca ggt ctc tcc ggg ttc gtc gtc atc atc atc  163
Leu Ala Thr Ile Ile Ala Gly Leu Ser Gly Phe Val Val Ile Ile Ile
               10               15               20

```

```

gct gcc tgg gcc ctt ggt gat tcc agc caa ctt tcc gaa gaa ttc acc  211
Ala Ala Trp Ala Leu Gly Asp Ser Ser Gln Leu Ser Glu Glu Phe Thr
               25               30               35

```

```

gcc tac tgg ggt ctg ttc ttt gca gga acc gga gtg ctg act ggg ttg  259
Ala Tyr Trp Gly Leu Phe Phe Ala Gly Thr Gly Val Leu Thr Gly Leu
               40               45               50

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```

acg cag gag acg acc cgc gcg gtg acg gcc ggt tct cgt ggt ggt tct  307
Thr Gln Glu Thr Thr Arg Ala Val Thr Ala Gly Ser Arg Gly Gly Ser
               55               60               65

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```

cgt ggt ggg cgt gct ggt tct gtt gtt gga ttt agg cgt ttt ttg ttt  355
Arg Gly Gly Arg Ala Gly Ser Val Val Gly Phe Arg Pro Phe Leu Phe
               70               75               80               85

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```

agc ttc gtg gtt gcg gcg ata gtg ctc gtg gtg ctt gcc gct tcg gcg  403
Ser Phe Val Val Ala Ala Ile Val Leu Val Val Leu Gly Ala Ser Ala
               90               95               100

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ccg ctg tgg atc gcc cag ctt tta agt aat ttg caa ggt gtt ggt gtt  451
Pro Leu Trp Ile Gly Gln Leu Leu Ser Asn Leu Gln Gly Val Gly Val

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	105	110	115	
	ggg cta ctt gct gta ggt ctt gct agc tac gcg atc caa gcg aca atc			499
	Gly Leu Leu Ala Val Gly Leu Ala Ser Tyr Ala Ile Gln Ala Thr Ile			
	120	125	130	
	tcc gcc att ttt gtc cgg ctg cca att gtg gaa aga gta tgc ctc gct			547
	Ser Gly Ile Phe Val Arg Leu Pro Ile Val Glu Arg Val Cys Leu Ala			
	135	140	145	
	gat ttc ttt gga cac cgg cgt gcg cat ggt ttt aac tgt tgc cgc ctg			595
	Asp Phe Phe Gly His Arg Arg Ala His Gly Phe Asn Cys Cys Arg Leu			
	150	155	160	165
	gtt gct ggg tta tca att gct ggc gtt ctt gat cat cac cgt tgt ggg			643
	Val Ala Gly Leu Ser Ile Ala Gly Val Leu Asp His His Arg Cys Gly			
	170	175	180	
	atc aat atc ctg gct ggt cat cgt gct gtg ctt cgg ttc ggt gcg ttc			691
	Ile Asn Ile Leu Ala Gly His Arg Ala Val Leu Arg Phe Gly Ala Phe			
	185	190	195	
	cgt ttt ggg atc ggt tgc tgatgtttca cggggcggtt tca			732
	Arg Phe Gly Ile Gly Cys			
	200			
	<210> 964			
	<211> 203			
	<212> PRT			
	<213> <i>Corynebacterium glutamicum</i>			
	<400> 964			
	Val Arg Tyr Leu Thr Leu Ala Thr Ile Ile Ala Gly Leu Ser Gly Phe			
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	Val Val Ile Ile Ile Ala Ala Trp Ala Leu Gly Asp Ser Ser Gln Leu			
	20	25	30	
	Ser Glu Glu Phe Thr Ala Tyr Trp Gly Leu Phe Phe Ala Gly Thr Gly			
	35	40	45	
	Val Leu Thr Gly Leu Thr Gln Glu Thr Thr Arg Ala Val Thr Ala Gly			
	50	55	60	
	Ser Arg Gly Gly Ser Arg Gly Gly Arg Ala Gly Ser Val Val Gly Phe			
	65	70	75	80
	Arg Pro Phe Leu Phe Ser Phe Val Val Ala Ala Ile Val Leu Val Val			
	85	90	95	
	Leu Gly Ala Ser Ala Pro Leu Trp Ile Gly Gln Leu Leu Ser Asn Leu			
	100	105	110	
	Gln Gly Val Gly Val Gly Leu Leu Ala Val Gly Leu Ala Ser Tyr Ala			
	115	120	125	
	Ile Gln Ala Thr Ile Ser Gly Ile Phe Val Arg Leu Pro Ile Val Glu			
	130	135	140	
	Arg Val Cys Leu Ala Asp Phe Phe Gly His Arg Arg Ala His Gly Phe			


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145                      150                      155                      160
Asn Cys Cys Arg Leu Val Ala Gly Leu Ser Ile Ala Gly Val Leu Asp
                      165                      170                      175

His His Arg Cys Gly Ile Asn Ile Leu Ala Gly His Arg Ala Val Leu
                      180                      185                      190

Arg Phe Gly Ala Phe Arg Phe Gly Ile Gly Cys
                      195                      200

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<210> 965
 <211> 570
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(547)
 <223> FRXA02049

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<400> 965
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atctggaggt gccggagttt ccttctgggt gttggacta gtg cgc tat ctg acg 115
                      Val Arg Tyr Leu Thr
                      1                      5

ctg gcc aca atc atc gca ggt ctc tcc ggg ttc gtc gtc atc atc atc 163
Leu Ala Thr Ile Ile Ala Gly Leu Ser Gly Phe Val Val Ile Ile Ile
                      10                      15                      20

gct gcc tgg gcc ctt ggt gat tcc agc caa ctt tcc gaa gaa ttc acc 211
Ala Ala Trp Ala Leu Gly Asp Ser Ser Gln Leu Ser Glu Glu Phe Thr
                      25                      30                      35

gcc tac tgg ggt ctg ttc ttt gca gga acc gga gtg ctg act ggg ttg 259
Ala Tyr Trp Gly Leu Phe Phe Ala Gly Thr Gly Val Leu Thr Gly Leu
                      40                      45                      50

acg cag gag acg acc cgc gcg gtg acg gcc ggt tct cgt ggt ggt tct 307
Thr Gln Glu Thr Thr Arg Ala Val Thr Ala Gly Ser Arg Gly Gly Ser
                      55                      60                      65

cgt ggt ggg cgt gct ggt tct gtt gtt gga ttt agg ccg ttt ttg ttt 355
Arg Gly Gly Arg Ala Gly Ser Val Val Gly Phe Arg Pro Phe Leu Phe
                      70                      75                      80                      85

agc ttc gtg gtt gcg gcg ata gtg ctc gtg gtg ctt ggc gct tcg gcg 403
Ser Phe Val Val Ala Ala Ile Val Leu Val Val Leu Gly Ala Ser Ala
                      90                      95                      100

ccg ctg tgg atc ggc cag ctt tta agt aat ttg caa ggt gtt ggt gtt 451
Pro Leu Trp Ile Gly Gln Leu Leu Ser Asn Leu Gln Gly Val Gly Val
                      105                      110                      115

ggg cta ctt gct gta ggt ctt gct agc tac gcg atc caa gcg aca atc 499
Gly Leu Leu Ala Val Gly Leu Ala Ser Tyr Ala Ile Gln Ala Thr Ile
                      120                      125                      130

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tcc ggc att ttt gtc cgg ctg cca att gtg gaa aag agt atg cct cgc 547
 Ser Gly Ile Phe Val Arg Leu Pro Ile Val Glu Lys Ser Met Pro Arg
 135 140 145

tgatttcttt ggacaccggc gtg 570

<210> 966

<211> 149

<212> PRT

<213> Corynebacterium glutamicum

<400> 966

Val Arg Tyr Leu Thr Leu Ala Thr Ile Ile Ala Gly Leu Ser Gly Phe
 1 5 10 15

Val Val Ile Ile Ile Ala Ala Trp Ala Leu Gly Asp Ser Ser Gln Leu
 20 25 30

Ser Glu Glu Phe Thr Ala Tyr Trp Gly Leu Phe Phe Ala Gly Thr Gly
 35 40 45

Val Leu Thr Gly Leu Thr Gln Thr Thr Arg Ala Val Thr Ala Gly
 50 55 60

Ser Arg Gly Gly Ser Arg Gly Gly Arg Ala Gly Ser Val Val Gly Phe
 65 70 75 80

Arg Pro Phe Leu Phe Ser Phe Val Val Ala Ala Ile Val Leu Val Val
 85 90 95

Leu Gly Ala Ser Ala Pro Leu Trp Ile Gly Gln Leu Leu Ser Asn Leu
 100 105 110

Gln Gly Val Gly Val Gly Leu Leu Ala Val Gly Leu Ala Ser Tyr Ala
 115 120 125

Ile Gln Ala Thr Ile Ser Gly Ile Phe Val Arg Leu Pro Ile Val Glu
 130 135 140

Lys Ser Met Pro Arg
 145

<210> 967

<211> 918

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(895)

<223> RXN02050

<400> 967

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cggtgccaa ttgtggaaag agtatgcctc gctgatttct ttg gac acc ggc gtg 115
 Leu Asp Thr Gly Val
 1 5

cgc atg gtt tta act gtt gcc gcc tgg ttg ctg ggt tat caa ttg ctg 163
 Arg Met Val Leu Thr Val Ala Ala Trp Leu Leu Gly Tyr Gln Leu Leu
 10 15 20

gcg ttc ttg atc atc acc gtt gtg gga tca ata tcc tgg ctg gtc atc 211
 Ala Phe Leu Ile Ile Thr Val Val Gly Ser Ile Ser Trp Leu Val Ile
 25 30 35

gtg ctg tgc ttc ggt tgg gtg cgt tcc gtt ttg gga tgg gtt gct gat 259
 Val Leu Cys Phe Gly Ser Val Arg Ser Val Leu Gly Ser Val Ala Asp
 40 45 50

gtt tca cgg ggc gtt ttc atc cga cag gct ctg ctt gcg atg gca gca 307
 Val Ser Arg Gly Val Phe Ile Arg Gln Ala Leu Leu Ala Met Ala Ala
 55 60 65

tcc ggc gcc acg gca gtg ctg att act ggt ttc ccg acc ctg ctg aaa 355
 Ser Gly Ala Thr Ala Val Leu Ile Thr Gly Phe Pro Thr Leu Leu Lys
 70 75 80 85

ttc acg aac cct tca gcg gtt gca gga ggg gtt tgg atg gcc gct gtt 403
 Phe Thr Asn Pro Ser Ala Val Ala Gly Gly Val Ser Met Ala Ala Val
 90 95 100

tcc tac gcc gtc atc ctg acc cgc gct ccc ctg ctg gtt ccg ctg cag 451
 Ser Tyr Ala Val Ile Leu Thr Arg Ala Pro Leu Leu Val Pro Leu Gln
 105 110 115

caa ttc caa tgg gcg atc atc gtt cgt ttt gtc aaa ggt acg tcc ggt 499
 Gln Phe Gln Ser Ala Ile Ile Val Arg Phe Val Lys Gly Thr Ser Gly
 120 125 130

cca ttg aaa act ttg gcg ggt ccg ttg gca att gtg tgg gca gtc gga 547
 Pro Leu Lys Thr Leu Ala Gly Pro Leu Ala Ile Val Trp Ala Val Gly
 135 140 145

ctt gtt gga gct ggt ctt gca tgg tta gtt gcc cca tgg atc ctg gac 595
 Leu Val Gly Ala Gly Leu Ala Trp Leu Val Gly Pro Trp Ile Leu Asp
 150 155 160 165

gtt gta ctc caa aag gaa ctc ttc gcg gtc cct gcc tgg cta ctc gcg 643
 Val Val Leu Gln Lys Glu Leu Phe Ala Val Pro Gly Trp Leu Leu Ala
 170 175 180

atg ctc acc tta gcc gcc acc acc acc gct tca ttg atg gtg tcc gcc 691
 Met Leu Thr Leu Gly Ala Thr Thr Thr Ala Ser Leu Met Val Ser Gly
 185 190 195

tgc gcg gcg atc gcc ttt gaa cgt cac ggg atc tat ctc acc gga tgg 739
 Cys Ala Ala Ile Ala Phe Glu Arg His Gly Ile Tyr Leu Thr Gly Trp
 200 205 210

gtt gtt gcc act gtt gtt gcc gtc gga ttc ttg ctg gga cct ttt gat 787
 Val Val Ala Thr Val Val Ala Val Gly Phe Leu Leu Gly Pro Phe Asp
 215 220 225

ttg gcc gtc gct gct gcc ctt gcg ctc att gtt gcc cca ctc tgc ggt 835
 Leu Gly Val Ala Ala Gly Leu Ala Leu Ile Val Gly Pro Leu Cys Gly
 230 235 240 245

ttg ctg gta cac atg gga gcg ttt gtt ggt ggg gat ccg aat ccg gtt 883

Leu Leu Val His Met Gly Ala Phe Val Gly Gly Asp Arg Asn Arg Val
 250 255 260

ttg act gcg gga tagtttggtt tgattggggg att
 Leu Thr Ala Gly
 265

918

<210> 968

<211> 265

<212> PRT

<213> Corynebacterium glutamicum

<400> 968

Leu Asp Thr Gly Val Arg Met Val Leu Thr Val Ala Ala Trp Leu Leu
 1 5 10 15

Gly Tyr Gln Leu Leu Ala Phe Leu Ile Ile Thr Val Val Gly Ser Ile
 20 25 30

Ser Trp Leu Val Ile Val Leu Cys Phe Gly Ser Val Arg Ser Val Leu
 35 40 45

Gly Ser Val Ala Asp Val Ser Arg Gly Val Phe Ile Arg Gln Ala Leu
 50 55 60

Leu Ala Met Ala Ala Ser Gly Ala Thr Ala Val Leu Ile Thr Gly Phe
 65 70 75 80

Pro Thr Leu Leu Lys Phe Thr Asn Pro Ser Ala Val Ala Gly Gly Val
 85 90 95

Ser Met Ala Ala Val Ser Tyr Ala Val Ile Leu Thr Arg Ala Pro Leu
 100 105 110

Leu Val Pro Leu Gln Gln Phe Gln Ser Ala Ile Ile Val Arg Phe Val
 115 120 125

Lys Gly Thr Ser Gly Pro Leu Lys Thr Leu Ala Gly Pro Leu Ala Ile
 130 135 140

Val Trp Ala Val Gly Leu Val Gly Ala Gly Leu Ala Trp Leu Val Gly
 145 150 155 160

Pro Trp Ile Leu Asp Val Val Leu Gln Lys Glu Leu Phe Ala Val Pro
 165 170 175

Gly Trp Leu Leu Ala Met Leu Thr Leu Gly Ala Thr Thr Thr Ala Ser
 180 185 190

Leu Met Val Ser Gly Cys Ala Ala Ile Ala Phe Glu Arg His Gly Ile
 195 200 205

Tyr Leu Thr Gly Trp Val Val Ala Thr Val Val Ala Val Gly Phe Leu
 210 215 220

Leu Gly Pro Phe Asp Leu Gly Val Ala Ala Gly Leu Ala Leu Ile Val
 225 230 235 240

Gly Pro Leu Cys Gly Leu Leu Val His Met Gly Ala Phe Val Gly Gly
 245 250 255

Asp Arg Asn Arg Val Leu Thr Ala Gly
260 265

<210> 969

<211> 495

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(472)

<223> FRXA02050

<400> 969

cgcgctcccc tgctgggtcc gctgcagcaa ttccaatcgg cgatcatcgt tegttttgtc 60

aaaggtaccg tccggtccat tgaaaacttt ggcgggtccg ttg gca att gtg tgg 115
Leu Ala Ile Val Trp
1 5

gca gtc gga ctt gtt gga gct ggt ctt gca tgg tta gtt ggc cca tgg 163
Ala Val Gly Leu Val Gly Ala Gly Leu Ala Trp Leu Val Gly Pro Trp
10 15 20

atc ctg gac gtt gta ctc caa aag gaa ctc ttc gcg gtc cct ggc tgg 211
Ile Leu Asp Val Val Leu Gln Lys Glu Leu Phe Ala Val Pro Gly Trp
25 30 35

cta ctc gcg atg ctc acc tta ggc gcc acc acc acc gct tca ttg atg 259
Leu Leu Ala Met Leu Thr Leu Gly Ala Thr Thr Thr Ala Ser Leu Met
40 45 50

gtg tcc ggc tgc gcg gcg atc gcc ttt gaa cgt cac ggg atc tat ctc 307
Val Ser Gly Cys Ala Ala Ile Ala Phe Glu Arg His Gly Ile Tyr Leu
55 60 65

acc gga tgg gtt gtt gcc act gtt gtt gcc gtc gga ttc ttg ctg gga 355
Thr Gly Trp Val Val Ala Thr Val Val Ala Val Gly Phe Leu Leu Gly
70 75 80 85

cct ttt gat ttg ggc gtc gct gct ggc ctt gcg ctc att gtt ggc cca 403
Pro Phe Asp Leu Gly Val Ala Ala Gly Leu Ala Leu Ile Val Gly Pro
90 95 100

ctc tgc ggt ttg ctg gta cac atg gga gcg ttt gtt ggt ggg gat cgg 451
Leu Cys Gly Leu Leu Val His Met Gly Ala Phe Val Gly Gly Asp Arg
105 110 115

aat cgg gtt ttg act gcg gga tagtttggtt tgattggggg att 495
Asn Arg Val Leu Thr Ala Gly
120

<210> 970

<211> 124

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 970

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Leu Ala Ile Val Trp Ala Val Gly Leu Val Gly Ala Gly Leu Ala Trp
 1             5             10             15

Leu Val Gly Pro Trp Ile Leu Asp Val Val Leu Gln Lys Glu Leu Phe
             20             25             30

Ala Val Pro Gly Trp Leu Leu Ala Met Leu Thr Leu Gly Ala Thr Thr
 35             40             45

Thr Ala Ser Leu Met Val Ser Gly Cys Ala Ala Ile Ala Phe Glu Arg
 50             55             60

His Gly Ile Tyr Leu Thr Gly Trp Val Val Ala Thr Val Val Ala Val
 65             70             75             80

Gly Phe Leu Leu Gly Pro Phe Asp Leu Gly Val Ala Ala Gly Leu Ala
 85             90             95

Leu Ile Val Gly Pro Leu Cys Gly Leu Leu Val His Met Gly Ala Phe
 100            105            110

Val Gly Gly Asp Arg Asn Arg Val Leu Thr Ala Gly
 115            120

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<210> 971

<211> 618

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(595)

<223> RXN02059

<400> 971

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tcgggaaatt ccaactcatga acgcctagtc tacgggaacc atttcaccag cgtgtacgtt 60
gtaaatgtga actgaaaaag tgaaaaggaa gatgataaag atg act caa cca cgg 115
              Met Thr Gln Pro Arg
              1             5

ccc gat gcc gca tct gtg tgc ctg gaa aag aag cgc cca gaa gga tgg 163
Pro Asp Ala Ala Ser Val Ser Leu Glu Lys Lys Arg Pro Glu Gly Trp
              10             15             20

cca gtg gga agc ttt gaa aca tac cca gaa gcc caa gca gca gtg gat 211
Pro Val Gly Ser Phe Glu Thr Tyr Pro Glu Ala Gln Ala Ala Val Asp
              25             30             35

ttg ctc agt gat aat gca ttc ccc gtc acc gaa ttg acc att gtt ggt 259
Leu Leu Ser Asp Asn Ala Phe Pro Val Thr Glu Leu Thr Ile Val Gly
 40             45             50

gtg gac ctg att gaa gtg gaa cgc gtt aca ggt cgt ctc acg tgg ggt 307
Val Asp Leu Ile Glu Val Glu Arg Val Thr Gly Arg Leu Thr Trp Gly
 55             60             65

cgt gtg att gcc gga gga atg gca tct ggc gca tgg ttg ggt ctg ttc 355
Arg Val Ile Ala Gly Gly Met Ala Ser Gly Ala Trp Leu Gly Leu Phe
 70             75             80             85

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ttt ggc att gtc atg gcc ttg atg tct gga ttc tgg ttc tct tcc atc 403
 Phe Gly Ile Val Met Ala Leu Met Ser Gly Phe Trp Phe Ser Ser Ile
 90 95 100

gca gcg gga ata ggt atg ggt ttg gtg ttt ggc att gtc ggt gca gca 451
 Ala Ala Gly Ile Gly Met Gly Leu Val Phe Gly Ile Val Gly Ala Ala
 105 110 115

gtt cct tat gct gct tcc aaa ggc aag cgg gac ttt acc tct tca act 499
 Val Pro Tyr Ala Ala Ser Lys Gly Lys Arg Asp Phe Thr Ser Ser Thr
 120 125 130

caa att gtg gcg ggg cgc tat gat gtg att tgt tcc cca gaa cgt gct 547
 Gln Ile Val Ala Gly Arg Tyr Asp Val Ile Cys Ser Pro Glu Arg Ala
 135 140 145

cgg gaa gct cga gac atg att gcc ctg aaa act cga gat ctc cgc caa 595
 Arg Glu Ala Arg Asp Met Ile Ala Leu Lys Thr Arg Asp Leu Arg Gln
 150 155 160 165

taagttaaac taacgcctat gaa 618

<210> 972

<211> 165

<212> PRT

<213> Corynebacterium glutamicum

<400> 972

Met Thr Gln Pro Arg Pro Asp Ala Ala Ser Val Ser Leu Glu Lys Lys
 1 5 10 15

Arg Pro Glu Gly Trp Pro Val Gly Ser Phe Glu Thr Tyr Pro Glu Ala
 20 25 30

Gln Ala Ala Val Asp Leu Leu Ser Asp Asn Ala Phe Pro Val Thr Glu
 35 40 45

Leu Thr Ile Val Gly Val Asp Leu Ile Glu Val Glu Arg Val Thr Gly
 50 55 60

Arg Leu Thr Trp Gly Arg Val Ile Ala Gly Gly Met Ala Ser Gly Ala
 65 70 75 80

Trp Leu Gly Leu Phe Phe Gly Ile Val Met Ala Leu Met Ser Gly Phe
 85 90 95

Trp Phe Ser Ser Ile Ala Ala Gly Ile Gly Met Gly Leu Val Phe Gly
 100 105 110

Ile Val Gly Ala Ala Val Pro Tyr Ala Ala Ser Lys Gly Lys Arg Asp
 115 120 125

Phe Thr Ser Ser Thr Gln Ile Val Ala Gly Arg Tyr Asp Val Ile Cys
 130 135 140

Ser Pro Glu Arg Ala Arg Glu Ala Arg Asp Met Ile Ala Leu Lys Thr
 145 150 155 160

Arg Asp Leu Arg Gln

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<210> 973
<211> 618
<212> DNA
<213> Cornebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(595)
<223> FRXA02059
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gtaaatgtga	actgaaaaag	tgaaaaaggaa	gatgataaag	atg	act	caa	cca	cgg												163	
				Met	Thr	Gln	Pro	Arg												211	
				1				5												259	
ccc gat gcc gca tct gtg tcg ctg gaa aag cgc cca gaa gga tgg																				307	
Pro Asp Ala Ala Ser Val Ser Leu Glu Lys Lys Arg Pro Glu Gly Trp																				355	
			10					15					20							403	
cca gtg gga agc ttt gaa aca tac cca gaa gcc caa gca gca gtg gat																				451	
Pro Val Gly Ser Phe Glu Thr Tyr Pro Glu Ala Gln Ala Ala Val Asp																				499	
			25					30					35							547	
ttg ctc agt gat aat gca ttc ccc gtc acc gaa ttg acc att gtt ggt																				595	
Leu Leu Ser Asp Asn Ala Phe Pro Val Thr Glu Leu Thr Ile Val Gly																				611	
			40				45					50									
gtg gac ctg att gaa gtg gaa cgc gtt aca ggt cgt ctc acg tgg ggt																					
Val Asp Leu Ile Glu Val Glu Arg Val Thr Gly Arg Leu Thr Trp Gly																					
			55			60				65											
cgt gtg att gcc gga gga atg gca tct ggc gca tgg ttg ggt ctg ttc																					
Arg Val Ile Ala Gly Gly Met Ala Ser Gly Ala Trp Leu Gly Leu Phe																					
			70		75			80													
ttt ggc att gtc atg gcc ttg atg tct gga ttc tgg ttc tct tcc atc																					
Phe Gly Ile Val Met Ala Leu Met Ser Gly Phe Thr Trp Phe Ser Ser Ile																					
				90				95													
gca gcg gga ata ggt atg ggt ttg gtg ttt ggc att gtc ggt gca gca																					
Ala Ala Gly Ile Gly Met Gly Leu Val Phe Gly Ile Val Gly Ala Ala																					
			105				110					115									
gtt cct tat gct gct tcc aaa ggc aag cgg gac ttt acc tct tca act																					
Val Pro Tyr Ala Ala Ser Lys Gly Lys Arg Asp Phe Thr Ser Ser Thr																					
			120			125					130										
caa att gtg gcg ggg cgc tat gat gtg att tgt tcc cca gaa cgt gct																					
Gln Ile Val Ala Gly Arg Tyr Asp Val Ile Cys Ser Pro Glu Arg Ala																					
			135			140					145										
cgg gaa gct cga gac atg att gcc ctg aaa act cga gat ctc cgc caa																					
Arg Glu Ala Arg Asp Met Ile Ala Leu Lys Thr Arg Asp Leu Arg Gln																					
				155					160												
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<210> 974

<211> 165

<212> PRT

<213> Corynebacterium glutamicum

<400> 974

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1 5 10 15Arg Pro Glu Gly Trp Pro Val Gly Ser Phe Glu Thr Tyr Pro Glu Ala
20 25 30Gln Ala Ala Val Asp Leu Leu Ser Asp Asn Ala Phe Pro Val Thr Glu
35 40 45Leu Thr Ile Val Gly Val Asp Leu Ile Glu Val Glu Arg Val Thr Gly
50 55 60Arg Leu Thr Trp Gly Arg Val Ile Ala Gly Gly Met Ala Ser Gly Ala
65 70 75 80Trp Leu Gly Leu Phe Phe Gly Ile Val Met Ala Leu Met Ser Gly Phe
85 90 95Trp Phe Ser Ser Ile Ala Ala Gly Ile Gly Met Gly Leu Val Phe Gly
100 105 110Ile Val Gly Ala Ala Val Pro Tyr Ala Ala Ser Lys Gly Lys Arg Asp
115 120 125Phe Thr Ser Ser Thr Gln Ile Val Ala Gly Arg Tyr Asp Val Ile Cys
130 135 140Ser Pro Glu Arg Ala Arg Glu Ala Arg Asp Met Ile Ala Leu Lys Thr
145 150 155 160Arg Asp Leu Arg Gln
165

<210> 975

<211> 615

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(592)

<223> RXN02066

<400> 975

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acatccttga aagtcgagac acaggaggtc atcggaagat atg ttc aat tcc gac 115
Met Phe Asn Ser Asp
1 5acc acc gcg aat ctc caa gct aaa agt cga gat cgt gca gga tct aaa 163
Thr Thr Ala Asn Leu Gln Ala Lys Ser Arg Asp Arg Ala Gly Ser Lys

	10	15	20	
	gca aag cgc agc agg cca agt ttt gat tca gta gcg cgg gat gtt ttg			211
	Ala Lys Arg Ser Arg Pro Ser Phe Asp Ser Val Ala Arg Asp Val Leu	25	30	35
	gat gtt cga aca aaa aca gca caa gtt aaa aac aag gct aaa gag ttt			259
	Asp Val Arg Thr Lys Thr Ala Gln Val Lys Asn Lys Ala Lys Glu Phe	40	45	50
	tcc tct gtt gat cac ctt tca gca gac gcc gca gcc atg ttt gta gac			307
	Ser Ser Val Asp His Leu Ser Ala Asp Ala Ala Ala Met Phe Val Asp	55	60	65
	aat gaa ctg tcc cgt gcc gcc atg cat cgc gcc agg ctg cac att gtg			355
	Asn Glu Leu Ser Arg Gly Ala Met His Arg Ala Arg Leu His Ile Val	70	75	80
	cac tgc gct gaa tgt agg gaa gag att aac cgt cag cgg gaa acc gtt			403
	His Cys Ala Glu Cys Arg Glu Glu Ile Asn Arg Gln Arg Glu Thr Val	90	95	100
	gat tat ctc cgc tca gag tgc aaa aac gaa gaa gtg tcc gcc cca atg			451
	Asp Tyr Leu Arg Ser Glu Cys Lys Asn Glu Glu Val Ser Ala Pro Met	105	110	115
	gac ctc aaa gca cgg ctt gcc agc ctc gcc act gag tgc atg cct gcc			499
	Asp Leu Lys Ala Arg Leu Ala Ser Leu Ala Thr Glu Cys Met Pro Gly	120	125	130
	cct gcc gca gag aat tta gca atg cag cgc cca gag tct ttt gtg gct			547
	Pro Gly Ala Glu Asn Leu Ala Met Gln Arg Pro Glu Ser Phe Val Ala	135	140	145
	aaa gtt gag tcc gta gtg cgc gca gtt cgt aag aac caa gcc cgc			592
	Lys Val Glu Ser Val Val Arg Ala Val Arg Lys Asn Gln Gly Arg	150	155	160
	taatttttaa tccttattta cat			615

<210> 976

<211> 164

<212> PRT

<213> Corynebacterium glutamicum

<400> 976

Met Phe Asn Ser Asp Thr Thr Ala Asn Leu Gln Ala Lys Ser Arg Asp

1

5

10

15

Arg Ala Gly Ser Lys Ala Lys Arg Ser Arg Pro Ser Phe Asp Ser Val

20

25

30

Ala Arg Asp Val Leu Asp Val Arg Thr Lys Thr Ala Gln Val Lys Asn

35

40

45

Lys Ala Lys Glu Phe Ser Ser Val Asp His Leu Ser Ala Asp Ala Ala

50

55

60

Ala Met Phe Val Asp Asn Glu Leu Ser Arg Gly Ala Met His Arg Ala

65

70

75

80

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<210> 977
<211> 615
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> {101}..(592)
<223> FRXA02066

<400> 977
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acatccttga aagtcgagac acaggaggtc atcggaagat atg ttc aat tcc gac 115
Met Phe Asn Ser Asp
1 5

acc acc gcg aat ctc caa gct aaa agt cga gat cgt gca gga tct aaa 163
Thr Thr Ala Asn Leu Gln Ala Lys Ser Arg Asp Arg Ala Gly Ser Lys
10 15 20

gca aag cgc agc agg cca agt ttt gat tca gta gcg cgg gat gtt ttg 211
Ala Lys Arg Ser Arg Pro Ser Phe Asp Ser Val Ala Arg Asp Val Leu
25 30 35

gat gtt cga aca aaa aca gca caa gtt aaa aac aag gct aaa gag ttt 259
Asp Val Arg Thr Lys Thr Ala Gln Val Lys Asn Lys Ala Lys Glu Phe
40 45 50

tcc tct gtt gat cac ctt tca gca gac gcc gca gcc atg ttt gta gac 307
Ser Ser Val Asp His Leu Ser Ala Asp Ala Ala Met Phe Val Asp
55 60 65

aat gaa ctg tcc cgt ggc gcc atg cat cgc gcc agg ctg cac att gtg 355
Asn Glu Leu Ser Arg Gly Ala Met His Arg Ala Arg Leu His Ile Val
70 75 80 85

cac tgc gct gaa tgt agg gaa gag att aac cgt cag cgg gaa acc gtt 403
His Cys Ala Glu Cys Arg Glu Glu Ile Asn Arg Gln Arg Glu Thr Val
90 95 100

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gat tat ctc cgc tca gag tgc aaa aac gaa gaa gtg tcc gcc cca atg 451
 Asp Tyr Leu Arg Ser Glu Cys Lys Asn Glu Glu Val Ser Ala Pro Met
 105 110 115

gac ctc aaa gca cgg ctt gcc agc ctc gcc act gag tgc atg cct gcc 499
 Asp Leu Lys Ala Arg Leu Ala Ser Leu Ala Thr Glu Cys Met Pro Gly
 120 125 130

cct gcc gca gag aat tta gca atg cag cgc cca gag tct ttt gtg gct 547
 Pro Gly Ala Glu Asn Leu Ala Met Gln Arg Pro Glu Ser Phe Val Ala
 135 140 145

aaa gtt gag tcc gta gtg cgc gca gtt cgt aag aac caa gcc cgc 592
 Lys Val Glu Ser Val Val Arg Ala Val Arg Lys Asn Gln Gly Arg
 150 155 160

taatttttaa tccttatatta cat 615

<210> 978

<211> 164

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 978

Met Phe Asn Ser Asp Thr Thr Ala Asn Leu Gln Ala Lys Ser Arg Asp
 1 5 10 15

Arg Ala Gly Ser Lys Ala Lys Arg Ser Arg Pro Ser Phe Asp Ser Val
 20 25 30

Ala Arg Asp Val Leu Asp Val Arg Thr Lys Thr Ala Gln Val Lys Asn
 35 40 45

Lys Ala Lys Glu Phe Ser Ser Val Asp His Leu Ser Ala Asp Ala Ala
 50 55 60

Ala Met Phe Val Asp Asn Glu Leu Ser Arg Gly Ala Met His Arg Ala
 65 70 75 80

Arg Leu His Ile Val His Cys Ala Glu Cys Arg Glu Glu Ile Asn Arg
 85 90 95

Gln Arg Glu Thr Val Asp Tyr Leu Arg Ser Glu Cys Lys Asn Glu Glu
 100 105 110

Val Ser Ala Pro Met Asp Leu Lys Ala Arg Leu Ala Ser Leu Ala Thr
 115 120 125

Glu Cys Met Pro Gly Pro Gly Ala Glu Asn Leu Ala Met Gln Arg Pro
 130 135 140

Glu Ser Phe Val Ala Lys Val Glu Ser Val Val Arg Ala Val Arg Lys
 145 150 155 160

Asn Gln Gly Arg

<210> 979

<211> 579

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(556)

<223> RXN02067

<400> 979

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tatttacatt	ttctgaaaga	cgggtctgat	gttttctagc	gtg	ggt	tgg	gga	gag	115
				Val	Gly	Trp	Gly	Glu	
				1				5	

atc	ttc	ctc	tta	gtc	gtt	gtg	ggc	ctt	gtt	gtc	atc	ggc	cgg	gaa	cgg	163
Ile	Phe	Leu	Leu	Val	Val	Gly	Leu	Val	Val	Ile	Gly	Pro	Glu	Arg		
			10			15							20			

ttg	cct	cgt	ttg	atc	cag	gac	gca	cgc	gct	gcg	ctg	ctc	gct	gca	cgt	211
Leu	Pro	Arg	Leu	Ile	Gln	Asp	Ala	Arg	Ala	Ala	Leu	Leu	Ala	Ala	Arg	
			25				30						35			

acc	gct	atc	gac	aat	gca	aag	cag	tcg	ttg	gac	agt	gat	ttt	ggt	tcg	259
Thr	Ala	Ile	Asp	Asn	Ala	Lys	Gln	Ser	Leu	Asp	Ser	Asp	Phe	Gly	Ser	
		40				45					50					

gaa	ttt	gat	gaa	atc	cga	aag	cca	cta	acc	cag	gtt	gca	cag	tac	agc	307
Glu	Phe	Asp	Glu	Ile	Arg	Lys	Pro	Leu	Thr	Gln	Val	Ala	Gln	Tyr	Ser	
	55				60					65						

cgg	atg	agc	ccc	aag	acg	gcc	atc	act	aag	gcg	tta	ttt	gat	aat	gat	355
Arg	Met	Ser	Pro	Lys	Thr	Ala	Ile	Thr	Lys	Ala	Leu	Phe	Asp	Asn	Asp	
	70				75				80					85		

tcc	tcg	ttc	ctg	gat	gac	ttt	gat	cca	aag	aag	atc	atg	gcc	gaa	gga	403
Ser	Ser	Phe	Leu	Asp	Asp	Phe	Asp	Pro	Lys	Lys	Ile	Met	Ala	Glu	Gly	
			90					95					100			

aca	gaa	ggc	gaa	gct	cag	cgc	aac	aag	cag	gca	gct	gac	aac	aat	gcg	451
Thr	Glu	Gly	Glu	Ala	Gln	Arg	Asn	Lys	Gln	Ala	Ala	Asp	Asn	Asn	Ala	
			105				110						115			

aat	gtg	gtg	gaa	cgt	cca	gct	gat	ggc	tcc	acc	gca	cgc	cca	acg	caa	499
Asn	Val	Val	Glu	Arg	Pro	Ala	Asp	Gly	Ser	Thr	Ala	Arg	Pro	Thr	Gln	
		120				125					130					

aac	gat	cca	aaa	gac	ggc	cgg	aat	tac	tca	ggc	gtc	tct	tgg	acc		547
Asn	Asp	Pro	Lys	Asp	Gly	Pro	Asn	Tyr	Ser	Gly	Val	Ser	Trp	Thr		
	135				140					145						

gat	att	att	tagcttttat	taaagccaa	gcc											579
Asp	Ile	Ile														
	150															

<210> 980

<211> 152

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 980

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Ile Gly Pro Glu Arg Leu Pro Arg Leu Ile Gln Asp Ala Arg Ala Ala
 20 25 30

Leu Leu Ala Ala Arg Thr Ala Ile Asp Asn Ala Lys Gln Ser Leu Asp
 35 40 45

Ser Asp Phe Gly Ser Glu Phe Asp Glu Ile Arg Lys Pro Leu Thr Gln
 50 55 60

Val Ala Gln Tyr Ser Arg Met Ser Pro Lys Thr Ala Ile Thr Lys Ala
 65 70 75 80

Leu Phe Asp Asn Asp Ser Ser Phe Leu Asp Asp Phe Asp Pro Lys Lys
 85 90 95

Ile Met Ala Glu Gly Thr Glu Gly Glu Ala Gln Arg Asn Lys Gln Ala
 100 105 110

Ala Asp Asn Asn Ala Asn Val Val Glu Arg Pro Ala Asp Gly Ser Thr
 115 120 125

Ala Arg Pro Thr Gln Asn Asp Pro Lys Asp Gly Pro Asn Tyr Ser Gly
 130 135 140

Gly Val Ser Trp Thr Asp Ile Ile
 145 150

<210> 981

<211> 579

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(556)

<223> FRXA02067

<400> 981

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tatttacatt ttctgaaga ccggtctgat gttttctagc gtg ggt tgg gga gag 115
 Val Gly Trp Gly Glu
 1 5

atc ttc ctc tta gtc gtt gtg ggc ctt gtt gtc atc ggc ccg gaa cgg 163
 Ile Phe Leu Leu Val Val Val Gly Leu Val Val Ile Gly Pro Glu Arg
 10 15 20

ttg cct cgt ttg atc cag gac gca cgc gct gcg ctg ctc gct gca cgt 211
 Leu Pro Arg Leu Ile Gln Asp Ala Arg Ala Ala Leu Leu Ala Ala Arg
 25 30 35

acc gct atc gac aat gca aag cag tcg ttg gac agt gat ttt ggt tcg 259
 Thr Ala Ile Asp Asn Ala Lys Gln Ser Leu Asp Ser Asp Phe Gly Ser
 40 45 50

gaa ttt gat gaa atc cga aag cca cta acc cag gtt gca cag tac agc 307
 Glu Phe Asp Glu Ile Arg Lys Pro Leu Thr Gln Val Ala Gln Tyr Ser
 55 60 65

cgg atg agc ccc aag acg gcc atc act aag gcg tta ttt gat aat gat 355
 Arg Met Ser Pro Lys Thr Ala Ile Thr Lys Ala Leu Phe Asp Asn Asp
 70 75 80 85

tcc tcg ttc ctg gat gac ttt gat cca aag aag atc atg gcc gaa gga 403
 Ser Ser Phe Leu Asp Asp Phe Asp Pro Lys Lys Ile Met Ala Glu Gly
 90 95 100

aca gaa ggc gaa gct cag cgc aac aag cag gca gct gac aac aat gcg 451
 Thr Glu Gly Glu Ala Gln Arg Asn Lys Gln Ala Ala Asp Asn Asn Ala
 105 110 115

aat gtg gtg gaa cgt cca gct gat ggt tcc acc gca cgc cca acg caa 499
 Asn Val Val Glu Arg Pro Ala Asp Gly Ser Thr Ala Arg Pro Thr Gln
 120 125 130

aac gat cca aaa gac ggc ccg aat tac tca ggt ggc gtc tct tgg acc 547
 Asn Asp Pro Lys Asp Gly Pro Asn Tyr Ser Gly Val Ser Trp Thr
 135 140 145

gat att att tagcttttat ttaacgccaa gcc 579
 Asp Ile Ile
 150

<210> 982
 <211> 152
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 982
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 1 5 10 15
 Ile Gly Pro Glu Arg Leu Pro Arg Leu Ile Gln Asp Ala Arg Ala Ala
 20 25 30
 Leu Leu Ala Ala Arg Thr Ala Ile Asp Asn Ala Lys Gln Ser Leu Asp
 35 40 45
 Ser Asp Phe Gly Ser Glu Phe Asp Glu Ile Arg Lys Pro Leu Thr Gln
 50 55 60
 Val Ala Gln Tyr Ser Arg Met Ser Pro Lys Thr Ala Ile Thr Lys Ala
 65 70 75 80
 Leu Phe Asp Asn Asp Ser Ser Phe Leu Asp Asp Phe Asp Pro Lys Lys
 85 90 95
 Ile Met Ala Glu Gly Thr Glu Gly Glu Ala Gln Arg Asn Lys Gln Ala
 100 105 110
 Ala Asp Asn Asn Ala Asn Val Val Glu Arg Pro Ala Asp Gly Ser Thr
 115 120 125
 Ala Arg Pro Thr Gln Asn Asp Pro Lys Asp Gly Pro Asn Tyr Ser Gly
 130 135 140

Gly Val Ser Trp Thr Asp Ile Ile
145 150

<210> 983
<211> 912
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (101)..(889)
<223> RXN02075

<400> 983
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ccatacgcat ggttcacagg atttcagtag gattaacccc atg tac aag gtc ttc 115
Met Tyr Lys Val Phe
1 5

gaa gca ctg gat gat tta gtt caa gcc gtt caa cgc gca tac ggc gtt 163
Glu Ala Leu Asp Asp Leu Val Gln Ala Val Gln Arg Ala Tyr Gly Val
10 15 20

ccc atg acc gga aat tgc gtg gtt ccc cgt cag gaa gtg ctt gcg ctt 211
Pro Met Thr Gly Asn Cys Val Val Pro Arg Gln Glu Val Leu Ala Leu
25 30 35

ctc gat gat tta cgt gat gcg ctt cct gta gaa ctt gat gat gca caa 259
Leu Asp Asp Leu Arg Asp Ala Leu Pro Val Glu Leu Asp Asp Ala Gln
40 45 50

gat gtg ctg gac cac cgt gat ggt gtg atc cgt gaa gct gaa gaa aag 307
Asp Val Leu Asp His Arg Asp Gly Val Ile Arg Glu Ala Glu Glu Lys
55 60 65

gcc att gcc ttg gtc gac gat gca gaa aac gag gcc cga aac ctc ctt 355
Ala Ile Ala Leu Val Asp Asp Ala Glu Asn Glu Ala Arg Asn Leu Leu
70 75 80 85

gca cgc gca act gag gag tca gat gcc atg gtg gaa gac gcc acc aag 403
Ala Arg Ala Thr Glu Glu Ser Asp Ala Met Val Glu Asp Ala Thr Lys
90 95 100

cat gcg cat tct gtc gtt gct aag gct aat gac aca gcg gat cgc atc 451
His Ala His Ser Val Val Ala Lys Ala Asn Asp Thr Ala Asp Arg Ile
105 110 115

gtg agt gac gct cgt cga gaa gca aac agc gtc acc gag cgc gcc cag 499
Val Ser Asp Ala Arg Arg Glu Ala Asn Ser Val Thr Glu Arg Ala Gln
120 125 130

gct gaa tct gag cgc ctg gtc aac tcc gcc aat gat gcg tat cgc cgc 547
Ala Glu Ser Glu Arg Leu Val Asn Ser Gly Asn Asp Ala Tyr Arg Arg
135 140 145

gog gtt gct gaa ggc cag gcc gag cag gat cgc ctg gtc agc gag gca 595
Ala Val Ala Glu Gly Gln Ala Glu Gln Asp Arg Leu Val Ser Glu Ala
150 155 160 165

gaa gtg gtg cgt cgc tcc acg gaa gaa gca cac cgc att gtg gat gca 643
 Glu Val Val Arg Arg Ser Thr Glu Glu Ala His Arg Ile Val Asp Ala
 170 175 180

gcg cac gct gac tcc aac aag ctg cgc aat gaa tgc gat gac tac gtg 691
 Ala His Ala Asp Ser Asn Lys Leu Arg Asn Glu Cys Asp Asp Tyr Val
 185 190 195

gat acc aag ttg gca gag ttt gaa acc tcg ctg tcc acc acg ttg cgt 739
 Asp Thr Lys Leu Ala Glu Phe Glu Thr Ser Leu Ser Thr Thr Leu Arg
 200 205 210

tct gtc act gct gat cgt tcc gca cta cgc cga gga gct gga gct act 787
 Ser Val Thr Ala Asp Arg Ser Ala Leu Arg Arg Gly Ala Gly Ala Thr
 215 220 225

ggc cgc gag ctg cgc gat gag caa ccg gca gcg cgt ggt gaa tat gag 835
 Gly Arg Glu Leu Arg Asp Glu Glu Gln Pro Ala Ala Arg Gly Glu Tyr Glu
 230 235 240 245

cgg gac tac gag cgt gat tat gaa cga ggc tac gaa cgc gac gat cga 883
 Arg Asp Tyr Glu Arg Asp Tyr Glu Arg Gly Tyr Glu Arg Asp Asp Arg
 250 255 260

gac tac tagtttccaa gaaaccattt agg 912
 Asp Tyr

<210> 984
 <211> 263
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 984
 Met Tyr Lys Val Phe Glu Ala Leu Asp Asp Leu Val Gln Ala Val Gln
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Arg Ala Tyr Gly Val Pro Met Thr Gly Asn Cys Val Val Pro Arg Gln
 20 25 30

Glu Val Leu Ala Leu Leu Asp Asp Leu Arg Asp Ala Leu Pro Val Glu
 35 40 45

Leu Asp Asp Ala Gln Asp Val Leu Asp His Arg Asp Gly Val Ile Arg
 50 55 60

Glu Ala Glu Glu Lys Ala Ile Ala Leu Val Asp Asp Ala Glu Asn Glu
 65 70 75 80

Ala Arg Asn Leu Leu Ala Arg Ala Thr Glu Glu Ser Asp Ala Met Val
 85 90 95

Glu Asp Ala Thr Lys His Ala His Ser Val Val Ala Lys Ala Asn Asp
 100 105 110

Thr Ala Asp Arg Ile Val Ser Asp Ala Arg Arg Glu Ala Asn Ser Val
 115 120 125

Thr Glu Arg Ala Gln Ala Glu Ser Glu Arg Leu Val Asn Ser Gly Asn

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130              135              140
Asp Ala Tyr Arg Arg Ala Val Ala Glu Gly Gln Ala Glu Gln Asp Arg
145              150              155              160
Leu Val Ser Glu Ala Glu Val Val Arg Arg Ser Thr Glu Glu Ala His
165              170              175
Arg Ile Val Asp Ala Ala His Ala Asp Ser Asn Lys Leu Arg Asn Glu
180              185              190
Cys Asp Asp Tyr Val Asp Thr Lys Leu Ala Glu Phe Glu Thr Ser Leu
195              200              205
Ser Thr Thr Leu Arg Ser Val Thr Ala Asp Arg Ser Ala Leu Arg Arg
210              215              220
Gly Ala Gly Ala Thr Gly Arg Glu Leu Arg Asp Glu Gln Pro Ala Ala
225              230              235              240
Arg Gly Glu Tyr Glu Arg Asp Tyr Glu Arg Asp Tyr Glu Arg Gly Tyr
245              250              255
Glu Arg Asp Asp Arg Asp Tyr
260

<210> 985
<211> 657
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(634)
<223> RXN02076

<400> 985
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tatgtagtca cgatgaggta cgagtaggat ctctcgtgtc atg aaa tct cca ttt 115
Met Lys Ser Pro Phe
1 5

att ttt gat gtc gcc gca ctc ctt cgt gga agt gcc ctt ccg gaa cac 163
Ile Phe Asp Val Ala Ala Leu Leu Arg Gly Ser Ala Leu Pro Glu His
10 15 20

ctc acc caa tca ggt cca agc cgg acc cgc att ggt ccg gaa atg atc 211
Leu Thr Gln Ser Gly Pro Ser Pro Thr Arg Ile Gly Pro Glu Met Ile
25 30 35

gcg atc ccc gag ggc gga aaa gtt atc gta gaa gcc cag atc att cca 259
Ala Ile Pro Glu Gly Gly Lys Val Ile Val Glu Ala Gln Ile Ile Pro
40 45 50

ctc ggt gga ggc ctg gcc gtc gaa gca gat atc gaa gcg cag ctt ctg 307
Leu Gly Gly Gly Leu Ala Val Glu Ala Asp Ile Glu Ala Gln Leu Leu
55 60 65

gga cag tgc tcc cgc tgc ctc cgc gaa ctc acc cca acc aag acg ctg 355

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Gly	Gln	Cys	Ser	Arg	Cys	Leu	Arg	Glu	Leu	Thr	Pro	Thr	Lys	Thr	Leu	
70					75					80					85	
cac	gtc	tct	gag	gtt	ttt	gct	gcc	gat	cca	gac	ttt	gtt	act	ggt	gaa	403
His	Val	Ser	Glu	Val	Phe	Ala	Ala	Asp	Pro	Asp	Phe	Val	Thr	Gly	Glu	
				90					95				100			
gat	gca	gca	gat	gac	gaa	gat	gag	ctg	cca	atg	gtt	aac	caa	gac	cag	451
Asp	Ala	Ala	Asp	Asp	Glu	Asp	Glu	Leu	Pro	Met	Val	Asn	Gln	Asp	Gln	
				105				110					115			
att	gat	ctg	ctt	cag	tct	gtc	att	gat	gaa	gct	ggt	ctg	acc	ttg	ccg	499
Ile	Asp	Leu	Leu	Gln	Ser	Val	Ile	Asp	Glu	Ala	Gly	Leu	Thr	Leu	Pro	
				120				125					130			
ttt	aac	cct	gtc	tcg	gaa	gaa	ctt	ggg	tac	ggc	gca	tcg	cag	gat	gat	547
Phe	Asn	Pro	Val	Cys	Glu	Glu	Leu	Gly	Tyr	Gly	Ala	Cys	Gln	Asp	Asp	
				135			140					145				
gaa	acg	cca	gct	cct	gac	ggg	gtc	tct	gaa	gaa	gta	gaa	gac	gag	gaa	595
Glu	Thr	Pro	Ala	Pro	Asp	Gly	Val	Ser	Glu	Glu	Val	Glu	Asp	Glu	Glu	
				150			155				160				165	
aag	gtc	gat	ccg	cgc	tgg	gct	ggg	ttg	gag	aag	ttc	ctg	tgagcaggaa			644
Lys	Val	Asp	Pro	Arg	Trp	Ala	Gly	Leu	Glu	Lys	Phe	Leu				
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aaagaatcgc	ctc															657

<210> 986
 <211> 178
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 986
 Met Lys Ser Pro Phe Ile Phe Asp Val Ala Ala Leu Leu Arg Gly Ser
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 Ala Leu Pro Glu His Leu Thr Gln Ser Gly Pro Ser Pro Thr Arg Ile
 20 25 30
 Gly Pro Glu Met Ile Ala Ile Pro Glu Gly Gly Lys Val Ile Val Glu
 35 40 45
 Ala Gln Ile Ile Pro Leu Gly Gly Gly Leu Ala Val Glu Ala Asp Ile
 50 55 60
 Glu Ala Gln Leu Leu Gly Gln Cys Ser Arg Cys Leu Arg Glu Leu Thr
 65 70 75 80
 Pro Thr Lys Thr Leu His Val Ser Glu Val Phe Ala Ala Asp Pro Asp
 85 90 95
 Phe Val Thr Gly Glu Asp Ala Ala Asp Asp Glu Asp Glu Leu Pro Met
 100 105 110
 Val Asn Gln Asp Gln Ile Asp Leu Leu Gln Ser Val Ile Asp Glu Ala
 115 120 125
 Gly Leu Thr Leu Pro Phe Asn Pro Val Cys Glu Glu Leu Gly Tyr Gly

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130          135          140
Ala Cys Gln Asp Asp Glu Thr Pro Ala Pro Asp Gly Val Ser Glu Glu
145          150          155          160
Val Glu Asp Glu Glu Lys Val Asp Pro Arg Trp Ala Gly Leu Glu Lys
165          170          175
Phe Leu

<210> 987
<211> 657
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(634)
<223> FRXA02076

<400> 987
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Met Lys Ser Pro Phe
1
att ttt gat gtc gcc gca ctc ctt cgt gga agt gcc ctt ccg gaa cac 163
Ile Phe Asp Val Ala Ala Leu Leu Arg Gly Ser Ala Leu Pro Glu His
10 15 20
ctc acc caa tca ggt cca agc ccg acc cgc att ggt ccg gaa atg atc 211
Leu Thr Gln Ser Gly Pro Ser Pro Thr Arg Ile Gly Pro Glu Met Ile
25 30 35
gcg atc ccc gag ggc gga aaa gtt atc gta gaa gcc cag atc att cca 259
Ala Ile Pro Glu Gly Gly Lys Val Ile Val Glu Ala Gln Ile Ile Pro
40 45 50
ctc ggt gga ggc ctg gcc gtc gaa gca gat atc gaa gcg cag ctt ctg 307
Leu Gly Gly Gly Leu Ala Val Glu Ala Asp Ile Glu Ala Gln Leu Leu
55 60 65
gga cag tgc tcc cgc tgc ctc cgc gaa ctc acc cca acc aag acg ctg 355
Gly Gln Cys Ser Arg Cys Leu Arg Glu Leu Thr Pro Thr Lys Thr Leu
70 75 80 85
cac gtc tct gag gtt ttt gct gcc gat cca gac ttt gtt act ggt gaa 403
His Val Ser Glu Val Phe Ala Ala Asp Pro Asp Phe Val Thr Gly Glu
90 95 100
gat gca gca gat gac gaa gat gag ctg cca atg gtt aac caa gac cag 451
Asp Ala Ala Asp Asp Glu Asp Leu Pro Met Val Asn Gln Asp Gln
105 110 115
att gat ctg ctt cag tct gtc att gat gaa gct ggt ctg acc ttg ccg 499
Ile Asp Leu Leu Gln Ser Val Ile Asp Glu Ala Gly Leu Thr Leu Pro
120 125 130

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ttt aac cct gtc tgc gaa gaa ctt ggg tac ggc gca tgc cag gat gat 547
 Phe Asn Pro Val Cys Glu Glu Leu Gly Tyr Gly Ala Cys Gln Asp Asp
 135 140 145

gaa acg cca gct cct gac ggt gtc tct gaa gaa gta gaa gac gag gaa 595
 Glu Thr Pro Ala Pro Asp Gly Val Ser Glu Glu Val Glu Asp Glu Glu
 150 155 160 165

aag gtc gat ccg cgc tgg gct ggt ttg gag aag ttc ctg tgagcaggaa 644
 Lys Val Asp Pro Arg Trp Ala Gly Leu Glu Lys Phe Leu
 170 175

aaagaatcgc ctc 657

<210> 988

<211> 178

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 988

Met Lys Ser Pro Phe Ile Phe Asp Val Ala Ala Leu Leu Arg Gly Ser
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Ala Leu Pro Glu His Leu Thr Gln Ser Gly Pro Ser Pro Thr Arg Ile
 20 25 30

Gly Pro Glu Met Ile Ala Ile Pro Glu Gly Gly Lys Val Ile Val Glu
 35 40 45

Ala Gln Ile Ile Pro Leu Gly Gly Gly Leu Ala Val Glu Ala Asp Ile
 50 55 60

Glu Ala Gln Leu Leu Gly Gln Cys Ser Arg Cys Leu Arg Glu Leu Thr
 65 70 75 80

Pro Thr Lys Thr Leu His Val Ser Glu Val Phe Ala Ala Asp Pro Asp
 85 90 95

Phe Val Thr Gly Glu Asp Ala Ala Asp Asp Glu Asp Glu Leu Pro Met
 100 105 110

Val Asn Gln Asp Gln Ile Asp Leu Leu Gln Ser Val Ile Asp Glu Ala
 115 120 125

Gly Leu Thr Leu Pro Phe Asn Pro Val Cys Glu Glu Leu Gly Tyr Gly
 130 135 140

Ala Cys Gln Asp Asp Glu Thr Pro Ala Pro Asp Gly Val Ser Glu Glu
 145 150 155 160

Val Glu Asp Glu Glu Lys Val Asp Pro Arg Trp Ala Gly Leu Glu Lys
 165 170 175

Phe Leu

<210> 989

<211> 840

<212> DNA

cga ctg atg cgc tac gca gtg aag gaa gta agc aag cgt ttc cgt tcg 691
Arg Leu Met Arg Tyr Ala Val Lys Glu Val Ser Lys Arg Phe Arg Ser
185 190 195

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gca ttg att ggc aaa att ctg ccg ttt ggt atc ggt gcg gtg ctg ggc 739
Ala Leu Ile Gly Lys Ile Leu Pro Phe Gly Ile Gly Ala Val Leu Gly
      200                      205                      210

acg atg gcc aac cgc aaa att gcc aag agg act gtc gga aac gca tac 787
Thr Met Ala Asn Arg Lys Ile Ala Lys Arg Thr Val Gly Asn Ala Tyr
      215                      220                      225

gac tct ctt ggt cct ctc ccc acc cat ttt taagtactca agacccttcc 837
Asp Ser Leu Gly Pro Leu Pro Thr His Phe
      230                      235

aac 840

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<210> 990
<211> 239
<212> PRT
<213> Corynebacterium glutamicum

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Ala Val Leu Glu Asp Asn Ala Gly Phe Ser Gly Lys Tyr Leu Ile Arg
      20              25              30

Ala Leu Asp Lys Ala Ala His Met Gln Thr Gly Ala Ile Glu Gly Tyr
      35              40              45

Ile Ser Trp Leu Arg Lys His Asn Pro Glu Lys Thr Pro Ala Gln Leu
      50              55              60

Gln Val Leu Val Asp Lys His Phe Met Arg Leu Ala Thr Gly Ser Gly
      65              70              75              80

Ala Gly Val Gly Met Ala Ala Ala Val Pro Gly Ile Gly Phe Val Thr
      85              90              95

Gly Ala Leu Ala Val Gly Ala Glu Ser Leu Val Phe Leu Asp Ala Ala
      100             105             110

Ala Phe Tyr Thr Met Ala Ser Ala His Leu Arg Gly Ile Asp Ile Arg
      115             120             125

His Pro Glu Arg Arg Arg Gly Leu Ile Leu Val Val Leu Leu Gly Thr
      130             135             140

Ala Gly Lys Ala Ile Val Asp Ala Gly Val Gly Asp Leu Ser Lys Lys
      145             150             155             160

Asn His Ala Pro Gly Ile Ala Ile Ser Arg Phe Asn Ile Gly Gly Leu
      165             170             175

Met Glu Val Asn Gly Arg Leu Met Arg Tyr Ala Val Lys Glu Val Ser
      180             185             190

Lys Arg Phe Arg Ser Ala Leu Ile Gly Lys Ile Leu Pro Phe Gly Ile
      195             200             205

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Gly Ala Val Leu Gly Thr Met Ala Asn Arg Lys Ile Ala Lys Arg Thr
210 215 220

Val Gly Asn Ala Tyr Asp Ser Leu Gly Pro Leu Pro Thr His Phe
225 230 235

<210> 991

<211> 840

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(817)

<223> FRXA02094

<400> 991

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tccaagtaaa tttctctccc ctatttttag gaggcaccac atg gct gaa cac aac 115
Met Ala Glu His Asn
1 5

gcc atc atc acg gat gca gta cat tcc gac ccc gct gtt tta gaa gac 163
Ala Ile Ile Thr Asp Ala Val His Ser Asp Pro Ala Val Leu Glu Asp
10 15 20

aac gcc ggg ttc agc gga aag tac cta atc cgt gcc ctg gac aag gca 211
Asn Ala Gly Phe Ser Gly Lys Tyr Leu Ile Arg Ala Leu Asp Lys Ala
25 30 35

gct cat atg caa aca ggt gcc atc gag gga tac att tct tgg ctt cgg 259
Ala His Met Gln Thr Gly Ala Ile Glu Gly Tyr Ile Ser Trp Leu Arg
40 45 50

aag cac aat cct gag aaa aca ccg gcg cag ctg cag gta ctc gtc gac 307
Lys His Asn Pro Glu Lys Thr Pro Ala Gln Leu Gln Val Leu Val Asp
55 60 65

aag cat ttt atg cgc ctt gcc acc gcc tct gcc gct ggt gtg ggc atg 355
Lys His Phe Met Arg Leu Ala Thr Gly Ser Gly Ala Gly Val Gly Met
70 75 80 85

gct gcg gcc gtg cca gcc att gcc ttt gtc acg ggt gct ctt gcc gtt 403
Ala Ala Ala Val Pro Gly Ile Gly Phe Val Thr Gly Ala Leu Ala Val
90 95 100

ggt gct gaa tcg ttg gtg ttt ttg gat gct gct gcg ttt tac acc atg 451
Gly Ala Glu Ser Leu Val Phe Leu Asp Ala Ala Ala Phe Tyr Thr Met
105 110 115

gca tcc gcg cac ctg cgt gcc atc gac atc cgc cat cct gaa cgc cga 499
Ala Ser Ala His Leu Arg Gly Ile Asp Ile Arg His Pro Glu Arg Arg
120 125 130

cgt ggt ttg att ttg gtg gtt ctg ctg gcc acc gca gcc aaa gcc att 547
Arg Gly Leu Ile Leu Val Val Leu Leu Gly Thr Ala Gly Lys Ala Ile
135 140 145

ggt gac gca gcc gtc ggt gat tta tcc aag aaa aac cac gcg ccg gcc 595

Val Asp Ala Gly Val Gly Asp Leu Ser Lys Lys Asn His Ala Pro Gly
 150 155 160 165
 att gcg att tcc cgg ttt aat atc ggt ggc ttg atg gaa gtc aac ggc 643
 Ile Ala Ile Ser Arg Phe Asn Ile Gly Gly Leu Met Glu Val Asn Gly
 170 175 180
 cga ctg atg cgc tac gca gtg aag gaa gta agc aag cgt ttc cgt tcg 691
 Arg Leu Met Arg Tyr Ala Val Lys Glu Val Ser Lys Arg Phe Arg Ser
 185 190 195
 gca ttg att ggc aaa att ctg ccg ttt ggt atc ggt cgc gtg ctg ggc 739
 Ala Leu Ile Gly Lys Ile Leu Pro Phe Gly Ile Gly Ala Val Leu Gly
 200 205 210
 acg atg gcc aac cgc aaa att gcc aag agg act gtc gga aac gca tac 787
 Thr Met Ala Asn Arg Lys Ile Ala Lys Arg Thr Val Gly Asn Ala Tyr
 215 220 225
 gac tct ctt ggt cct ctc ccc acc cat ttt taagtactca agacccttcc 837
 Asp Ser Leu Gly Pro Leu Pro Thr His Phe
 230 235
 aac 840
 <210> 992
 <211> 239
 <212> PRT
 <213> *Corynebacterium glutamicum*
 <400> 992
 Met Ala Glu His Asn Ala Ile Ile Thr Asp Ala Val His Ser Asp Pro
 1 5 10 15
 Ala Val Leu Glu Asp Asn Ala Gly Phe Ser Gly Lys Tyr Leu Ile Arg
 20 25 30
 Ala Leu Asp Lys Ala Ala His Met Gln Thr Gly Ala Ile Glu Gly Tyr
 35 40 45
 Ile Ser Trp Leu Arg Lys His Asn Pro Glu Lys Thr Pro Ala Gln Leu
 50 55 60
 Gln Val Leu Val Asp Lys His Phe Met Arg Leu Ala Thr Gly Ser Gly
 65 70 75 80
 Ala Gly Val Gly Met Ala Ala Ala Val Pro Gly Ile Gly Phe Val Thr
 85 90 95
 Gly Ala Leu Ala Val Gly Ala Glu Ser Leu Val Phe Leu Asp Ala Ala
 100 105 110
 Ala Phe Tyr Thr Met Ala Ser Ala His Leu Arg Gly Ile Asp Ile Arg
 115 120 125
 His Pro Glu Arg Arg Arg Gly Leu Ile Leu Val Val Leu Leu Gly Thr
 130 135 140
 Ala Gly Lys Ala Ile Val Asp Ala Gly Val Gly Asp Leu Ser Lys Lys
 145 150 155 160

```

Asn His Ala Pro Gly Ile Ala Ile Ser Arg Phe Asn Ile Gly Gly Leu
      165                      170                      175

Met Glu Val Asn Gly Arg Leu Met Arg Tyr Ala Val Lys Glu Val Ser
      180                      185                      190

Lys Arg Phe Arg Ser Ala Leu Ile Gly Lys Ile Leu Pro Phe Gly Ile
      195                      200                      205

Gly Ala Val Leu Gly Thr Met Ala Asn Arg Lys Ile Ala Lys Arg Thr
      210                      215                      220

Val Gly Asn Ala Tyr Asp Ser Leu Gly Pro Leu Pro Thr His Phe
      225                      230                      235

```

<210> 993

<211> 1245

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> {101}..{1222}

<223> RXN02104

<400> 993

catggattcc catttggagc ettatttaca caggccacct ggcttgtttc ccaccgcgat 60

```

gtgccacaat aacgccataa cagaaaggca tactgacaca atg tcc aac tcc ccc 115
                                     Met Ser Asn Ser Pro
                                     1                      5

```

```

acc gac gtt tca acg agc gca cct cga att atg atc gcg cca gat tcc 163
Thr Asp Val Ser Thr Ser Ala Pro Arg Ile Met Ile Ala Pro Asp Ser
                        10                      15                      20

```

```

tac aaa gga acc gct acc gca tca gaa gct gcg caa tac tta ggc gaa 211
Tyr Lys Gly Thr Ala Thr Ala Ser Glu Ala Ala Gln Tyr Leu Gly Glu
                        25                      30                      35

```

```

ggc gtg ttg gaa att ttg ccc aac gcc tcc att acg ttg gca ccc atg 259
Gly Val Leu Glu Ile Leu Pro Asn Ala Ser Ile Thr Leu Ala Pro Met
                        40                      45                      50

```

```

gcc gac ggt ggc gaa gga aca tcc tca gtt ttc ggc ggg cag gtc ata 307
Ala Asp Gly Gly Glu Gly Thr Ser Ser Val Phe Gly Gly Gln Val Ile
                        55                      60                      65

```

```

aca tta ccc acg aca aat gcc gcg gga cgc ctc acc gaa gcc agc tac 355
Thr Leu Pro Thr Thr Asn Ala Ala Gly Arg Leu Thr Glu Ala Ser Tyr
                        70                      75                      80                      85

```

```

acc tta gat tcc gaa aca aac act gcc tac att gac atc gcc gca gcc 403
Thr Leu Asp Ser Glu Thr Asn Thr Ala Tyr Ile Asp Ile Ala Ala Ala
                        90                      95                      100

```

```

tcc ggt ttg ccc gcc gtt gca gac gat cta gtc ccc acc acc gcc gat 451
Ser Gly Leu Pro Ala Val Ala Asp Asp Leu Val Pro Thr Thr Gly Asp
                        105                      110                      115

```

acc tac ggc acc ggc gtt ttg atc gca gac gcg gtc acc cgt ggc gca	499
Thr Tyr Gly Thr Gly Val Leu Ile Ala Asp Ala Val Thr Arg Gly Ala	
120 125 130	
act cgc att gct tta ggc ctt ggc gga tca gcc aca act gac gcc ggc	547
Thr Arg Ile Ala Leu Gly Leu Gly Gly Ser Ala Thr Thr Asp Ala Gly	
135 140 145	
tca gga att ctc atc gcc ctc ggc gcc gtc cca cgc aac aaa gag ggc	595
Ser Gly Ile Leu Ile Ala Leu Gly Ala Val Pro Arg Asn Lys Glu Gly	
150 155 160 165	
tac gca cta cga acc ggt ggc gcc gac ctc atc aac ctc gat tac atc	643
Tyr Ala Leu Arg Thr Gly Gly Ala Asp Leu Ile Asn Leu Asp Tyr Ile	
170 175 180	
gat acc gcc gaa ctc aac atc ccc gca gcc gcc gtc gaa tgg atc ctg	691
Asp Thr Ala Glu Leu Asn Ile Pro Ala Ala Ala Val Glu Trp Ile Leu	
185 190 195	
ctc acc gat gtc gac gcc ccc gcc acc ggc ccg cag ggc gcg gcc acc	739
Leu Thr Asp Val Asp Ala Pro Ala Thr Gly Pro Gln Gly Ala Ala Thr	
200 205 210	
gta ttc ggg ccc caa aaa ggt gcc acc gaa aaa gac att tcg ctt ctc	787
Val Phe Gly Pro Gln Lys Gly Ala Thr Glu Lys Asp Ile Ser Leu Leu	
215 220 225	
gac gcc gcc ctc cac gcc tgc gcc caa ctg gaa gtt gat ggc aca	835
Asp Ala Ala Leu His His Ala Cys Ala Gln Leu Glu Val Asp Gly Thr	
230 235 240 245	
aag cca ggt atg ggc gca gcc ggg ggc att gca atc gga ctg acg tgg	883
Lys Pro Gly Met Gly Ala Ala Gly Gly Ile Ala Ile Gly Leu Thr Trp	
250 255 260	
ctg tcc acc ctc atg cac ggc aac gac caa cag atc cat atc ctc ccc	931
Leu Ser Thr Leu Met His Gly Asn Asp Gln Gln Ile His Ile Leu Pro	
265 270 275	
ggc gcg cca ctg att gcc cgc tcc aac gga atc gag gat gcg ctg cca	979
Gly Ala Pro Leu Ile Ala Arg Ser Asn Gly Ile Glu Asp Ala Leu Pro	
280 285 290	
gaa act gac ttg ttg atc acc ggt gaa ggc cga cta gat tcc caa tcg	1027
Glu Thr Asp Leu Leu Ile Thr Gly Glu Gly Arg Leu Asp Ser Gln Ser	
295 300 305	
ttc acc gga aag gtt gtg ggc acc ctc cac ggt tta gct aaa gcc cac	1075
Phe Thr Gly Lys Val Val Gly Thr Leu His Gly Leu Ala Lys Ala His	
310 315 320 325	
gat gtg gat ctc gct gtt gcg gcc gcc atc gtg gaa ggc ggt att ccc	1123
Asp Val Asp Leu Ala Val Ala Ala Gly Ile Val Glu Gly Gly Ile Pro	
330 335 340	
gat gat ttc cta gcg gta gaa atg att aaa tcc tcc gac gtt gca gca	1171
Asp Asp Phe Leu Ala Val Glu Met Ile Lys Ser Ser Asp Val Ala Ala	
345 350 355	

caa tta cgt gat gca ggc cga agg atc gct caa gaa tac gta gct caa 1219
 Gln Leu Arg Asp Ala Gly Arg Arg Ile Ala Gln Glu Tyr Val Ala Gln
 360 365 370

aac tagcgaagga tctccacagt cca 1245
 Asn

<210> 994

<211> 374

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 994

Met Ser Asn Ser Pro Thr Asp Val Ser Thr Ser Ala Pro Arg Ile Met
 1 5 10 15

Ile Ala Pro Asp Ser Tyr Lys Gly Thr Ala Thr Ala Ser Glu Ala Ala
 20 25 30

Gln Tyr Leu Gly Glu Gly Val Leu Glu Ile Leu Pro Asn Ala Ser Ile
 35 40 45

Thr Leu Ala Pro Met Ala Asp Gly Gly Glu Gly Thr Ser Ser Val Phe
 50 55 60

Gly Gly Gln Val Ile Thr Leu Pro Thr Thr Asn Ala Ala Gly Arg Leu
 65 70 75 80

Thr Glu Ala Ser Tyr Thr Leu Asp Ser Glu Thr Asn Thr Ala Tyr Ile
 85 90 95

Asp Ile Ala Ala Ala Ser Gly Leu Pro Ala Val Ala Asp Asp Leu Val
 100 105 110

Pro Thr Thr Gly Asp Thr Tyr Gly Thr Gly Val Leu Ile Ala Asp Ala
 115 120 125

Val Thr Arg Gly Ala Thr Arg Ile Ala Leu Gly Leu Gly Gly Ser Ala
 130 135 140

Thr Thr Asp Ala Gly Ser Gly Ile Leu Ile Ala Leu Gly Ala Val Pro
 145 150 155 160

Arg Asn Lys Glu Gly Tyr Ala Leu Arg Thr Gly Gly Ala Asp Leu Ile
 165 170 175

Asn Leu Asp Tyr Ile Asp Thr Ala Glu Leu Asn Ile Pro Ala Ala Ala
 180 185 190

Val Glu Trp Ile Leu Leu Thr Asp Val Asp Ala Pro Ala Thr Gly Pro
 195 200 205

Gln Gly Ala Ala Thr Val Phe Gly Pro Gln Lys Gly Ala Thr Glu Lys
 210 215 220

Asp Ile Ser Leu Leu Asp Ala Ala Leu His His Ala Cys Ala Gln Leu
 225 230 235 240

Glu Val Asp Gly Thr Lys Pro Gly Met Gly Ala Ala Gly Gly Ile Ala

245	250	255
Ile Gly Leu Thr Trp Leu Ser Thr Leu Met His Gly Asn Asp Gln Gln		
260	265	270
Ile His Ile Leu Pro Gly Ala Pro Leu Ile Ala Arg Ser Asn Gly Ile		
275	280	285
Glu Asp Ala Leu Pro Glu Thr Asp Leu Leu Ile Thr Gly Glu Gly Arg		
290	295	300
Leu Asp Ser Gln Ser Phe Thr Gly Lys Val Val Gly Thr Leu His Gly		
305	310	315
Leu Ala Lys Ala His Asp Val Asp Leu Ala Val Ala Ala Gly Ile Val		
325	330	335
Glu Gly Gly Ile Pro Asp Asp Phe Leu Ala Val Glu Met Ile Lys Ser		
340	345	350
Ser Asp Val Ala Ala Gln Leu Arg Asp Ala Gly Arg Ile Ala Gln		
355	360	365
Glu Tyr Val Ala Gln Asn		
370		

<210> 995
 <211> 443
 <212> DNA
 <213> *Corynebacterium glutamicum*
 <220>
 <221> CDS
 <222> (1)..(420)
 <223> FRXA02104
 <400> 995

cac gcc tgc gcc caa ctg gaa gtt gat ggc aca aag cca ggt atg ggc	48
His Ala Cys Ala Gln Leu Glu Val Asp Gly Thr Lys Pro Gly Met Gly	
1 5 10 15	
gca gcc ggg ggc att gca atc gga ctg acg tgg ctg tcc acc ctc atg	96
Ala Ala Gly Gly Ile Ala Ile Gly Leu Thr Trp Leu Ser Thr Leu Met	
20 25 30	
cac ggc aac gac caa cag atc cat atc ctc ccc ggc gcg cca ctg att	144
His Gly Asn Asp Gln Gln Ile His Ile Leu Pro Gly Ala Pro Leu Ile	
35 40 45	
gcc cgc tcc aac gga atc gag gat gcg ctg cca gaa act gac ttg ttg	192
Ala Arg Ser Asn Gly Ile Glu Asp Ala Leu Pro Glu Thr Asp Leu Leu	
50 55 60	
atc acc ggt gaa ggc cga cta gat tcc caa tcg ttc acc gga aag gtt	240
Ile Thr Gly Glu Gly Arg Leu Asp Ser Gln Ser Phe Thr Gly Lys Val	
65 70 75 80	
gtg ggc acc ctc cac ggt tta gct aaa gcc cac gat gtg gat ctc gct	288
Val Gly Thr Leu His Gly Leu Ala Lys Ala His Asp Val Asp Leu Ala	
85 90 95	

```

gtt gcg gcc gcc atc gtg gaa ggc ggt att ccc gat gat ttc cta gcg 336
Val Ala Ala Gly Ile Val Glu Gly Gly Ile Pro Asp Asp Phe Leu Ala
      100      105      110

gta gaa atg att aaa tcc tcc gac gtt gca gca caa tta cgt gat gca 384
Val Glu Met Ile Lys Ser Ser Asp Val Ala Ala Gln Leu Arg Asp Ala
      115      120      125

ggc cga agg atc gct caa gaa tac gta gct caa aac tagcgaagga 430
Gly Arg Arg Ile Ala Gln Glu Tyr Val Ala Gln Asn
      130      135      140

tctccacagt cca 443

```

```

<210> 996
<211> 140
<212> PRT
<213> Corynebacterium glutamicum

```

```

<400> 996
His Ala Cys Ala Gln Leu Glu Val Asp Gly Thr Lys Pro Gly Met Gly
  1          5          10          15

Ala Ala Gly Gly Ile Ala Ile Gly Leu Thr Trp Leu Ser Thr Leu Met
      20          25          30

His Gly Asn Asp Gln Gln Ile His Ile Leu Pro Gly Ala Pro Leu Ile
      35          40          45

Ala Arg Ser Asn Gly Ile Glu Asp Ala Leu Pro Glu Thr Asp Leu Leu
      50          55          60

Ile Thr Gly Glu Gly Arg Leu Asp Ser Gln Ser Phe Thr Gly Lys Val
      65          70          75          80

Val Gly Thr Leu His Gly Leu Ala Lys Ala His Asp Val Asp Leu Ala
      85          90          95

Val Ala Ala Gly Ile Val Glu Gly Gly Ile Pro Asp Asp Phe Leu Ala
      100          105          110

Val Glu Met Ile Lys Ser Ser Asp Val Ala Ala Gln Leu Arg Asp Ala
      115          120          125

Gly Arg Arg Ile Ala Gln Glu Tyr Val Ala Gln Asn
      130          135          140

```

```

<210> 997
<211> 553
<212> DNA
<213> Corynebacterium glutamicum

```

```

<220>
<221> CDS
<222> (101)..(553)
<223> FRXA02071

```

```

<400> 997

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catggattcc catttggagc cttatttaca caggccacct ggcttgtttc ccaccgcgat 60

gtgccacaat aacgccataa cagaaaggca tactgacaca atg tcc aac tcc ccc 115
Met Ser Asn Ser Pro
1 5

acc gac gtt tca acg agc gca cct cga att atg atc gcg cca gat tcc 163
Thr Asp Val Ser Thr Ser Ala Pro Arg Ile Met Ile Ala Pro Asp Ser
10 15 20

tac aaa gga acc gct acc gca tca gaa gct gcg caa tac tta ggc gaa 211
Tyr Lys Gly Thr Ala Thr Ala Ser Glu Ala Ala Gln Tyr Leu Gly Glu
25 30 35

ggc gtg ttg gaa att ttg ccc aac gcc tcc att acg ttg gca ccc atg 259
Gly Val Leu Glu Ile Leu Pro Asn Ala Ser Ile Thr Leu Ala Pro Met
40 45 50

gcc gac ggt ggc gaa gga aca tcc tca gtt ttc ggc ggg cag gtc ata 307
Ala Asp Gly Gly Glu Gly Thr Ser Ser Val Phe Gly Gly Gln Val Ile
55 60 65

aca tta ccc acg aca aat gcc gcg gga cgc ctc acc gaa gcc agc tac 355
Thr Leu Pro Thr Thr Asn Ala Ala Gly Arg Leu Thr Glu Ala Ser Tyr
70 75 80 85

acc tta gat tcc gaa aca aac act gcc tac att gac atc gcc gca gcc 403
Thr Leu Asp Ser Glu Thr Asn Thr Ala Tyr Ile Asp Ile Ala Ala Ala
90 95 100

tcc ggt ttg ccc gcc gtt gca gac gat cta gtc ccc acc acc ggc gat 451
Ser Gly Leu Pro Ala Val Ala Asp Asp Leu Val Pro Thr Thr Gly Asp
105 110 115

acc tac ggc acc ggc gtt ttg atc gca gac gcg gtc acc cgt ggc gca 499
Thr Tyr Gly Thr Gly Val Leu Ile Ala Asp Ala Val Thr Arg Gly Ala
120 125 130

act cgc att gct tta ggc ctt ggc gga tca gcc aca act gac gcc ggc 547
Thr Arg Ile Ala Leu Gly Leu Gly Gly Ser Ala Thr Thr Asp Ala Gly
135 140 145

tca gga 553
Ser Gly
150

<210> 998
<211> 151
<212> PRT
<213> Corynebacterium glutamicum

<400> 998
Met Ser Asn Ser Pro Thr Asp Val Ser Thr Ser Ala Pro Arg Ile Met
1 5 10 15
Ile Ala Pro Asp Ser Tyr Lys Gly Thr Ala Thr Ala Ser Glu Ala Ala
20 25 30
Gln Tyr Leu Gly Glu Gly Val Leu Glu Ile Leu Pro Asn Ala Ser Ile
35 40 45

```

Thr Leu Ala Pro Met Ala Asp Gly Gly Glu Gly Thr Ser Ser Val Phe
  50                      55                      60

Gly Gly Gln Val Ile Thr Leu Pro Thr Thr Asn Ala Ala Gly Arg Leu
  65                      70                      75                      80

Thr Glu Ala Ser Tyr Thr Leu Asp Ser Glu Thr Asn Thr Ala Tyr Ile
                      85                      90                      95

Asp Ile Ala Ala Ala Ser Gly Leu Pro Ala Val Ala Asp Asp Leu Val
  100                    105                    110

Pro Thr Thr Gly Asp Thr Tyr Gly Thr Gly Val Leu Ile Ala Asp Ala
  115                    120                    125

Val Thr Arg Gly Ala Thr Arg Ile Ala Leu Gly Leu Gly Gly Ser Ala
  130                    135                    140

Thr Thr Asp Ala Gly Ser Gly
  145                    150

```

```

<210> 999
<211> 465
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(442)
<223> RXN02107

<400> 999
aagaagtaga gctcagcgat gaagatttcg cggcaggcca cgacctagta aaaaccaa 60
acgcaccga ggagtggaact aagcgagttc aatagtttct atg gat ctg cac aag 115
                                         Met Asp Leu His Lys
                                         1                      5

gta gct gca gcg cac gcg gcg act ctt ccc ctg agc acc aaa gag ttt 163
Val Ala Ala Ala His Ala Ala Thr Leu Pro Leu Ser Thr Lys Glu Phe
                      10                      15                      20

cct ttc gga ccc gag cac gaa gtg tac aaa gtg cgg ggc aag gta ttt 211
Pro Phe Gly Pro Glu His Glu Val Tyr Lys Val Arg Gly Lys Val Phe
                      25                      30                      35

ttg ctg ctc acg ata cta aat gat gag cgg att atc acg ctg aaa tca 259
Leu Leu Leu Thr Ile Leu Asn Asp Glu Pro Ile Ile Thr Leu Lys Ser
                      40                      45                      50

gac ccc gag att ggc gct tca cta cgc agt ggc ttc ccc acc atc cag 307
Asp Pro Glu Ile Gly Ala Ser Leu Arg Ser Gly Phe Pro Thr Ile Gln
                      55                      60                      65

gct gga tat cac atg aac aaa gtg cac tgg ctg agc att agc gat ggt 355
Ala Gly Tyr His Met Asn Lys Val His Trp Leu Ser Ile Ser Asp Gly
                      70                      75                      80

gaa cgg atc acg aaa gac ttc atc gaa ggt ctc gtg gaa gag tcc tat 403

```


Glu Arg Ile Thr	90	Leu Asp Phe Ile	Glu Gly	95	Leu Val Glu Glu Ser Tyr	100	
gaa ctg gta att	tcc acc ttg ccg	aag tat aaa agg	cct taacttggtt				452
Glu Leu Val Ile	Ser Thr Leu Pro	Lys Tyr Lys Arg	Pro	110			
gcttgccgggt ggc							465

```
<210> 1000
<211> 114
<212> PRT
<213> Corynebacterium glutamicum
```

400> 1000
Met Asp Leu His Lys Val Ala Ala Ala His Ala Ala Thr Leu Pro Leu
1 5 10 15
Ser Thr Lys Glu Phe Pro Phe Gly Pro Glu His Glu Val Tyr Lys Val
20 25 30
Arg Gly Lys Val Phe Leu Leu Leu Thr Ile Leu Asn Asp Glu Pro Ile
35 40 45
Ile Thr Leu Lys Ser Asp Pro Glu Ile Gly Ala Ser Leu Arg Ser Gly
50 55 60
Phe Pro Thr Ile Gln Ala Gly Tyr His Met Asn Lys Val His Trp Leu
65 70 75 80
Ser Ile Ser Asp Gly Glu Arg Ile Thr Lys Asp Phe Ile Glu Gly Leu
85 90 95
Val Glu Glu Ser Tyr Glu Leu Val Ile Ser Thr Leu Pro Lys Tyr Lys
100 105 110
Arg Pro

```
<210> 1001
<211> 465
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(442)
<223> FRXA02107
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<400> 1001
aagaagtaga gctcagcgat gaagatttgc cggcaggcca cgacctagta aaaaccaaatt 60
acgccaccga ggagtggact aagcgagttc aatagtttct atg gat ctg cac aag 115
Met Asp Leu His Lys
1 5
gta gct gca gcg cac gcg gcg act ctt ccc ctg agc acc aaa gag ttt 163
Val Ala Ala Ala His Ala Ala Thr Leu Pro Leu Ser Thr Lys Glu Phe
10 15 20

```

gta gct gca gcg cac gcg gcg act ctt ccc ctg agc acc aaa gag ttt 163
Val Ala Ala Ala His Ala Ala Thr Leu Pro Leu Ser Thr Lys Glu Phe
10 15 20

```

cct ttc gga ccc gag cac gaa gtg tac aaa gtg cgg ggc aag gta ttt 211
Pro Phe Gly Pro Glu His Glu Val Tyr Lys Val Arg Gly Lys Val Phe
      25              30              35

ttg ctg ctc acg ata cta aat gat gag ccg att atc acg ctg aaa tca 259
Leu Leu Leu Thr Ile Leu Asn Asp Glu Pro Ile Ile Thr Leu Lys Ser
      40              45              50

gac ccc gag att ggc gct tca cta cgc agt ggc ttc ccc acc atc cag 307
Asp Pro Glu Ile Gly Ala Ser Leu Arg Ser Gly Phe Pro Thr Ile Gln
      55              60              65

gct gga tat cac atg aac aaa gtg cac tgg ctg agc att agc gat ggt 355
Ala Gly Tyr His Met Asn Lys Val His Trp Leu Ser Ile Ser Asp Gly
      70              75              80              85

gaa cgg atc acg aaa gac ttc atc gaa ggt ctc gtg gaa gag tcc tat 403
Glu Arg Ile Thr Lys Asp Phe Ile Glu Gly Leu Val Glu Glu Ser Tyr
      90              95              100

gaa ctg gta att tcc acc ttg ccg aag tat aaa agg cct taacttggtt 452
Glu Leu Val Ile Ser Thr Leu Pro Lys Tyr Lys Arg Pro
      105              110

gcttgccgggt ggc 465

<210> 1002
<211> 114
<212> PRT
<213> Corynebacterium glutamicum

<400> 1002
Met Asp Leu His Lys Val Ala Ala Ala His Ala Ala Thr Leu Pro Leu
  1              5              10              15

Ser Thr Lys Glu Phe Pro Phe Gly Pro Glu His Glu Val Tyr Lys Val
      20              25              30

Arg Gly Lys Val Phe Leu Leu Leu Thr Ile Leu Asn Asp Glu Pro Ile
      35              40              45

Ile Thr Leu Lys Ser Asp Pro Glu Ile Gly Ala Ser Leu Arg Ser Gly
      50              55              60

Phe Pro Thr Ile Gln Ala Gly Tyr His Met Asn Lys Val His Trp Leu
      65              70              75              80

Ser Ile Ser Asp Gly Glu Arg Ile Thr Lys Asp Phe Ile Glu Gly Leu
      85              90              95

Val Glu Glu Ser Tyr Glu Leu Val Ile Ser Thr Leu Pro Lys Tyr Lys
      100              105              110

Arg Pro

```

<210> 1003

<211> 732

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> {101}..{709}

<223> RXN02108

<400> 1003

aagacttcat cgaagggtctc gtggaagagt cctatgaact ggtaatttcc accttgccga 60

agataaaag gccttaactt ggttgcttgc ggggtggcaag atg ggt gat atg aaa 115
 Met Gly Asp Met Lys
 1 5

att acc cgc cac atc cat gca tgc gtt gag atc tca cag gga aac gat 163
 Ile Thr Arg His Ile His Ala Cys Val Glu Ile Ser Gln Gly Asn Asp
 10 15 20

cga atc att att gat ccc ggt act ttt ggc gcc cca gat tta tgt ggc 211
 Arg Ile Ile Ile Asp Pro Gly Thr Phe Gly Ala Pro Asp Leu Cys Gly
 25 30 35

gcg acc atc ctg gtc acc cac aat cat gcc gat cac gtt gat ccc gag 259
 Ala Thr Ile Leu Val Thr His Asn His Ala Asp His Val Asp Pro Glu
 40 45 50

ttg ctc aag ccc ggc atg acg att tac gcg cct cga tca gta gca cat 307
 Leu Leu Lys Pro Gly Met Thr Ile Tyr Ala Pro Arg Ser Val Ala His
 55 60 65

tca att cca gta gaa tgc cac atc gtg gaa cac ggc cga aac ttt acc 355
 Ser Ile Pro Val Glu Cys His Ile Val Glu His Gly Arg Asn Phe Thr
 70 75 80 85

gtt ggg tcc cta tcc gtt gag gtt ctt ggt tct gaa cat gcg atg ctc 403
 Val Gly Ser Leu Ser Val Glu Val Leu Gly Ser Glu His Ala Met Leu
 90 95 100

acc cat tcc atg ccg atc gcg gaa aac gtt gga tac tta atc aac ggc 451
 Thr His Ser Met Pro Ile Ala Glu Asn Val Gly Tyr Leu Ile Asn Gly
 105 110 115

cga gtg ctc cac ccc ggc gat acc ttc caa ccc att aaa gat gtc gaa 499
 Arg Val Leu His Pro Gly Asp Thr Phe Gln Pro Ile Lys Asp Val Glu
 120 125 130

ctc gcc ctg gtt cct gtc aac ggc ccc tgg gtg aaa atg ctg gat gtg 547
 Leu Ala Leu Val Pro Val Asn Gly Pro Trp Val Lys Met Leu Asp Val
 135 140 145

gaa ggc tat ttg aag aaa ttt cca cca aag cgt ttc atc ggc att cac 595
 Glu Gly Tyr Leu Lys Lys Phe Pro Pro Lys Arg Phe Ile Gly Ile His
 150 155 160 165

gat ggc att gtt aat gat cgc ggt ttg gcg atc aac aag aag ttc tta 643
 Asp Gly Ile Val Asn Asp Arg Gly Leu Ala Ile Asn Lys Lys Phe Leu
 170 175 180

acg cat ctt ggt gaa acc tat ggc tcg gaa tac tcg ccg ctt gaa gag 691
 Thr His Leu Gly Glu Thr Tyr Gly Ser Glu Tyr Ser Pro Leu Glu Glu

185

190

195

gga gag tcg ttg gaa att tagattcttg gtttagattc ttg
 Gly Glu Ser Leu Glu Ile
 200

732

<210> 1004

<211> 203

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1004

Met Gly Asp Met Lys Ile Thr Arg His Ile His Ala Cys Val Glu Ile
 1 5 10 15

Ser Gln Gly Asn Asp Arg Ile Ile Ile Asp Pro Gly Thr Phe Gly Ala
 20 25 30

Pro Asp Leu Cys Gly Ala Thr Ile Leu Val Thr His Asn His Ala Asp
 35 40 45

His Val Asp Pro Glu Leu Leu Lys Pro Gly Met Thr Ile Tyr Ala Pro
 50 55 60

Arg Ser Val Ala His Ser Ile Pro Val Glu Cys His Ile Val Glu His
 65 70 75 80

Gly Arg Asn Phe Thr Val Gly Ser Leu Ser Val Glu Val Leu Gly Ser
 85 90 95

Glu His Ala Met Leu Thr His Ser Met Pro Ile Ala Glu Asn Val Gly
 100 105 110

Tyr Leu Ile Asn Gly Arg Val Leu His Pro Gly Asp Thr Phe Gln Pro
 115 120 125

Ile Lys Asp Val Glu Leu Ala Leu Val Pro Val Asn Gly Pro Trp Val
 130 135 140

Lys Met Leu Asp Val Glu Gly Tyr Leu Lys Lys Phe Pro Pro Lys Arg
 145 150 155 160

Phe Ile Gly Ile His Asp Gly Ile Val Asn Asp Arg Gly Leu Ala Ile
 165 170 175

Asn Lys Lys Phe Leu Thr His Leu Gly Glu Thr Tyr Gly Ser Glu Tyr
 180 185 190

Ser Pro Leu Glu Glu Gly Glu Ser Leu Glu Ile
 195 200

<210> 1005

<211> 558

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(535)

<223> FRXA02108

<400> 1005

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 tcatgccgat cacgttgatc ccgagttgct caagcccgcg atg acg att tac gcg 115
 Met Thr Ile Tyr Ala
 1 5
 cct cga tca gta gca cat tca att cca gta gaa tgc cac atc gtg gaa 163
 Pro Arg Ser Val Ala His Ser Ile Pro Val Glu Cys His Ile Val Glu
 10 15 20
 cac ggc cga aac ttt acc gtt ggg tcc cta tcc gtt gag gtt ctt ggt 211
 His Gly Arg Asn Phe Thr Val Gly Ser Leu Ser Val Glu Val Leu Gly
 25 30 35
 tct gaa cat gcg atg ctc acc cat tcc atg ccg atc gcg gaa aac gtt 259
 Ser Glu His Ala Met Leu Thr His Ser Met Pro Ile Ala Glu Asn Val
 40 45 50
 gga tac tta atc aac ggc cga gtg ctc cac ccc ggc gat acc ttc caa 307
 Gly Tyr Leu Ile Asn Gly Arg Val Leu His Pro Gly Asp Thr Phe Gln
 55 60 65
 ccc att aaa gat gtc gaa ctc gcc ctg gtt cct gtc aac ggc ccc tgg 355
 Pro Ile Lys Asp Val Glu Leu Ala Leu Val Pro Val Asn Gly Pro Trp
 70 75 80 85
 gtg aaa atg ctg gat gtg gaa ggc tat ttg aag aaa ttt cca cca aag 403
 Val Lys Met Leu Asp Val Glu Gly Tyr Leu Lys Lys Phe Pro Pro Lys
 90 95 100
 cgt ttc atc ggc att cac gat ggc att gtt aat gat cgc ggt ttg gcg 451
 Arg Phe Ile Gly Ile His Asp Gly Ile Val Asn Asp Arg Gly Leu Ala
 105 110 115
 atc aac aag aag ttc tta acg cat ctt ggt gaa acc tat ggc tcg gaa 499
 Ile Asn Lys Lys Phe Leu Thr His Leu Gly Glu Thr Tyr Gly Ser Glu
 120 125 130
 tac tcg ccg ctt gaa gag gga gag tcg ttg gaa att tagattcttg 545
 Tyr Ser Pro Leu Glu Glu Gly Glu Ser Leu Glu Ile
 135 140 145
 gtttagattc ttg 558

<210> 1006

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 1006

Met Thr Ile Tyr Ala Pro Arg Ser Val Ala His Ser Ile Pro Val Glu
 1 5 10 15
 Cys His Ile Val Glu His Gly Arg Asn Phe Thr Val Gly Ser Leu Ser
 20 25 30
 Val Glu Val Leu Gly Ser Glu His Ala Met Leu Thr His Ser Met Pro

35		40		45
Ile Ala Glu Asn Val Gly Tyr	Leu Ile Asn Gly Arg Val Leu His Pro			
50	55	60		
Gly Asp Thr Phe Gln Pro	Ile Lys Asp Val Glu Leu Ala Leu Val Pro			
65	70	75	80	
Val Asn Gly Pro Trp Val Lys Met Leu Asp Val Glu Gly Tyr Leu Lys				
85	90	95		
Lys Phe Pro Pro Lys Arg Phe Ile Gly Ile His Asp Gly Ile Val Asn				
100	105	110		
Asp Arg Gly Leu Ala Ile Asn Lys Lys Phe Leu Thr His Leu Gly Glu				
115	120	125		
Thr Tyr Gly Ser Glu Tyr Ser Pro Leu Glu Glu Gly Glu Ser Leu Glu				
130	135	140		

Ile
145

<210> 1007
<211> 509
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(486)
<223> RXN02114

<400> 1007	
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Ser Ile Gly Tyr Ala Trp Thr Thr Ala Phe His Ala Leu Thr Pro Gly	
1 5 10 15	
ctt ggc ggc atc gcc att ggt att tgg ctg ctc ggt ggt gtg ctc ggt	96
Leu Gly Gly Ile Ala Ile Gly Ile Trp Leu Leu Gly Gly Val Leu Gly	
20 25 30	
ggg ttg gtt atc cgc aag ccg ggt gcc gca att ttc gtt gaa gta gtg	144
Gly Leu Val Ile Arg Lys Pro Gly Ala Ala Ile Phe Val Glu Val Val	
35 40 45	
gcc gca tgt gtc tct gca gcg ctt gct tca cag ttt ggt atc tcc acc	192
Ala Ala Cys Val Ser Ala Ala Leu Ala Ser Gln Phe Gly Ile Ser Thr	
50 55 60	
att tac tcc ggc ttg gcg cag gga atc ggc gct gaa atc atc ttc gcg	240
Ile Tyr Ser Gly Leu Ala Gln Gly Ile Gly Ala Glu Ile Ile Phe Ala	
65 70 75 80	
ctg ttc ctc tac cgt cgc tac agc ctg ccc acc acc atg ctt gca ggt	288
Leu Phe Leu Tyr Arg Arg Tyr Ser Leu Pro Thr Thr Met Leu Ala Gly	
85 90 95	
atg ggc gca ggt ggc gcc gca att ttc ctg gaa atg ttc ttc tac gga	336
Met Gly Ala Gly Gly Gly Ala Ile Phe Leu Glu Met Phe Phe Tyr Gly	

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100          105          110
aac ctc gca aag acg atg tcc ttc aac atc atc tat tcc acc act gtc 384
Asn Leu Ala Lys Thr Met Ser Phe Asn Ile Ile Tyr Ser Thr Thr Val
115          120          125

ctt att tcc ggt gcg atc ctt gcc gcc ctg ctc agc tgg tac ctg gtc 432
Leu Ile Ser Gly Ala Ile Leu Ala Gly Leu Leu Ser Trp Tyr Leu Val
130          135          140

cgc gcg ttg gcg agg act ggt gca ctt gat cgt ttc gcc gct gcc cgc 480
Arg Ala Leu Ala Arg Thr Gly Ala Leu Asp Arg Phe Ala Ala Gly Arg
145          150          155

gag gta taaatgacca cgcacttgg aac 509
Glu Val

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<210> 1008
<211> 162
<212> PRT
<213> Corynebacterium glutamicum

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<400> 1008
Ser Ile Gly Tyr Ala Trp Thr Thr Ala Phe His Ala Leu Thr Pro Gly
1      5      10
Leu Gly Gly Ile Ala Ile Gly Ile Trp Leu Leu Gly Gly Val Leu Gly
20     25     30
Gly Leu Val Ile Arg Lys Pro Gly Ala Ala Ile Phe Val Glu Val Val
35     40     45
Ala Ala Cys Val Ser Ala Ala Leu Ala Ser Gln Phe Gly Ile Ser Thr
50     55     60
Ile Tyr Ser Gly Leu Ala Gln Gly Ile Gly Ala Glu Ile Ile Phe Ala
65     70     75     80
Leu Phe Leu Tyr Arg Arg Tyr Ser Leu Pro Thr Thr Met Leu Ala Gly
85     90     95
Met Gly Ala Gly Gly Gly Ala Ile Phe Leu Glu Met Phe Phe Tyr Gly
100    105    110
Asn Leu Ala Lys Thr Met Ser Phe Asn Ile Ile Tyr Ser Thr Thr Val
115    120    125
Leu Ile Ser Gly Ala Ile Leu Ala Gly Leu Leu Ser Trp Tyr Leu Val
130    135    140
Arg Ala Leu Ala Arg Thr Gly Ala Leu Asp Arg Phe Ala Ala Gly Arg
145    150    155    160
Glu Val

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<210> 1009
<211> 509

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<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> {1}..(486)

<223> FRXA02114

<400> 1009

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Ser	Ile	Gly	Tyr	Ala	Trp	Thr	Thr	Ala	Phe	His	Ala	Leu	Thr	Pro	Gly	
1				5					10					15		

ctt	ggc	ggc	atc	gcc	att	ggt	att	tgg	ctg	ctc	ggt	ggt	gtg	ctc	ggt	96
Leu	Gly	Gly	Ile	Ala	Ile	Gly	Ile	Trp	Leu	Leu	Gly	Gly	Val	Leu	Gly	
			20					25					30			

ggg	tgt	ggt	atc	cgc	aag	cgc	ggt	gcc	gca	att	ttc	ggt	gaa	gta	gtg	144
Gly	Leu	Val	Ile	Arg	Lys	Pro	Gly	Ala	Ala	Ile	Phe	Val	Glu	Val	Val	
		35					40					45				

gcc	gca	tgt	gtc	tct	gca	gcg	ctt	gct	tca	cag	ttt	ggt	atc	tcc	acc	192
Ala	Ala	Cys	Val	Ser	Ala	Ala	Leu	Ala	Ser	Gln	Phe	Gly	Ile	Ser	Thr	
	50					55					60					

att	tac	tcc	ggc	tgt	gcg	cag	gga	atc	ggc	gct	gaa	atc	atc	ttc	gcg	240
Ile	Tyr	Ser	Gly	Leu	Ala	Gln	Gly	Ile	Gly	Ala	Glu	Ile	Ile	Phe	Ala	
	65				70				75					80		

ctg	ttc	ctc	tac	cgt	cgc	tac	agc	ctg	ccc	acc	acc	atg	ctt	gca	ggt	288
Leu	Phe	Leu	Tyr	Arg	Arg	Tyr	Ser	Leu	Pro	Thr	Thr	Met	Leu	Ala	Gly	
				85					90					95		

atg	ggc	gca	ggt	ggc	ggc	gca	att	ttc	ctg	gaa	atg	ttc	ttc	tac	gga	336
Met	Gly	Ala	Gly	Gly	Gly	Ala	Ile	Phe	Leu	Glu	Met	Phe	Phe	Tyr	Gly	
			100				105						110			

aac	ctc	gca	aag	acg	atg	tcc	ttc	aac	atc	atc	tat	tcc	acc	act	gtc	384
Asn	Leu	Ala	Lys	Thr	Met	Ser	Phe	Asn	Ile	Ile	Tyr	Ser	Thr	Thr	Val	
		115					120					125				

ctt	att	tcc	ggt	gcg	atc	ctt	gcc	ggc	ctg	ctc	agc	tgg	tac	ctg	gtc	432
Leu	Ile	Ser	Gly	Ala	Ile	Leu	Ala	Gly	Leu	Leu	Ser	Trp	Tyr	Leu	Val	
	130					135					140					

cgc	gcg	tgt	gcg	agg	act	ggt	gca	ctt	gat	cgt	ttc	gcc	gct	ggc	cgc	480
Arg	Ala	Leu	Ala	Arg	Thr	Gly	Ala	Leu	Asp	Arg	Phe	Ala	Ala	Gly	Arg	
145					150				155					160		

gag	gta	taaatgacca	cgcacttgg	aac												509
Glu	Val															

<210> 1010

<211> 162

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1010

Ser Ile Gly Tyr Ala Trp Thr Thr Ala Phe His Ala Leu Thr Pro Gly

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Leu Gly Gly Ile Ala Ile Gly Ile Trp Leu Leu Gly Gly Val Leu Gly
20 25 30

Gly Leu Val Ile Arg Lys Pro Gly Ala Ala Ile Phe Val Glu Val Val
35 40 45

Ala Ala Cys Val Ser Ala Ala Leu Ala Ser Gln Phe Gly Ile Ser Thr
50 55 60

Ile Tyr Ser Gly Leu Ala Gln Gly Ile Gly Ala Glu Ile Ile Phe Ala
65 70 75 80

Leu Phe Leu Tyr Arg Arg Tyr Ser Leu Pro Thr Thr Met Leu Ala Gly
85 90 95

Met Gly Ala Gly Gly Gly Ala Ile Phe Leu Glu Met Phe Phe Tyr Gly
100 105 110

Asn Leu Ala Lys Thr Met Ser Phe Asn Ile Ile Tyr Ser Thr Thr Val
115 120 125

Leu Ile Ser Gly Ala Ile Leu Ala Gly Leu Leu Ser Trp Tyr Leu Val
130 135 140

Arg Ala Leu Ala Arg Thr Gly Ala Leu Asp Arg Phe Ala Ala Gly Arg
145 150 155 160

Glu Val

<210> 1011
<211> 828
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (101)..(805)
<223> RXN02121

<400> 1011
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tgggatacct tcgagacaaa ctctcgaaaag ctccgcgaacc atg atc acc tca cca 115
Met Ile Thr Ser Pro
1 5
ttt gag cgc gag ctg aag ctg ctc aac gag ggg gaa ctg ggt att gtc 163
Phe Glu Arg Glu Leu Lys Leu Leu Asn Glu Gly Glu Leu Gly Ile Val
10 15 20
cag cag ttg gtg gaa tca agc aac atc gga ttc atc gtc gat ctt gaa 211
Gln Gln Leu Val Glu Ser Ser Asn Ile Gly Phe Ile Val Asp Leu Glu
25 30 35
tta gat ggc gat tat ggg tgg gcg gtc tac aaa ccg gaa ttg ggg gag 259
Leu Asp Gly Asp Tyr Gly Trp Ala Val Tyr Lys Pro Glu Leu Gly Glu
40 45 50

caa ccc ctg tgg gat ttc cct cct ggc ctg tac aaa cgt gaa cgt gca 307
 Gln Pro Leu Trp Asp Phe Pro Pro Gly Leu Tyr Lys Arg Glu Arg Ala
 55 60 65
 gcc ttt gtg atc agt gag ttt ttg ggt tgg aac atc gtg cct cca acg 355
 Ala Phe Val Ile Ser Glu Phe Leu Gly Trp Asn Ile Val Pro Pro Thr
 70 75 80 85
 gtg atc atg cac gat gcc cgg gct ggt gtg ggc tcg gtg cag tgg ttt 403
 Val Ile Met His Asp Ala Pro Ala Gly Val Gly Ser Val Gln Trp Phe
 90 95 100
 att gaa aac aat ggc gaa cac tat ttt cca ctg ttt gac acc cgc gct 451
 Ile Glu Asn Asn Gly Glu His Tyr Phe Pro Leu Phe Asp Thr Arg Ala
 105 110 115
 gac ctg cat cgg cag ttt gtc cgc atg gct gtg ttt gat ctg ttg tgc 499
 Asp Leu His Pro Gln Phe Val Arg Met Ala Val Phe Asp Leu Leu Cys
 120 125 130
 aac aac act gac cgg aaa gcg ggc cat gtg ttg tta gac ggc gat cat 547
 Asn Asn Thr Asp Arg Lys Ala Gly His Val Leu Leu Asp Gly Asp His
 135 140 145
 att tgg ggc atc gat cac ggg ttg tgt ttt tcc gtc gaa cgg aag ctg 595
 Ile Trp Gly Ile Asp His Gly Leu Cys Phe Ser Val Glu Pro Lys Leu
 150 155 160 165
 cgc acg gtg att tgg gat ttc gca ggc tgc acc att cca gat gac ttg 643
 Arg Thr Val Ile Trp Asp Phe Ala Gly Cys Thr Ile Pro Asp Asp Leu
 170 175 180
 gtg aca gat gtt gag cag ctt ttg gag gac gtc cgg gaa gaa ctt cat 691
 Val Thr Asp Val Glu Gln Leu Leu Glu Asp Val Pro Glu Glu Leu His
 185 190 195
 cag ctt ctt cat ccc gca gaa att gat gcg ctg cag cgc cgt gcc tca 739
 Gln Leu Leu His Pro Ala Glu Ile Asp Ala Leu Gln Arg Arg Ala Ser
 200 205 210
 aga atc agc agg tta cgg ttc ctt cgg cag gcg aaa tcg cat cgt caa 787
 Arg Ile Ser Arg Leu Pro Phe Leu Pro Gln Ala Lys Ser His Arg Gln
 215 220 225
 ttc cct tgg cca ctt gtt tgagtaggct ggcgggcagg tgc 828
 Phe Pro Trp Pro Leu Val
 230 235

<210> 1012

<211> 235

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1012

Met Ile Thr Ser Pro Phe Glu Arg Glu Leu Lys Leu Leu Asn Glu Gly
 1 5 10 15

Glu Leu Gly Ile Val Gln Gln Leu Val Glu Ser Ser Asn Ile Gly Phe
 20 25 30

Ile	Val	Asp	Leu	Glu	Leu	Asp	Gly	Asp	Tyr	Gly	Trp	Ala	Val	Tyr	Lys
		35					40					45			
Pro	Glu	Leu	Gly	Glu	Gln	Pro	Leu	Trp	Asp	Phe	Pro	Pro	Gly	Leu	Tyr
		50				55					60				
Lys	Arg	Glu	Arg	Ala	Ala	Phe	Val	Ile	Ser	Glu	Phe	Leu	Gly	Trp	Asn
		65			70					75					80
Ile	Val	Pro	Pro	Thr	Val	Ile	Met	His	Asp	Ala	Pro	Ala	Gly	Val	Gly
				85					90					95	
Ser	Val	Gln	Trp	Phe	Ile	Glu	Asn	Asn	Gly	Glu	His	Tyr	Phe	Pro	Leu
			100					105					110		
Phe	Asp	Thr	Arg	Ala	Asp	Leu	His	Pro	Gln	Phe	Val	Arg	Met	Ala	Val
							120					125			
Phe	Asp	Leu	Leu	Cys	Asn	Asn	Thr	Asp	Arg	Lys	Ala	Gly	His	Val	Leu
						135					140				
Leu	Asp	Gly	Asp	His	Ile	Trp	Gly	Ile	Asp	His	Gly	Leu	Cys	Phe	Ser
					150					155				160	
Val	Glu	Pro	Lys	Leu	Arg	Thr	Val	Ile	Trp	Asp	Phe	Ala	Gly	Cys	Thr
					165				170					175	
Ile	Pro	Asp	Asp	Leu	Val	Thr	Asp	Val	Glu	Gln	Leu	Leu	Glu	Asp	Val
			180					185					190		
Pro	Glu	Glu	Leu	His	Gln	Leu	Leu	His	Pro	Ala	Glu	Ile	Asp	Ala	Leu
			195				200					205			
Gln	Arg	Arg	Ala	Ser	Arg	Ile	Ser	Arg	Leu	Pro	Phe	Leu	Pro	Gln	Ala
						215					220				
Lys	Ser	His	Arg	Gln	Phe	Pro	Trp	Pro	Leu	Val					
					230					235					

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<210> 1013
<211> 828
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(805)  
<223> FRXA02121
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tgggatacct togagacaaa cttccgaaag ctccgcaacc atg atc acc tca cca 115
Met Ile Thr Ser Pro
1 5
ttt gag cgc gag ctg aag ctg ctc aac gag ggg gaa ctg ggt att gtc 163
Phe Glu Arg Glu Leu Lys Leu Leu Asn Glu Gly Glu Leu Gly Ile Val
10 15 20
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cag cag ttg gtg gaa tca agc aac atc gga ttc atc gtc gat ctt gaa 211
Gln Gln Leu Val Glu Ser Ser Asn Ile Gly Phe Ile Val Asp Leu Glu
25 30 35

tta gat ggc gat tat ggg tgg gcg gtc tac aaa ccg gaa ttg ggg gag 259
Leu Asp Gly Asp Tyr Gly Trp Ala Val Tyr Lys Pro Glu Leu Gly Glu
40 45 50

caa ccc ctg tgg gat ttc cct cct ggc ctg tac aaa cgt gaa cgt gca 307
Gln Pro Leu Trp Asp Phe Pro Pro Gly Leu Tyr Lys Arg Glu Arg Ala
55 60 65

gcc ttt gtg atc agt gag ttt ttg ggt tgg aac atc gtg cct cca acg 355
Ala Phe Val Ile Ser Glu Phe Leu Gly Trp Asn Ile Val Pro Pro Thr
70 75 80 85

gtg atc atg cac gat gcc ccg gct ggt gtg ggc tcg gtg cag tgg ttt 403
Val Ile Met His Asp Ala Pro Ala Gly Val Gly Ser Val Gln Trp Phe
90 95 100

att gaa aac aat ggc gaa cac tat ttt cca ctg ttt gac acc cgc gct 451
Ile Glu Asn Asn Gly Glu His Tyr Phe Pro Leu Phe Asp Thr Arg Ala
105 110 115

gac ctg cat ccg cag ttt gtc cgc atg gct gtg ttt gat ctg ttg tgc 499
Asp Leu His Pro Gln Phe Val Arg Met Ala Val Phe Asp Leu Leu Cys
120 125 130

aac aac act gac ccg aaa tcg ggc cat gtg ttg cta gac ggc gat cat 547
Asn Asn Thr Asp Arg Lys Ser Gly His Val Leu Leu Asp Gly Asp His
135 140 145

att tgg ggc atc gat cac ggg ttg tgt ttt tcc gtc gaa ccg aag ctg 595
Ile Trp Gly Ile Asp His Gly Leu Cys Phe Ser Val Glu Pro Lys Leu
150 155 160 165

cgc acg gtg att tgg gat ttc gca ggc tgc acc att cca gat gac ttg 643
Arg Thr Val Ile Trp Asp Phe Ala Gly Cys Thr Ile Pro Asp Asp Leu
170 175 180

gtg aca gat gtt gag cag ctt ttg gag gac gtc ccg gaa gaa ctt cat 691
Val Thr Asp Val Glu Gln Leu Leu Glu Asp Val Pro Glu Glu Leu His
185 190 195

cag ctt ctt cat ccc gca gaa att gat gcg ctg cag cgc cgt gcc tca 739
Gln Leu Leu His Pro Ala Glu Ile Asp Ala Leu Gln Arg Arg Ala Ser
200 205 210

aga atc agc agg tta ccg ttc ctt ccg cag gcg aaa tcg cat cgt caa 787
Arg Ile Ser Arg Leu Pro Phe Leu Pro Gln Ala Lys Ser His Arg Gln
215 220 225

ttc cct tgg cca ctt gtt tgagtaggct ggccgggcagg tgc 828
Phe Pro Trp Pro Leu Val
230 235

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<210> 1014

<211> 235

<212> PRT

<213> Corynebacterium glutamicum

<400> 1014

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Glu	Leu	Gly	Ile	Val	Gln	Gln	Leu	Val	Glu	Ser	Ser	Asn	Ile	Gly	Phe
			20					25					30		

Ile	Val	Asp	Leu	Glu	Leu	Asp	Gly	Asp	Tyr	Gly	Trp	Ala	Val	Tyr	Lys
		35					40					45			

Pro	Glu	Leu	Gly	Glu	Gln	Pro	Leu	Trp	Asp	Phe	Pro	Pro	Gly	Leu	Tyr
	50					55					60				

Lys	Arg	Glu	Arg	Ala	Ala	Phe	Val	Ile	Ser	Glu	Phe	Leu	Gly	Trp	Asn
65					70					75					80

Ile	Val	Pro	Pro	Thr	Val	Ile	Met	His	Asp	Ala	Pro	Ala	Gly	Val	Gly
				85					90					95	

Ser	Val	Gln	Trp	Phe	Ile	Glu	Asn	Asn	Gly	Glu	His	Tyr	Phe	Pro	Leu
				100					105					110	

Phe	Asp	Thr	Arg	Ala	Asp	Leu	His	Pro	Gln	Phe	Val	Arg	Met	Ala	Val
		115					120					125			

Phe	Asp	Leu	Leu	Cys	Asn	Asn	Thr	Asp	Arg	Lys	Ser	Gly	His	Val	Leu
	130						135				140				

Leu	Asp	Gly	Asp	His	Ile	Trp	Gly	Ile	Asp	His	Gly	Leu	Cys	Phe	Ser
145					150					155					160

Val	Glu	Pro	Lys	Leu	Arg	Thr	Val	Ile	Trp	Asp	Phe	Ala	Gly	Cys	Thr
			165						170					175	

Ile	Pro	Asp	Asp	Leu	Val	Thr	Asp	Val	Glu	Gln	Leu	Leu	Glu	Asp	Val
			180					185					190		

Pro	Glu	Glu	Leu	His	Gln	Leu	Leu	His	Pro	Ala	Glu	Ile	Asp	Ala	Leu
			195				200					205			

Gln	Arg	Arg	Ala	Ser	Arg	Ile	Ser	Arg	Leu	Pro	Phe	Leu	Pro	Gln	Ala
	210					215					220				

Lys	Ser	His	Arg	Gln	Phe	Pro	Trp	Pro	Leu	Val
225				230					235	

<210> 1015

<211> 465

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(442)

<223> RXN02138

<400> 1015

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Met Thr Ala Pro Ser
1 5

acc aac acc ggt gtt atc ttg acc gag tcc gca gcg tcc aaa gct aag 163
Thr Asn Thr Gly Val Ile Leu Thr Glu Ser Ala Ala Ser Lys Ala Lys
10 15 20

gca ctc atc gat cag gaa ggc cgc gac gac ctc tct ctg cgt atc gcc 211
Ala Leu Ile Asp Gln Glu Gly Arg Asp Asp Leu Ser Leu Arg Ile Ala
25 30 35

gtt cag cct ggc ggc tgc tct ggc ctt cgt tac cag ctt tac ttc gac 259
Val Gln Pro Gly Gly Cys Ser Gly Leu Arg Tyr Gln Leu Tyr Phe Asp
40 45 50

gac cgc acc ctt gat ggc gat aag gaa gac atc gtc ggt ggc gtt cgc 307
Asp Arg Thr Leu Asp Gly Asp Lys Glu Asp Ile Val Gly Gly Val Arg
55 60 65

ctt gtc gtt gac aag atg agc acc cca tac ttg ctc ggc gct cag atc 355
Leu Val Val Asp Lys Met Ser Thr Pro Tyr Leu Leu Gly Ala Gln Ile
70 75 80 85

gac ttc gct gac acc atc gag cag cag ggc ttc acc atc gac aac cca 403
Asp Phe Ala Asp Thr Ile Glu Gln Gln Gly Phe Thr Ile Asp Asn Pro
90 95 100

aac gca ggc agc tct tgc gct tgt ggt gac tcc ttc aac taaagagatt 452
Asn Ala Gly Ser Ser Cys Ala Cys Gly Asp Ser Phe Asn
105 110

ccgttatgta gga 465

<210> 1016
<211> 114
<212> PRT
<213> Corynebacterium glutamicum

<400> 1016
Met Thr Ala Pro Ser Thr Asn Thr Gly Val Ile Leu Thr Glu Ser Ala
1 5 10 15

Ala Ser Lys Ala Lys Ala Leu Ile Asp Gln Glu Gly Arg Asp Asp Leu
20 25 30

Ser Leu Arg Ile Ala Val Gln Pro Gly Gly Cys Ser Gly Leu Arg Tyr
35 40 45

Gln Leu Tyr Phe Asp Asp Arg Thr Leu Asp Gly Asp Lys Glu Asp Ile
50 55 60

Val Gly Gly Val Arg Leu Val Val Asp Lys Met Ser Thr Pro Tyr Leu
65 70 75 80

Leu Gly Ala Gln Ile Asp Phe Ala Asp Thr Ile Glu Gln Gln Gly Phe
85 90 95

Thr Ile Asp Asn Pro Asn Ala Gly Ser Ser Cys Ala Cys Gly Asp Ser

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100

105

110

Phe Asn

<210> 1017

<211> 465

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(442)

<223> FRXA02138

<400> 1017

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aaagtaattc aaagggccaa cagttaagga gactaaagcg atg acc gct cca tca 115
 Met Thr Ala Pro Ser
 1 5

acc aac acc ggt gtt atc ttg acc gag tcc gca gcg tcc aaa gct aag 163
 Thr Asn Thr Gly Val Ile Leu Thr Glu Ser Ala Ala Ser Lys Ala Lys
 10 15 20

gca ctc atc gat cag gaa ggc cgc gac gac ctc tct ctg cgt atc gcc 211
 Ala Leu Ile Asp Gln Glu Gly Arg Asp Asp Leu Ser Leu Arg Ile Ala
 25 30 35

gtt cag cct ggc ggc tgc tct ggc ctt cgt tac cag ctt tac ttc gac 259
 Val Gln Pro Gly Gly Cys Ser Gly Leu Arg Tyr Gln Leu Tyr Phe Asp
 40 45 50

gac cgc acc ctt gat ggc gat aag gaa gac atc gtc ggt ggc gtt cgc 307
 Asp Arg Thr Leu Asp Gly Asp Lys Glu Asp Ile Val Gly Gly Val Arg
 55 60 65

ctt gtc gtt gac aag atg agc acc cca tac ttg ctc ggc gct cag atc 355
 Leu Val Val Asp Lys Met Ser Thr Pro Tyr Leu Gly Ala Gln Ile
 70 75 80 85

gac ttc gct gac acc atc gag cag cag ggc ttc acc atc gac aac cca 403
 Asp Phe Ala Asp Thr Ile Glu Gln Gln Gly Phe Thr Ile Asp Asn Pro
 90 95 100

aac gca ggc agc tct tgc gct tgt ggt gac tcc ttc aac taaagagatt 452
 Asn Ala Gly Ser Ser Cys Ala Cys Gly Asp Ser Phe Asn
 105 110

ccgttatgta gga 465

<210> 1018

<211> 114

<212> PRT

<213> Corynebacterium glutamicum

<400> 1018

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90 100	
gga aca tgg gaa tgg tac agc ggc tcg atg ctc tcg gcc acc aat atg Gly Thr Trp Glu Trp Tyr Ser Gly Ser Met Leu Ser Ala Thr Asn Met	451
105 110 115	
tac tgg ttc ctc tac ttc ttg gtc atc ttc aac cta ttt tta tgg gca Tyr Trp Phe Leu Tyr Phe Leu Val Ile Phe Asn Leu Phe Leu Trp Ala	499
120 125 130	
acg aga aaa ctc cca gct tgg gca att gtg gcg ttg gtg gcc tca ctg Thr Arg Lys Leu Pro Ala Trp Ala Ile Val Ala Leu Val Ala Ser Leu	547
135 140 145	
tgg cta ctt atg ccg gct tat agc gag att gag att cta cgc aag tcc Trp Leu Leu Met Pro Ala Tyr Ser Glu Ile Glu Ile Leu Arg Lys Ser	595
150 155 160 165	
att att tac ttg cct aca ttc ctc att ggc gct tac ttc cgc cca ctg Ile Ile Tyr Leu Pro Thr Phe Leu Ile Gly Ala Tyr Phe Arg Pro Leu	643
170 175 180	
att tcg cgt ttt gca gaa gcc gca aca agg cca aaa gca ata gtg ttt Ile Ser Arg Phe Ala Glu Ala Ala Thr Arg Pro Lys Ala Ile Val Phe	691
185 190 195	
gca gcg gtc ctt tat gtc tcg gga ctt gct ttg ggc gtg atc tca aat Ala Ala Val Leu Tyr Val Ser Gly Leu Ala Leu Gly Val Ile Ser Asn	739
200 205 210	
ggg ctg cgc gac agc gaa aac cat ggc gca agc gtg ctg tgg ctg atg Gly Leu Arg Asp Ser Glu Asn His Gly Ala Ser Val Leu Trp Leu Met	787
215 220 225	
aac ctc cgc gat act ttt gct cat gca ctc ggc ggc aac ctc act gga Asn Leu Arg Asp Thr Phe Ala His Ala Leu Gly Gly Asn Leu Thr Gly	835
230 235 240 245	
ttc gat atg gat cac ctt cct gga atg atc att cgg att gtt tcc ctg Phe Asp Met Asp His Leu Pro Gly Met Ile Ile Arg Ile Val Ser Leu	883
250 255 260	
cct gca gga att gtg ttg tgc gta tgg ctt ggc cga ata aag cca gta Pro Ala Gly Ile Val Leu Cys Val Trp Leu Gly Arg Ile Lys Pro Val	931
265 270 275	
ggg gag ttt ttg aaa ctt att ggt agg cac acc ctt ccc atc tac att Gly Glu Phe Leu Lys Leu Ile Gly Arg His Thr Leu Pro Ile Tyr Ile	979
280 285 290	
ggg cat gca aca gga cta tcg ctg att ttt ggt ttc ggc ttg cgc tgg Gly His Ala Thr Gly Leu Ser Leu Ile Phe Gly Phe Gly Leu Arg Trp	1027
295 300 305	
aat ttc atg gag att gat aac ttc tct gac agt ttg tgg cac cac acc Asn Phe Met Glu Ile Asp Asn Phe Ser Asp Ser Leu Trp His His Thr	1075
310 315 320 325	
aat acg tgg atg gtc atc gcg ttt gcc tgc gcg atg ctc ggc ggg tac	1123

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Asn Thr Trp Met Val Ile Ala Phe Ala Cys Ala Met Leu Gly Gly Tyr
      330                      335                      340

ctg acc tat ctg atc tcg cga gtt cca gtg ctg gga tgg act ctt gtt 1171
Leu Thr Tyr Leu Ile Ser Arg Val Pro Val Leu Gly Trp Thr Leu Val
      345                      350                      355

ccc cct aaa ctg cca gaa cca gat aaa act cca gct aaa gca caa gct 1219
Pro Pro Lys Leu Pro Glu Pro Asp Lys Thr Pro Ala Lys Ala Gln Ala
      360                      365                      370

gat tct cac gtt aaa gct cag tct gcg aag cct atg aat gct tct acc 1267
Asp Ser His Val Lys Ala Gln Ser Ala Lys Pro Met Asn Ala Ser Thr
      375                      380                      385

tct tct aag acg tac ggt ata taactgaagc ataacctgtg tga 1311
Ser Ser Lys Thr Tyr Gly Ile
      390                      395

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<210> 1020

<211> 396

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1020

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Met Asp Trp Pro Asp Ile Ala Lys Gly Ile Ser Ile Leu Gly Val Val
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Leu Leu His Val Ser Leu Ala Ile Pro Gly Gly Gln Asp Thr Met Met
      20          25          30

Ser His Leu Asn Ala Leu Leu Asp Pro Leu Arg Met Pro Leu Phe Phe
      35          40          45

Met Val Ser Gly Phe Phe Ala Val Lys Val Leu Asn Gln Ser Phe Gly
      50          55          60

Glu Leu Phe Arg Gly Arg Leu Trp Phe Tyr Leu Val Pro Tyr Leu Leu
      65          70          75          80

Trp Thr Pro Val Asn Leu Tyr Leu His Arg Leu Glu Gly Thr Val Phe
      85          90          95

Thr Gly Arg Ala Pro Gly Thr Trp Glu Trp Tyr Ser Gly Ser Met Leu
      100          105          110

Ser Ala Thr Asn Met Tyr Trp Phe Leu Tyr Phe Leu Val Ile Phe Asn
      115          120          125

Leu Phe Leu Trp Ala Thr Arg Lys Leu Pro Ala Trp Ala Ile Val Ala
      130          135          140

Leu Val Ala Ser Leu Trp Leu Leu Met Pro Ala Tyr Ser Glu Ile Glu
      145          150          155          160

Ile Leu Arg Lys Ser Ile Ile Tyr Leu Pro Thr Phe Leu Ile Gly Ala
      165          170          175

Tyr Phe Arg Pro Leu Ile Ser Arg Phe Ala Glu Ala Ala Thr Arg Pro
      180          185          190

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Lys Ala Ile Val Phe Ala Ala Val Leu Tyr Val Ser Gly Leu Ala Leu
    195                      200                      205

Gly Val Ile Ser Asn Gly Leu Arg Asp Ser Glu Asn His Gly Ala Ser
    210                      215                      220

Val Leu Trp Leu Met Asn Leu Arg Asp Thr Phe Ala His Ala Leu Gly
    225                      230                      235                      240

Gly Asn Leu Thr Gly Phe Asp Met Asp His Leu Pro Gly Met Ile Ile
    245                      250                      255

Arg Ile Val Ser Leu Pro Ala Gly Ile Val Leu Cys Val Trp Leu Gly
    260                      265                      270

Arg Ile Lys Pro Val Gly Glu Phe Leu Lys Leu Ile Gly Arg His Thr
    275                      280                      285

Leu Pro Ile Tyr Ile Gly His Ala Thr Gly Leu Ser Leu Ile Phe Gly
    290                      295                      300

Phe Gly Leu Arg Trp Asn Phe Met Glu Ile Asp Asn Phe Ser Asp Ser
    305                      310                      315                      320

Leu Trp His His Thr Asn Thr Trp Met Val Ile Ala Phe Ala Cys Ala
    325                      330                      335

Met Leu Gly Gly Tyr Leu Thr Tyr Leu Ile Ser Arg Val Pro Val Leu
    340                      345                      350

Gly Trp Thr Leu Val Pro Pro Lys Leu Pro Glu Pro Asp Lys Thr Pro
    355                      360                      365

Ala Lys Ala Gln Ala Asp Ser His Val Lys Ala Gln Ser Ala Lys Pro
    370                      375                      380

Met Asn Ala Ser Thr Ser Ser Lys Thr Tyr Gly Ile
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<210> 1021

<211> 1311

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1288)

<223> FRXA02151

<400> 1021

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agccccacag caggtgacgg ctccccagaa caaggctcgt atg gat tgg cca gac    115
                Met Asp Trp Pro Asp
                        1                      5

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atc gcc aag gga ata tcc atc cta ggt gtc gtg tta cta cac gtg tgg    163
Ile Ala Lys Gly Ile Ser Ile Leu Gly Val Val Leu Leu His Val Ser
        10                      15                      20

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ttg gca att cca ggt ggc cag gac acc atg atg tcc cac ctg aac gca 211
 Leu Ala Ile Pro Gly Gly Gln Asp Thr Met Met Ser His Leu Asn Ala
 25 30 35

ctg ctt gat cca ctt cgg atg cca tta ttt ttt atg gtg agt gga ttt 259
 Leu Leu Asp Pro Leu Arg Met Pro Leu Phe Phe Met Val Ser Gly Phe
 40 45 50

ttt gca gtt aaa gtt ctg aat caa agc ttt ggt gaa ctt ttc cgc ggg 307
 Phe Ala Val Lys Val Leu Asn Gln Ser Phe Gly Glu Leu Phe Arg Gly
 55 60 65

cga ctg tgg ttc tac ctg gtt cca tat ttg ctg tgg act cca gtg aat 355
 Arg Leu Trp Phe Tyr Leu Val Pro Tyr Leu Leu Trp Thr Pro Val Asn
 70 75 80 85

ctt tat cta cac cgc ctc gag ggc aca gtt ttt acc ggt aga gca cgc 403
 Leu Tyr Leu His Arg Leu Glu Gly Thr Val Phe Thr Gly Arg Ala Pro
 90 95 100

gga aca tgg gaa tgg tac agc ggc tgc atg ctc tgc gcc acc aat atg 451
 Gly Thr Trp Glu Trp Tyr Ser Gly Ser Met Leu Ser Ala Thr Asn Met
 105 110 115

tac tgg ttc ctc tac ttc ttg gtc atc ttc aac cta ttt tta tgg gca 499
 Tyr Trp Phe Leu Tyr Phe Leu Val Ile Phe Asn Leu Phe Leu Trp Ala
 120 125 130

acg aga aaa ctc cca gct tgg gca att gtg gcg ttg gtg gcc tca ctg 547
 Thr Arg Lys Leu Pro Ala Trp Ala Ile Val Ala Leu Val Ala Ser Leu
 135 140 145

tgg cta ctt atg ccg gct tat agc gag att gag att cta cgc aag tcc 595
 Trp Leu Leu Met Pro Ala Tyr Ser Glu Ile Glu Ile Leu Arg Lys Ser
 150 155 160 165

att att tac ttg cct aca ttc ctc att ggc gct tac ttc cgc cca ctg 643
 Ile Ile Tyr Leu Pro Thr Phe Leu Ile Gly Ala Tyr Phe Arg Pro Leu
 170 175 180

att tgc cgt ttt gca gaa gcc gca aca agg cca aaa gca ata gtg ttt 691
 Ile Ser Arg Phe Ala Glu Ala Ala Thr Arg Pro Lys Ala Ile Val Phe
 185 190 195

gca gcg gtc ctt tat gtc tgc gga ctt gct ttg ggc gtg atc tca aat 739
 Ala Ala Val Leu Tyr Val Ser Gly Leu Ala Leu Gly Val Ile Ser Asn
 200 205 210

ggg ctg cgc gac agc gaa aac cat ggc gca agc gtg ctg tgg ctg atg 787
 Gly Leu Arg Asp Ser Glu Asn His Gly Ala Ser Val Leu Trp Leu Met
 215 220 225

aac ctc cgc gat act ttt gct cat gca ctc ggc ggc aac ctc act gga 835
 Asn Leu Arg Asp Thr Phe Ala His Ala Leu Gly Gly Asn Leu Thr Gly
 230 235 240 245

ttc gat atg gat cac ctt cct gga atg atc att cgg att gtt tcc ctg 883
 Phe Asp Met Asp His Leu Pro Gly Met Ile Ile Arg Ile Val Ser Leu
 250 255 260

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cct gca gga att gtg ttg tgc gta tgg ctt ggc cga ata aag cca gta 931
Pro Ala Gly Ile Val Leu Cys Val Trp Leu Gly Arg Ile Lys Pro Val
      265                               270                               275

ggg gag ttt ttg aaa ctt att ggt agg cac acc ctt ccc atc tac att 979
Gly Glu Phe Leu Lys Leu Ile Gly Arg His Thr Leu Pro Ile Tyr Ile
      280                               285                               290

ggg cat gca aca gga cta tgc ctg att ttt ggt ttc ggc ttg cgc tgg 1027
Gly His Ala Thr Gly Leu Ser Leu Ile Phe Gly Phe Gly Leu Arg Trp
      295                               300                               305

aat ttc atg gag att gat aac ttc tct gac agt ttg tgg cac cac acc 1075
Asn Phe Met Glu Ile Asp Asn Phe Ser Asp Ser Leu Trp His His Thr
      310                               315                               320                               325

aat acg tgg atg gtc atc gcg ttt gcc tgc gcg atg ctc ggc ggg tac 1123
Asn Thr Trp Met Val Ile Ala Phe Ala Cys Ala Met Leu Gly Gly Tyr
      330                               335                               340

ctg acc tat ctg atc tgc cga gtt cca gtg ctg gga tgg act ctt gtt 1171
Leu Thr Tyr Leu Ile Ser Arg Val Pro Val Leu Gly Trp Thr Leu Val
      345                               350                               355

ccc cct aaa ctg cca gaa cca gat aaa act cca gct aaa gca caa gct 1219
Pro Pro Lys Leu Pro Glu Pro Asp Lys Thr Pro Ala Lys Ala Gln Ala
      360                               365                               370

gat tct cac gtt aaa gct cag tct gcg aag cct atg aat gct tct acc 1267
Asp Ser His Val Lys Ala Gln Ser Ala Lys Pro Met Asn Ala Ser Thr
      375                               380                               385

tct tct aag acg tac ggt ata taactgaagc ataacctgtg tga 1311
Ser Ser Lys Thr Tyr Gly Ile
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<212> PRT
<213> Corynebacterium glutamicum

<400> 1022
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  20           25           30

Ser His Leu Asn Ala Leu Leu Asp Pro Leu Arg Met Pro Leu Phe Phe
  35           40           45

Met Val Ser Gly Phe Phe Ala Val Lys Val Leu Asn Gln Ser Phe Gly
  50           55           60

Glu Leu Phe Arg Gly Arg Leu Trp Phe Tyr Leu Val Pro Tyr Leu Leu
  65           70           75           80

Trp Thr Pro Val Asn Leu Tyr Leu His Arg Leu Glu Gly Thr Val Phe
  85           90           95

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Thr Gly Arg Ala Pro Gly Thr Trp Glu Trp Tyr Ser Gly Ser Met Leu
 100 105 110
 Ser Ala Thr Asn Met Tyr Trp Phe Leu Tyr Phe Leu Val Ile Phe Asn
 115 120 125
 Leu Phe Leu Trp Ala Thr Arg Lys Leu Pro Ala Trp Ala Ile Val Ala
 130 135 140
 Leu Val Ala Ser Leu Trp Leu Leu Met Pro Ala Tyr Ser Glu Ile Glu
 145 150 155 160
 Ile Leu Arg Lys Ser Ile Ile Tyr Leu Pro Thr Phe Leu Ile Gly Ala
 165 170 175
 Tyr Phe Arg Pro Leu Ile Ser Arg Phe Ala Glu Ala Ala Thr Arg Pro
 180 185 190
 Lys Ala Ile Val Phe Ala Ala Val Leu Tyr Val Ser Gly Leu Ala Leu
 195 200 205
 Gly Val Ile Ser Asn Gly Leu Arg Asp Ser Glu Asn His Gly Ala Ser
 210 215 220
 Val Leu Trp Leu Met Asn Leu Arg Asp Thr Phe Ala His Ala Leu Gly
 225 230 235 240
 Gly Asn Leu Thr Gly Phe Asp Met Asp His Leu Pro Gly Met Ile Ile
 245 250 255
 Arg Ile Val Ser Leu Pro Ala Gly Ile Val Leu Cys Val Trp Leu Gly
 260 265 270
 Arg Ile Lys Pro Val Gly Glu Phe Leu Lys Leu Ile Gly Arg His Thr
 275 280 285
 Leu Pro Ile Tyr Ile Gly His Ala Thr Gly Leu Ser Leu Ile Phe Gly
 290 295 300
 Phe Gly Leu Arg Trp Asn Phe Met Glu Ile Asp Asn Phe Ser Asp Ser
 305 310 315 320
 Leu Trp His His Thr Asn Thr Trp Met Val Ile Ala Phe Ala Cys Ala
 325 330 335
 Met Leu Gly Gly Tyr Leu Thr Tyr Leu Ile Ser Arg Val Pro Val Leu
 340 345 350
 Gly Trp Thr Leu Val Pro Pro Lys Leu Pro Glu Pro Asp Lys Thr Pro
 355 360 365
 Ala Lys Ala Gln Ala Asp Ser His Val Lys Ala Gln Ser Ala Lys Pro
 370 375 380
 Met Asn Ala Ser Thr Ser Ser Lys Thr Tyr Gly Ile
 385 390 395

<210> 1023

<211> 969

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(946)

<223> RXN02169

<400> 1023

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ctgttactgg tgggattaat acctattttt gggagaactt ttg gac atg caa ata 115
 Leu Asp Met Gln Ile
 1 5

aac cgc cga ggc ttc tta aaa gcc acc aca gga ctt gcc act atc ggc 163
 Asn Arg Arg Gly Phe Leu Lys Ala Thr Thr Gly Leu Ala Thr Ile Gly
 10 15 20

gct gcc agc atg ttt atg cca aag gcc aac gcc ctt gga gca atc aag 211
 Ala Ala Ser Met Phe Met Pro Lys Ala Asn Ala Leu Gly Ala Ile Lys
 25 30 35

ggc acc gtc atc gac tac gca gca ggc gtc ccc agc gca gca tcc att 259
 Gly Thr Val Ile Asp Tyr Ala Ala Gly Val Pro Ser Ala Ala Ser Ile
 40 45 50

aaa aat gca ggg cac ctt gga gct gtc cgt tac gtg tca cag cga cgc 307
 Lys Asn Ala Gly His Leu Gly Ala Val Arg Tyr Val Ser Gln Arg Arg
 55 60 65

ccc ggc act gaa tcc tgg atg atc gcc aag cca gtc aca ctg gca gaa 355
 Pro Gly Thr Glu Ser Trp Met Ile Gly Lys Pro Val Thr Leu Ala Glu
 70 75 80 85

acc cga gct ttt gaa caa aac ggc ctc aaa acc gca tcc gtc tat caa 403
 Thr Arg Ala Phe Glu Gln Asn Gly Leu Lys Thr Ala Ser Val Tyr Gln
 90 95 100

tac gga aag gca gag acc gcc gat tgg aag aac ggc gcc gca gga gcg 451
 Tyr Gly Lys Ala Glu Thr Ala Asp Trp Lys Asn Gly Ala Ala Gly Ala
 105 110 115

gca acc cac gct cca cag gca att gcg ctt cac gtg gca gct ggt ggc 499
 Ala Thr His Ala Pro Gln Ala Ile Ala Leu His Val Ala Ala Gly Gly
 120 125 130

cct aaa aat cgc ccc atc tac gtg gcg atc gac gac aac cca agc tgg 547
 Pro Lys Asn Arg Pro Ile Tyr Val Ala Ile Asp Asp Asn Pro Ser Trp
 135 140 145

tct gaa tac acc aat cag att cgc ccc tac ctc cag gca ttc aat gtt 595
 Ser Glu Tyr Thr Asn Gln Ile Arg Pro Tyr Leu Gln Ala Phe Asn Val
 150 155 160 165

gcg ctg tcc gct gcc ggc tac cag tta ggt gtc tac ggc aac tac aac 643
 Ala Leu Ser Ala Ala Gly Tyr Gln Leu Gly Val Tyr Gly Asn Tyr Asn
 170 175 180

gtc att aat tgg gct atc gcc gac ggc ctt gga gaa ttc ttc tgg atg 691
 Val Ile Asn Trp Ala Ile Ala Asp Gly Leu Gly Glu Phe Phe Trp Met
 185 190 195

cac aac tgg gga tca gaa gga aag atc cac cca cgc acc acc atc cac 739
 His Asn Trp Gly Ser Glu Gly Lys Ile His Pro Arg Thr Thr Ile His
 200 205 210

cag atc cgc att gat aag gac acc ctc gac gga gtc ggc atc gac atg 787
 Gln Ile Arg Ile Asp Lys Asp Thr Leu Asp Gly Val Gly Ile Asp Met
 215 220 225

aac aat gtc tat gca gac gac tgg ggt cag tgg acc cca ggc aac gcg 835
 Asn Asn Val Tyr Ala Asp Asp Trp Gly Gln Trp Thr Pro Gly Asn Ala
 230 235 240 245

gtt gac gat gcc atc ccc acc att cct gga aac tcc aac acg gga aca 883
 Val Asp Asp Ala Ile Pro Thr Ile Pro Gly Asn Ser Asn Thr Gly Thr
 250 255 260

ggt act gga att gat gct gac acc atc aac caa gta atc aag att ctt 931
 Gly Thr Gly Ile Asp Ala Asp Thr Ile Asn Gln Val Ile Lys Ile Leu
 265 270 275

ggc acc cta tct agc taaactagcc gtgctgactc aca 969
 Gly Thr Leu Ser Ser
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<210> 1024
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 20 25 30

Leu Gly Ala Ile Lys Gly Thr Val Ile Asp Tyr Ala Ala Gly Val Pro
 35 40 45

Ser Ala Ala Ser Ile Lys Asn Ala Gly His Leu Gly Ala Val Arg Tyr
 50 55 60

Val Ser Gln Arg Arg Pro Gly Thr Glu Ser Trp Met Ile Gly Lys Pro
 65 70 75 80

Val Thr Leu Ala Glu Thr Arg Ala Phe Glu Gln Asn Gly Leu Lys Thr
 85 90 95

Ala Ser Val Tyr Gln Tyr Gly Lys Ala Glu Thr Ala Asp Trp Lys Asn
 100 105 110

Gly Ala Ala Gly Ala Ala Thr His Ala Pro Gln Ala Ile Ala Leu His
 115 120 125

Val Ala Ala Gly Gly Pro Lys Asn Arg Pro Ile Tyr Val Ala Ile Asp
 130 135 140

Asp Asn Pro Ser Trp Ser Glu Tyr Thr Asn Gln Ile Arg Pro Tyr Leu
 145 150 155 160

Gln Ala Phe Asn Val Ala Leu Ser Ala Ala Gly Tyr Gln Leu Gly Val
 165 170 175

Tyr Gly Asn Tyr Asn Val Ile Asn Trp Ala Ile Ala Asp Gly Leu Gly
 180 185 190

Glu Phe Phe Trp Met His Asn Trp Gly Ser Glu Gly Lys Ile His Pro
 195 200 205

Arg Thr Thr Ile His Gln Ile Arg Ile Asp Lys Asp Thr Leu Asp Gly
 210 215 220

Val Gly Ile Asp Met Asn Asn Val Tyr Ala Asp Asp Trp Gly Gln Trp
 225 230 235 240

Thr Pro Gly Asn Ala Val Asp Asp Ala Ile Pro Thr Ile Pro Gly Asn
 245 250 255

Ser Asn Thr Gly Thr Gly Thr Gly Ile Asp Ala Asp Thr Ile Asn Gln
 260 265 270

Val Ile Lys Ile Leu Gly Thr Leu Ser Ser
 275 280

<210> 1025

<211> 969

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(946)

<223> FRXA02169

<400> 1025

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 Leu Asp Met Gln Ile
 1 5

aac cgc cga ggc ttc tta aaa gcc acc aca gga ctt gcc act atc ggc 163
 Asn Arg Arg Gly Phe Leu Lys Ala Thr Thr Gly Leu Ala Thr Ile Gly
 10 15 20

gct gcc agc atg ttt atg cca aag gcc aac gcc ctt gga gca atc aag 211
 Ala Ala Ser Met Phe Met Pro Lys Ala Asn Ala Leu Gly Ala Ile Lys
 25 30 35

ggc acc gtc atc gac tac gca gca ggc gtc ccc agc gca gca tcc att 259
 Gly Thr Val Ile Asp Tyr Ala Ala Gly Val Pro Ser Ala Ala Ser Ile
 40 45 50

aaa aat gca ggg cac ctt gga gct gtc cgt tac gtg tca cag cga cgc 307
 Lys Asn Ala Gly His Leu Gly Ala Val Arg Tyr Val Ser Gln Arg Arg
 55 60 65

ccc ggc act gaa tcc tgg atg atc ggc aag cca gtc aca ctg gca gaa 355
 Pro Gly Thr Glu Ser Trp Met Ile Gly Lys Pro Val Thr Leu Ala Glu

70	75	80	85	
acc cga gct ttt gaa caa aac ggc ctc aaa acc gca tcc gtc tat caa				403
Thr Arg Ala Phe Glu Gln Asn Gly Leu Lys Thr Ala Ser Val Tyr Gln	90	95	100	
tac gga aag gca gag acc gcc gat tgg aag aac ggc gcc gca gga gcg				451
Tyr Gly Lys Ala Glu Thr Ala Asp Trp Lys Asn Gly Ala Ala Gly Ala	105	110	115	
gca acc cac gct cca cag gca att gcg ctt cac gtg gca gct ggt ggc				499
Ala Thr His Ala Pro Gln Ala Ile Ala Leu His Val Ala Ala Gly Gly	120	125	130	
cct aaa aat cgc ccc atc tac gtg gcg atc gac gac aac cca agc tgg				547
Pro Lys Asn Arg Pro Ile Tyr Val Ala Ile Asp Asp Asn Pro Ser Trp	135	140	145	
tct gaa tac acc aat cag att cgc ccc tac ctc cag gca ttc aat gtt				595
Ser Glu Tyr Thr Asn Gln Ile Arg Pro Tyr Leu Gln Ala Phe Asn Val	150	155	160	165
gcg ctg tcc gct gcc ggc tac cag tta ggt gtc tac ggc aac tac aac				643
Ala Leu Ser Ala Ala Gly Tyr Gln Leu Gly Val Tyr Gly Asn Tyr Asn	170	175	180	
gtc att aat tgg gct atc gcc gac ggc ctt gga gaa ttc ttc tgg atg				691
Val Ile Asn Trp Ala Ile Ala Asp Gly Leu Gly Glu Phe Thr Trp Met	185	190	195	
cac aac tgg gga tca gaa gga aag atc cac cca cgc acc acc atc cac				739
His Asn Trp Gly Ser Glu Gly Lys Ile His Pro Arg Thr Thr Ile His	200	205	210	
cag atc cgc att gat aag gac acc ctc gac gga gtc ggc atc gac atg				787
Gln Ile Arg Ile Asp Lys Asp Thr Leu Asp Gly Val Gly Ile Asp Met	215	220	225	
aac aat gtc tat gca gac gac tgg ggt cag tgg acc cca ggc aac gcg				835
Asn Asn Val Tyr Ala Asp Asp Trp Gly Gln Trp Thr Pro Gly Asn Ala	230	235	240	245
gtt gac gat gcc atc ccc acc att cct gga aac tcc aac acg gga aca				883
Val Asp Asp Ala Ile Pro Thr Ile Pro Gly Asn Ser Asn Thr Gly Thr	250	255	260	
ggt act gga att gat gct gac acc atc aac caa gta atc aag att ctt				931
Gly Thr Gly Ile Asp Ala Asp Thr Ile Asn Gln Val Ile Lys Ile Leu	265	270	275	
ggc acc cta tct agc taaactagcc gtgctgactc aca				969
Gly Thr Leu Ser Ser	280			

<210> 1026

<211> 282

<212> PRT

<213> Corynebacterium glutamicum

<400> 1026

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 Leu Ala Thr Ile Gly Ala Ala Ser Met Phe Met Pro Lys Ala Asn Ala
 20 25 30
 Leu Gly Ala Ile Lys Gly Thr Val Ile Asp Tyr Ala Ala Gly Val Pro
 35 40 45
 Ser Ala Ala Ser Ile Lys Asn Ala Gly His Leu Gly Ala Val Arg Tyr
 50 55 60
 Val Ser Gln Arg Arg Pro Gly Thr Glu Ser Trp Met Ile Gly Lys Pro
 65 70 75 80
 Val Thr Leu Ala Glu Thr Arg Ala Phe Glu Gln Asn Gly Leu Lys Thr
 85 90 95
 Ala Ser Val Tyr Gln Tyr Gly Lys Ala Glu Thr Ala Asp Trp Lys Asn
 100 105 110
 Gly Ala Ala Gly Ala Ala Thr His Ala Pro Gln Ala Ile Ala Leu His
 115 120 125
 Val Ala Ala Gly Gly Pro Lys Asn Arg Pro Ile Tyr Val Ala Ile Asp
 130 135 140
 Asp Asn Pro Ser Trp Ser Glu Tyr Thr Asn Gln Ile Arg Pro Tyr Leu
 145 150 155 160
 Gln Ala Phe Asn Val Ala Leu Ser Ala Ala Gly Tyr Gln Leu Gly Val
 165 170 175
 Tyr Gly Asn Tyr Asn Val Ile Asn Trp Ala Ile Ala Asp Gly Leu Gly
 180 185 190
 Glu Phe Phe Trp Met His Asn Trp Gly Ser Glu Gly Lys Ile His Pro
 195 200 205
 Arg Thr Thr Ile His Gln Ile Arg Ile Asp Lys Asp Thr Leu Asp Gly
 210 215 220
 Val Gly Ile Asp Met Asn Asn Val Tyr Ala Asp Asp Trp Gly Gln Trp
 225 230 235 240
 Thr Pro Gly Asn Ala Val Asp Asp Ala Ile Pro Thr Ile Pro Gly Asn
 245 250 255
 Ser Asn Thr Gly Thr Gly Thr Gly Ile Asp Ala Asp Thr Ile Asn Gln
 260 265 270
 Val Ile Lys Ile Leu Gly Thr Leu Ser Ser
 275 280

<210> 1027

<211> 1581

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1558)

<223> RXN02180

<400> 1027

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agctttctca caacttgaat agaaattgag gtatccggca atg acg tca ggg aaa 115
                                         Met Thr Ser Gly Lys
                                         1      5

tca acg agt act agg gga gcc cta gac cgg tat ttc aaa atc tcg gag 163
Ser Thr Ser Thr Arg Gly Ala Leu Asp Arg Tyr Phe Lys Ile Ser Glu
                        10                        15                        20

cga gga tca agc att ggc acg gaa atc cgt gca ggt gtg gtc aca ttc 211
Arg Gly Ser Ser Ile Gly Thr Glu Ile Arg Ala Gly Val Val Thr Phe
                        25                        30                        35

ttc gcg atg gcc tac atc atc atc ctc aac ccc ttg atc ctt ggc acc 259
Phe Ala Met Ala Tyr Ile Ile Ile Leu Asn Pro Leu Ile Leu Gly Thr
                        40                        45                        50

acc cct gac gta gag ggc aac acc cta ggc atc gca cag gtt gca gcg 307
Thr Pro Asp Val Glu Gly Asn Thr Leu Gly Ile Ala Gln Val Ala Ala
                        55                        60                        65

gca aca gcg ctt gcc gct ggt gtc atg acc atc gcg ttt ggt ttg att 355
Ala Thr Ala Leu Ala Ala Gly Val Met Thr Ile Ala Phe Gly Leu Ile
                        70                        75                        80                        85

gcg cgt tat cca ttc ggc att gct gct ggc ctg gga att aac acc atg 403
Ala Arg Tyr Pro Phe Gly Ile Ala Ala Gly Leu Gly Ile Asn Thr Met
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gtc gcc gtg aca ctg gtt tca ggt gag ggc ctg acc tgg cgg gaa gca 451
Val Ala Val Thr Leu Val Ser Gly Glu Gly Leu Thr Trp Pro Glu Ala
                        105                        110                        115

atg gga ctt gtg gtc ctt gac ggt gtg gtc att gtt att ttg gct gtg 499
Met Gly Leu Val Val Leu Asp Gly Val Val Ile Val Ile Leu Ala Val
                        120                        125                        130

tcc ggc ttc cgt gtt gct gtg ttc cgt gcg atc cca gca tcc atg aag 547
Ser Gly Phe Arg Val Ala Val Phe Arg Ala Ile Pro Ala Ser Met Lys
                        135                        140                        145

gcg gcc atc agc gtg ggt atc ggc ctg ttc atc gcc atg atc ggc ctc 595
Ala Ala Ile Ser Val Gly Ile Gly Leu Phe Ile Ala Met Ile Gly Leu
                        150                        155                        160                        165

gtg gat gca ggc ttt gtt cgc cgt att cca gat gct gcc ggt act act 643
Val Asp Ala Gly Phe Val Arg Arg Ile Pro Asp Ala Ala Gly Thr Thr
                        170                        175                        180

gtg cca gtg act ttg ggc att gat ggt tcc att gcg tct tgg cca acg 691
Val Pro Val Thr Leu Gly Ile Asp Gly Ser Ile Ala Ser Trp Pro Thr
                        185                        190                        195

ttc gtg ttc gtt gtc ggt gtt ctt ctc tgt ggc atc ctt gtt gtc cgt 739
Phe Val Phe Val Val Gly Val Leu Leu Cys Gly Ile Leu Val Val Arg

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200	205	210	
cga gtt cgc ggt gga ctg ttt atc ggc att ttg gga acc acc att ttg Arg Val Arg Gly Gly Leu Phe Ile Gly Ile Leu Gly Thr Thr Ile Leu 215 220 225			787
gcg atc atc gca gaa gca atc ttt gat tcc ggt gcg tcc ttt gaa aat Ala Ile Ile Ala Glu Ala Ile Phe Asp Ser Gly Ala Ser Phe Glu Asn 230 235 240 245			835
ggt gaa gca aac gca gaa ggc tgg tca ctc gcc gtt cct ggt ctc cca Gly Glu Ala Asn Ala Glu Gly Trp Ser Leu Ala Val Pro Gly Leu Pro 250 255 260			883
gac tcc ttc ggt ggc atc ccg gat ctt tcc atc gtc ggc gca gtt gat Asp Ser Phe Gly Gly Ile Pro Asp Leu Ser Ile Val Gly Ala Val Asp 265 270 275			931
ttg atc ggt gcg ttc agc cgc atc ggt gtg gtc gcc gcg acc ttg ctg Leu Ile Gly Ala Phe Ser Arg Ile Gly Val Val Ala Thr Leu Leu 280 285 290			979
atc ttt acc ctg gtc ctt gca aac ttc ttc gac gcc atg ggc acc atg Ile Phe Thr Leu Val Leu Ala Asn Phe Phe Asp Met Gly Thr Met 295 300 305			1027
acc gct ctt ggt aag cag ggc aac ttg gtt gat gat gaa ggc aac ctt Thr Ala Leu Gly Lys Gln Gly Asn Leu Val Asp Asp Glu Gly Asn Leu 310 315 320 325			1075
cca gac att aag aag gca ctg gtt gtg gaa ggc gca ggt gcc att gtc Pro Asp Ile Lys Lys Ala Leu Val Val Glu Gly Ala Gly Ala Ile Val 330 335 340			1123
ggt ggt gct ttc tct gca tcc tcc aac acc gtg ttc gct gac tct tct Gly Gly Ala Phe Ser Ala Ser Ser Asn Thr Val Phe Ala Asp Ser Ser 345 350 355			1171
gca ggt gtt gca gac ggc gca cga acc ggc ctt gcc aac gtg gtc acc Ala Gly Val Ala Asp Gly Ala Arg Thr Gly Leu Ala Asn Val Val Thr 360 365 370			1219
ggc tcc ttg ttc ttg gct gcc atg ttc ttg acc cca ctg tat gaa atc Gly Ser Leu Phe Leu Ala Ala Met Phe Leu Thr Pro Leu Tyr Glu Ile 375 380 385			1267
gtc ccc atc gaa gca gca gca cca gtg ctt gta gtt gtt ggc gcg atg Val Pro Ile Glu Ala Ala Ala Pro Val Leu Val Val Val Gly Ala Met 390 395 400 405			1315
atg atg ggg cag gtt acc gag att gat ttc tcc aag ttc tac atc gca Met Met Gly Gln Val Thr Glu Ile Asp Phe Ser Lys Phe Tyr Ile Ala 410 415 420			1363
ttc cca gcg ttc ttg acc att gtg atc atg cct ttc acc tac tcc att Phe Pro Ala Phe Leu Thr Ile Val Ile Met Pro Phe Thr Tyr Ser Ile 425 430 435			1411
gca aac ggc att ggc gtt gga ttc atc atg tac gcc atc atg gct gca Ala Asn Gly Ile Gly Val Gly Phe Ile Met Tyr Ala Ile Met Ala Ala 440 445 450			1459

gcg gca ggc aaa gca aag caa gtg cac tgg ctg atg tgg ctg gtc gct 1507
 Ala Ala Gly Lys Ala Lys Gln Val His Trp Leu Met Trp Leu Val Ala
 455 460 465

gga ctc ttc gtc gtg ttc ttc gcg att gat ccc atc atg gaa gct gtc 1555
 Gly Leu Phe Val Val Phe Phe Ala Ile Asp Pro Ile Met Glu Ala Val
 470 475 480 485

ggc taatgacaac gcgcacggta att 1581
 Gly

<210> 1028

<211> 486

<212> PRT

<213> Corynebacterium glutamicum

<400> 1028

Met Thr Ser Gly Lys Ser Thr Ser Thr Arg Gly Ala Leu Asp Arg Tyr
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Phe Lys Ile Ser Glu Arg Gly Ser Ser Ile Gly Thr Glu Ile Arg Ala
 20 25 30

Gly Val Val Thr Phe Phe Ala Met Ala Tyr Ile Ile Ile Leu Asn Pro
 35 40 45

Leu Ile Leu Gly Thr Thr Pro Asp Val Glu Gly Asn Thr Leu Gly Ile
 50 55 60

Ala Gln Val Ala Ala Ala Thr Ala Leu Ala Ala Gly Val Met Thr Ile
 65 70 75 80

Ala Phe Gly Leu Ile Ala Arg Tyr Pro Phe Gly Ile Ala Ala Gly Leu
 85 90 95

Gly Ile Asn Thr Met Val Ala Val Thr Leu Val Ser Gly Glu Gly Leu
 100 105 110

Thr Trp Pro Glu Ala Met Gly Leu Val Val Leu Asp Gly Val Val Ile
 115 120 125

Val Ile Leu Ala Val Ser Gly Phe Arg Val Ala Val Phe Arg Ala Ile
 130 135 140

Pro Ala Ser Met Lys Ala Ala Ile Ser Val Gly Ile Gly Leu Phe Ile
 145 150 155 160

Ala Met Ile Gly Leu Val Asp Ala Gly Phe Val Arg Arg Ile Pro Asp
 165 170 175

Ala Ala Gly Thr Thr Val Pro Val Thr Leu Gly Ile Asp Gly Ser Ile
 180 185 190

Ala Ser Trp Pro Thr Phe Val Phe Val Val Gly Val Leu Leu Cys Gly
 195 200 205

Ile Leu Val Val Arg Arg Val Arg Gly Gly Leu Phe Ile Gly Ile Leu
 210 215 220

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Gly Thr Thr Ile Leu Ala Ile Ile Ala Glu Ala Ile Phe Asp Ser Gly
225                230                235                240

Ala Ser Phe Glu Asn Gly Glu Ala Asn Ala Glu Gly Trp Ser Leu Ala
                245                250                255

Val Pro Gly Leu Pro Asp Ser Phe Gly Gly Ile Pro Asp Leu Ser Ile
                260                265                270

Val Gly Ala Val Asp Leu Ile Gly Ala Phe Ser Arg Ile Gly Val Val
                275                280                285

Ala Ala Thr Leu Leu Ile Phe Thr Leu Val Leu Ala Asn Phe Phe Asp
290                295                300

Ala Met Gly Thr Met Thr Ala Leu Gly Lys Gln Gly Asn Leu Val Asp
305                310                315                320

Asp Glu Gly Asn Leu Pro Asp Ile Lys Lys Ala Leu Val Val Glu Gly
                325                330                335

Ala Gly Ala Ile Val Gly Gly Ala Phe Ser Ala Ser Ser Asn Thr Val
                340                345                350

Phe Ala Asp Ser Ser Ala Gly Val Ala Asp Gly Ala Arg Thr Gly Leu
                355                360                365

Ala Asn Val Val Thr Gly Ser Leu Phe Leu Ala Ala Met Phe Leu Thr
                370                375                380

Pro Leu Tyr Glu Ile Val Pro Ile Glu Ala Ala Pro Val Leu Val
385                390                395                400

Val Val Gly Ala Met Met Met Gly Gln Val Thr Glu Ile Asp Phe Ser
                405                410                415

Lys Phe Tyr Ile Ala Phe Pro Ala Phe Leu Thr Ile Val Ile Met Pro
                420                425                430

Phe Thr Tyr Ser Ile Ala Asn Gly Ile Gly Val Gly Phe Ile Met Tyr
                435                440                445

Ala Ile Met Ala Ala Ala Ala Gly Lys Ala Lys Gln Val His Trp Leu
                450                455                460

Met Trp Leu Val Ala Gly Leu Phe Val Val Phe Phe Ala Ile Asp Pro
465                470                475                480

Ile Met Glu Ala Val Gly
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<210> 1029

<211> 1581

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1558)

<400> 1029

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agcttttcca	caacttgaat	agaaattgag	gtatccggca	atg	acg tca ggg aaa	115
				Met Thr Ser Gly Lys		
				1	5	
tca acg agt act agg gga gcc cta gac cgg tat ttc aaa atc tcg gag						163
Ser Thr Ser Thr Arg Gly Ala Leu Asp Arg Tyr Phe Lys Ile Ser Glu						
	10		15		20	
cga gga tca agc att ggc acg gaa atc cgt gca ggt gtg gtc aca ttc						211
Arg Gly Ser Ser Ile Gly Thr Glu Ile Arg Ala Gly Val Val Thr Phe						
	25		30		35	
ttc gcg atg gcc tac atc atc atc ctc aac ccc ttg atc ctt ggc acc						259
Phe Ala Met Ala Tyr Ile Ile Ile Leu Asn Pro Leu Ile Leu Thr						
	40		45		50	
acc cct gac gta gag ggc aac acc cta ggc atc gca cag gtt gca gcg						307
Thr Pro Asp Val Glu Gly Asn Thr Leu Gly Ile Ala Gln Val Ala Ala						
	55		60		65	
gca aca gcg ctt gcc gct ggt gtc atg acc atc gcg ttt ggt ttg att						355
Ala Thr Ala Leu Ala Ala Gly Val Met Thr Ile Ala Phe Gly Leu Ile						
	70		75		80	85
gcg cgt tat cca ttc ggc att gct gct ggc ctg gga att aac acc atg						403
Ala Arg Tyr Pro Phe Gly Ile Ala Ala Gly Leu Gly Ile Asn Thr Met						
	90		95		100	
gtc gcc gtg aca ctg gtt tca ggt gag ggc ctg acc tgg ccg gaa gca						451
Val Ala Val Thr Leu Val Ser Gly Glu Gly Leu Thr Trp Pro Glu Ala						
	105		110		115	
atg gga ctt gtg gtc ctt gac ggt gtg gtc att gtt att ttg gct gtg						499
Met Gly Leu Val Val Leu Asp Gly Val Val Ile Val Ile Leu Ala Val						
	120		125		130	
tcc gcc ttc cgt gtt gct gtg ttc cgt gcg atc cca gca tcc atg aag						547
Ser Gly Phe Arg Val Ala Val Phe Arg Ala Ile Pro Ala Ser Met Lys						
	135		140		145	
gcg gcc atc agc gtg ggt atc ggc ctg ttc atc gcc atg atc ggc ctc						595
Ala Ala Ile Ser Val Gly Ile Gly Leu Phe Ile Ala Met Ile Gly Leu						
	150		155		160	165
gtg gat gca ggc ttt gtt cgc cgt att cca gat gct gcc ggt act act						643
Val Asp Ala Gly Phe Val Arg Arg Ile Pro Asp Ala Ala Gly Thr Thr						
	170		175		180	
gtg cca gtg act ttg ggc att gat ggt tcc att gcg tct tgg cca acg						691
Val Pro Val Thr Leu Gly Ile Asp Gly Ser Ile Ala Ser Trp Pro Thr						
	185		190		195	
ttc gtg ttc gtt gtc ggt gtt ctt ctc tgt ggc atc ctt gtt gtc cgt						739
Phe Val Phe Val Val Gly Val Leu Leu Cys Gly Ile Leu Val Val Arg						
	200		205		210	

cga gtt cgc ggt gga ctg ttt atc ggc att ttg gga acc acc att ttg	787
Arg Val Arg Gly Gly Leu Phe Ile Gly Ile Leu Gly Thr Thr Ile Leu	
215 220 225	
gcg atc atc gca gaa gca atc ttt gat tcc ggt gcg tcc ttt gaa aat	835
Ala Ile Ile Ala Glu Ala Ile Phe Asp Ser Gly Ala Ser Phe Glu Asn	
230 235 240 245	
ggg gaa gca aac gca gaa ggc tgg tca ctc gcc gtt cct ggt ctc cca	883
Gly Glu Ala Asn Ala Glu Gly Trp Ser Leu Ala Val Pro Gly Leu Pro	
250 255 260	
gac tcc ttc ggt ggc atc ccg gat ctt tcc atc gtc ggc gca gtt gat	931
Asp Ser Phe Gly Gly Ile Pro Asp Leu Ser Ile Val Gly Ala Val Asp	
265 270 275	
ttg atc ggt gcg ttc agc cgc atc ggt gtg gtc gcc gcg acc ttg ctg	979
Leu Ile Gly Ala Phe Ser Arg Ile Gly Val Val Ala Ala Thr Leu Leu	
280 285 290	
atc ttt acc ctg gtc ctt gca aac ttc ttc gac gcc atg ggc acc atg	1027
Ile Phe Thr Leu Val Leu Ala Asn Phe Phe Asp Ala Met Gly Thr Met	
295 300 305	
acc gct ctt ggt aag cag ggc aac ttg gtt gat gat gaa ggc aac ctt	1075
Thr Ala Leu Gly Lys Gln Gly Asn Leu Val Asp Asp Glu Gly Asn Leu	
310 315 320 325	
cca gac att aag aag gca ctg gtt gtg gaa ggc gca ggt gcc att gtc	1123
Pro Asp Ile Lys Lys Ala Leu Val Val Glu Gly Ala Gly Ala Ile Val	
330 335 340	
ggg ggt gct ttc tct gca tcc tcc aac acc gtg ttc gct gac tct tct	1171
Gly Gly Ala Phe Ser Ala Ser Ser Asn Thr Val Phe Ala Asp Ser Ser	
345 350 355	
gca ggt gtt gca gac ggc gca cga acc ggc ctt gcc aac gtg gtc acc	1219
Ala Gly Val Ala Asp Gly Ala Arg Thr Gly Leu Ala Asn Val Val Thr	
360 365 370	
ggc tcc ttg ttc ttg gct gcc atg ttc ttg acc cca ctg tat gaa atc	1267
Gly Ser Leu Phe Leu Ala Ala Met Phe Leu Thr Pro Leu Tyr Glu Ile	
375 380 385	
gtc ccc atc gaa gca gca gca cca gtg ctt gta gtt gtt ggc gcg atg	1315
Val Pro Ile Glu Ala Ala Ala Pro Val Leu Val Val Val Gly Ala Met	
390 395 400 405	
atg atg ggg cag gtt acc gag att gat ttc tcc aag ttc tac atc gca	1363
Met Met Gly Gln Val Thr Glu Ile Asp Phe Ser Lys Phe Tyr Ile Ala	
410 415 420	
ttc cca gcg ttc ttg acc att gtg atc atg cct ttc acc tac tcc att	1411
Phe Pro Ala Phe Leu Thr Ile Val Ile Met Pro Phe Thr Tyr Ser Ile	
425 430 435	
gca aac ggc att ggc gtt gga ttc atc atg tac gcc atc atg gct gca	1459
Ala Asn Gly Ile Gly Val Gly Phe Ile Met Tyr Ala Ile Met Ala Ala	
440 445 450	
gcg gca ggc aaa gca aag caa gtg cac tgg ctg atg tgg ctg gtc gct	1507

Ala Ala Gly Lys Ala Lys Gln Val His Trp Leu Met Trp Leu Val Ala
 455 460 465

gga ctc ttc gtc gtg ttc ttc gcg att gat ccc atc atg gaa gct gtc 1555
 Gly Leu Phe Val Val Phe Phe Ala Ile Asp Pro Ile Met Glu Ala Val
 470 475 480 485

ggc taatgacaac gcgcacggta att 1581
 Gly

<210> 1030

<211> 486

<212> PRT

<213> Corynebacterium glutamicum

<400> 1030

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Phe Lys Ile Ser Glu Arg Gly Ser Ser Ile Gly Thr Glu Ile Arg Ala
 20 25 30

Gly Val Val Thr Phe Phe Ala Met Ala Tyr Ile Ile Ile Leu Asn Pro
 35 40 45

Leu Ile Leu Gly Thr Thr Pro Asp Val Glu Gly Asn Thr Leu Gly Ile
 50 55 60

Ala Gln Val Ala Ala Ala Thr Ala Leu Ala Ala Gly Val Met Thr Ile
 65 70 75 80

Ala Phe Gly Leu Ile Ala Arg Tyr Pro Phe Gly Ile Ala Ala Gly Leu
 85 90 95

Gly Ile Asn Thr Met Val Ala Val Thr Leu Val Ser Gly Glu Gly Leu
 100 105 110

Thr Trp Pro Glu Ala Met Gly Leu Val Val Leu Asp Gly Val Val Ile
 115 120 125

Val Ile Leu Ala Val Ser Gly Phe Arg Val Ala Val Phe Arg Ala Ile
 130 135 140

Pro Ala Ser Met Lys Ala Ala Ile Ser Val Gly Ile Gly Leu Phe Ile
 145 150 155 160

Ala Met Ile Gly Leu Val Asp Ala Gly Phe Val Arg Arg Ile Pro Asp
 165 170 175

Ala Ala Gly Thr Thr Val Pro Val Thr Leu Gly Ile Asp Gly Ser Ile
 180 185 190

Ala Ser Trp Pro Thr Phe Val Phe Val Val Gly Val Leu Leu Cys Gly
 195 200 205

Ile Leu Val Val Arg Arg Val Arg Gly Gly Leu Phe Ile Gly Ile Leu
 210 215 220

Gly Thr Thr Ile Leu Ala Ile Ile Ala Glu Ala Ile Phe Asp Ser Gly

225		230		235		240
Ala Ser Phe	Glu Asn Gly	Glu Ala Asn Ala	Glu Gly Trp Ser	Leu Ala		
	245		250		255	
Val Pro Gly	Leu Pro Asp Ser	Phe Gly Gly Ile	Pro Asp Leu Ser	Ile		
	260		265		270	
Val Gly Ala	Val Asp Leu Ile	Gly Ala Phe Ser	Arg Ile Gly Val	Val		
	275		280		285	
Ala Ala Thr	Leu Leu Ile Phe	Thr Leu Val Leu	Ala Asn Phe Phe	Asp		
	290		295		300	
Ala Met Gly	Thr Met Thr Ala	Leu Gly Lys Gln	Gly Asn Leu Val	Asp		
	305		310		315	
Asp Glu Gly	Asn Leu Pro Asp	Ile Lys Lys Ala	Leu Val Val Glu	Gly		
	325		330		335	
Ala Gly Ala	Ile Val Gly Gly	Ala Phe Ser Ala	Ser Ser Asn Thr	Val		
	340		345		350	
Phe Ala Asp	Ser Ser Ala Gly	Val Ala Asp Gly	Ala Arg Thr Gly	Leu		
	355		360		365	
Ala Asn Val	Val Thr Gly Ser	Leu Phe Leu Ala	Ala Met Phe Leu	Thr		
	370		375		380	
Pro Leu Tyr	Glu Ile Val Pro	Ile Glu Ala Ala	Ala Pro Val Leu	Val		
	385		390		395	
Val Val Gly	Ala Met Met Met	Gly Gln Val Thr	Glu Ile Asp Phe	Ser		
	405		410		415	
Lys Phe Tyr	Ile Ala Phe Pro	Ala Phe Leu Thr	Ile Val Ile Met	Pro		
	420		425		430	
Phe Thr Tyr	Ser Ile Ala Asn	Gly Ile Gly Val	Gly Phe Ile Met	Tyr		
	435		440		445	
Ala Ile Met	Ala Ala Ala Ala	Gly Lys Ala Lys	Gln Val His Trp	Leu		
	450		455		460	
Met Trp Leu	Val Ala Gly Leu	Phe Val Val Phe	Phe Ala Ile Asp	Pro		
	465		470		475	
Ile Met Glu	Ala Val Gly					
	485					

<210> 1031

<211> 702

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(679)

<223> RXN02185

[illegible]

<213> *Corynebacterium glutamicum*

<400> 1032

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		20					25						30		

Ala	Ser	Ala	Ala	Pro	Asp	Ser	Asp	Trp	Asp	Arg	Leu	Ala	Gln	Cys	Glu
	35					40					45				

Ser	Gly	Gly	Asn	Trp	Ala	Ile	Asn	Thr	Gly	Asn	Gly	Tyr	His	Gly	Gly
	50					55					60				

Leu	Gln	Phe	Ser	Ala	Ser	Thr	Trp	Ala	Ala	Tyr	Gly	Gly	Gln	Glu	Phe
65					70					75					80

Ala	Thr	Tyr	Ala	Tyr	Gln	Ala	Thr	Arg	Glu	Gln	Gln	Ile	Ala	Val	Ala
			85						90					95	

Glu	Arg	Thr	Leu	Ala	Gly	Gln	Gly	Trp	Gly	Ala	Trp	Pro	Ala	Cys	Ser
			100					105					110		

Ala	Ser	Leu	Gly	Leu	Asn	Ser	Ala	Pro	Thr	Gln	Arg	Asp	Leu	Ser	Ala
		115					120					125			

Thr	Thr	Ser	Thr	Pro	Glu	Pro	Ala	Ala	Ala	Pro	Ala	Val	Ala	Glu	
		130				135					140				

Tyr	Asn	Ala	Pro	Ala	Ala	Asn	Ile	Ala	Val	Gly	Ser	Thr	Asp	Leu	Asn
145						150				155				160	

Thr	Ile	Lys	Ser	Thr	Tyr	Gly	Ala	Val	Thr	Gly	Thr	Leu	Ala	Gln	Tyr
				165					170					175	

Gly	Ile	Thr	Val	Pro	Ala	Glu	Val	Glu	Ser	Tyr	Tyr	Asn	Ala	Phe	Val
			180					185					190		

Gly

<210> 1033

<211> 702

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(679)

<223> FRXA02185

<400> 1033

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				Met Gly Arg His Ser	
				1	5

act aag act agc tcc gcg ttc acc aag etc gca gct tcc acc atc gct 163

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Thr Lys Thr Ser Ser Ala Phe Thr Lys Leu Ala Ala Ser Thr Ile Ala
          10          15          20
ttc ggt gct gct gca acc atc atg gct cct tct gca tct gct gca cct 211
Phe Gly Ala Ala Ala Thr Ile Met Ala Pro Ser Ala Ser Ala Ala Pro
          25          30          35
gat tcc gac tgg gat cgc etc gca cag tgc gag tcc ggt ggt aac tgg 259
Asp Ser Asp Trp Asp Arg Leu Ala Gln Cys Glu Ser Gly Gly Asn Trp
          40          45          50
gca atc aac acc ggt aac ggc tac cac ggt ggt ctg cag ttc tcc gct 307
Ala Ile Asn Thr Gly Asn Gly Tyr His Gly Gly Leu Gln Phe Ser Ala
          55          60          65
agc acc tgg gct gct tac ggc ggc cag gag ttc gct acc tac gca tac 355
Ser Thr Trp Ala Ala Tyr Gly Gly Gln Glu Phe Ala Thr Tyr Ala Tyr
          70          75          85
cag gca acc cgt gag cag cag atc gct gtt gca gag cgc acc ttg gct 403
Gln Ala Thr Arg Glu Gln Gln Ile Ala Val Ala Glu Arg Thr Leu Ala
          90          95          100
ggt cag ggc tgg ggc gca tgg cct gct tgc tcc gct tcc ctt gga ctg 451
Gly Gln Gly Trp Gly Ala Trp Pro Ala Cys Ser Ala Ser Leu Gly Leu
          105          110          115
aac tcc gct cca acc cag cgt gac etc tcc gct acc acc tcc acc cca 499
Asn Ser Ala Pro Thr Gln Arg Asp Leu Ser Ala Thr Thr Ser Thr Pro
          120          125          130
gag cca gct gca gct gca cca gct gtt gct gag tac aac gct cct gca 547
Glu Pro Ala Ala Ala Pro Ala Val Ala Glu Tyr Asn Ala Pro Ala
          135          140          145
gcc aac atc gca gtt ggc tcc acc gac ttg aac acc atc aag tcc acc 595
Ala Asn Ile Ala Val Gly Ser Thr Asp Leu Asn Thr Ile Lys Ser Thr
          150          155          160
tac ggc gct gtc acc ggc acc etc gct cag tac ggc atc acc gtt cca 643
Tyr Gly Ala Val Thr Gly Thr Leu Ala Gln Tyr Gly Ile Thr Val Pro
          170          175          180
gct gag gtt gag tct tac tac aac gct ttc gtc ggc taaatctagc 689
Ala Glu Val Glu Ser Tyr Tyr Asn Ala Phe Val Gly
          185          190
tgcaacttttt aaa 702

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<210> 1034

<211> 193

<212> PRT

<213> Corynebacterium glutamicum

<400> 1034

```

Met Gly Arg His Ser Thr Lys Thr Ser Ser Ala Phe Thr Lys Leu Ala
  1              5              10              15

```

```

Ala Ser Thr Ile Ala Phe Gly Ala Ala Ala Thr Ile Met Ala Pro Ser
  20              25              30

```

```

Tyr Asn Ala Pro Ala Ala Asn Ile Ala Val Gly Ser Thr Asp Leu Asn
145                150                155                160
Tyr Ile Lys Ser Thr Tyr Gly Ala Val Thr Gly Thr Leu Ala Gln Tyr
                165                170                175
Gly Ile Thr Val Pro Ala Glu Val Glu Ser Tyr Tyr Asn Ala Phe Val
                180                185                190
Gly
#
<210> 1035
<211> 321
<212> DNA
<213> Corynebacterium glutamicum

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gcg tcc agc cca tgg ggc gat gac aaq gaa ttc cca gtt tct gca gaa 259

Ala Ser Ser Pro Tip Gly Asp Asp Lys Glu Phe Pro Val Ser Ala Glu
40 50
gag acc gga tac gtt cac ccg tac acc cgg atc aac cgc taagaaaactt 308
Glu Thr Gly Tyr Val His Pro Tyr Thr Arg Ile Asn Arg 65
55
aaaaaaaaaggc caa 321

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<210> 1036
<211> 66
<212> PRT
<213> Corynebacterium glutamicum
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<400> 1036
Met Tyr Asp Met Ala Asn Val Glu Lys Lys His Phe Val Asp Pro Ala
 1              5              10              15
Trp Pro Glu His Asn Pro Ala Asp Gly His Val Val Thr Glu Leu Ile
      20              25              30
Ser Lys Val Ala Gly Ala Ser Ser Pro Trp Gly Asp Asp Lys Glu Phe
      35              40              45
Pro Val Ser Ala Glu Glu Thr Gly Tyr Val His Pro Tyr Thr Arg Ile
      50              55              60
Asn Arg
63

```

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<210> 1037
<211> 342
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(319)
<223> FRXA02186
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#400> 1037
agctgatcat cactttgagt atccaaccac cccttgaggg tggggatggg ggagtccttt 60
ttcatgatgt tgtaagttt aagccttgtt gaggtgaact ttg ttc cca gag ttt 115
                                     Leu Phe Pro Glu Phe
                                      1                    5
gaa aga atg tat gac atg gca aac gta gag aag aag cac ttc gtc gat 163
Glu Arg Met Tyr Asp Asn Ala Asn Val Glu Lys Lys His Phe Val Asp
                               10                      15                20
ccg gca tgg ccg gag cac aat cca gct gac gga cac gtc gtt act gaa 211
Pro Ala Trp Pro Glu His Asn Pro Ala Asp Gly His Val Val Thr Glu
                                25                      30                35
ctc atc tcc aag gtc gca gcc gcg tcc agc cca tgg gcc gat gac aag 259
Leu Ile Ser Lys Val Ala Gly Ala Ser Ser Pro Trp Gly Asp Asp Lys
                              40                      45                50

```


gaa ttc cca gtt tct gca gaa gag acc gga tac gtt cac ccg tac acc 307
 Glu Phe Pro Val Ser Ala Glu Glu Thr Gly Tyr Val His Pro Tyr Thr
 55 60 65

cgg atc aac cgc taagaaactt aaaaaagagg caa 342
 Arg Ile Asn Arg
 70

<210> 1038

<211> 73

<212> PRT

<213> Corynebacterium glutamicum

<400> 1038

Leu Phe Pro Glu Phe Glu Arg Met Tyr Asp Met Ala Asn Val Glu Lys
 1 5 10 15

Lys His Phe Val Asp Pro Ala Trp Pro Glu His Asn Pro Ala Asp Gly
 20 25 30

His Val Val Thr Glu Leu Ile Ser Lys Val Ala Gly Ala Ser Ser Pro
 35 40 45

Trp Gly Asp Asp Lys Glu Phe Pro Val Ser Ala Glu Glu Thr Gly Tyr
 50 55 60

Val His Pro Tyr Thr Arg Ile Asn Arg
 65 70

<210> 1039

<211> 898

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(898)

<223> RXN02207

<400> 1039

gaatcggtga ctttgccaac accaatcaca caagcccttg atgatgtctc cctgtgactt 60

ggtccaatta cattcactgg taatctgaaa ccttgtgaat atg cgc cgt cga tcc 115
 Met Arg Arg Arg Ser
 1 5

cgt gtg tcc cgt ttg ctt ccc gcc aca gct ttg ctg gcc tca act gca 163
 Arg Val Ser Arg Leu Leu Pro Ala Thr Ala Leu Leu Ala Ser Thr Ala
 10 15 20

ctt ctt tta agt gca tgt acg caa ggg gta acg gac tcc ccg gat atg 211
 Leu Leu Leu Ser Ala Cys Thr Gln Gly Val Thr Asp Ser Pro Asp Met
 25 30 35

ggc aag gca act ccc gct gtc tcc ccc gca gca agc aac ccg gat ggc 259
 Gly Lys Ala Thr Pro Ala Val Ser Pro Ala Ala Ser Asn Pro Asp Gly
 40 45 50

caa gta att gag ttc ggc aac atc act gac atg gaa gtc act gat ggt 307

Gln	Val	Ile	Glu	Phe	Gly	Asn	Ile	Thr	Asp	Met	Glu	Val	Thr	Asp	Gly	
55						60					65					
gac	atc	ctc	ggt	gta	cgc	acc	gaa	gac	gca	ctc	gct	att	ggt	aca	gtc	355
Asp	Ile	Leu	Gly	Val	Arg	Thr	Glu	Asp	Ala	Leu	Ala	Ile	Gly	Thr	Val	
70					75				80					85		
tcc	gac	ttc	gaa	gcg	ggt	agc	cag	gtg	gaa	ctg	gac	gtc	gat	aag	caa	403
Ser	Asp	Phe	Glu	Ala	Gly	Ser	Gln	Val	Glu	Leu	Asp	Val	Asp	Lys	Gln	
				90					95					100		
tgc	ggc	gac	ctg	acc	gca	acc	ggc	ggc	act	ttc	gtg	ctc	ccc	tgc	gcc	451
Cys	Gly	Asp	Leu	Thr	Ala	Thr	Gly	Gly	Thr	Phe	Val	Leu	Pro	Cys	Ala	
			105				110						115			
gat	ggc	gtt	tat	ttg	att	gat	gcc	aag	gac	ccg	gat	ctg	gat	gag	ttg	499
Asp	Gly	Val	Tyr	Leu	Ile	Asp	Ala	Lys	Asp	Pro	Asp	Leu	Asp	Glu	Leu	
		120					125					130				
cgt	gca	act	gac	aag	cca	gtc	acg	gtg	gca	gcc	ttg	acc	agc	gat	gat	547
Arg	Ala	Thr	Asp	Lys	Pro	Val	Thr	Val	Ala	Ala	Leu	Thr	Ser	Asp	Asp	
		135				140					145					
cag	ctt	ctg	gtg	ggc	aat	ggg	gaa	gat	gaa	gaa	ctc	acc	atc	tac	cgc	595
Gln	Leu	Leu	Val	Gly	Asn	Gly	Glu	Asp	Glu	Glu	Leu	Thr	Ile	Tyr	Arg	
150					155				160					165		
gag	ggc	gaa	gag	cca	gaa	acc	ttc	acc	gtc	gcg	ggg	ccc	aat	acc	cag	643
Glu	Gly	Glu	Glu	Pro	Glu	Thr	Phe	Thr	Val	Ala	Gly	Pro	Asn	Thr	Gln	
				170					175					180		
ctc	atc	gcc	gtt	cct	gtc	att	gat	cgc	cac	gac	gcc	gtt	gtg	cgc	acc	691
Leu	Ile	Ala	Val	Pro	Val	Ile	Asp	Arg	His	Asp	Ala	Val	Val	Arg	Thr	
			185				190						195			
tgg	aac	gaa	aac	acc	acg	att	caa	gat	gtg	gac	tac	ccc	aac	gac	cgt	739
Trp	Asn	Glu	Asn	Thr	Thr	Ile	Gln	Asp	Val	Asp	Tyr	Pro	Asn	Asp	Arg	
		200					205					210				
gaa	ggc	gcg	acc	ctt	cgc	gtg	gga	ctc	ggc	gtt	ggg	caa	atg	gct	ggg	787
Glu	Gly	Ala	Thr	Leu	Arg	Val	Gly	Leu	Gly	Val	Gly	Gln	Met	Ala	Gly	
	215					220				225						
ggc	gaa	gac	ggc	ctg	ctg	gtg	gtc	tct	gat	gaa	atg	ggg	ggc	caa	att	835
Gly	Glu	Asp	Gly	Leu	Leu	Val	Val	Ser	Asp	Glu	Met	Gly	Gly	Gln	Ile	
230					235				240					245		
gcc	atc	tac	aac	gct	gat	gat	gtc	atc	cga	ctt	caa	aat	gac	cgc	ccc	883
Ala	Ile	Tyr	Asn	Ala	Asp	Asp	Val	Ile	Arg	Leu	Gln	Asn	Asp	Arg	Pro	
			250						255					260		
cac	cga	cga	gga	acc												898
His	Arg	Arg	Gly	Thr												
			265													

<210> 1040

<211> 266

<212> PRT

<213> Corynebacterium glutamicum

<400> 1040

Met Arg Arg Arg Ser Arg Val Ser Arg Leu Leu Pro Ala Thr Ala Leu
 1 5 10 15

Leu Ala Ser Thr Ala Leu Leu Leu Ser Ala Cys Thr Gln Gly Val Thr
 20 25 30

Asp Ser Pro Asp Met Gly Lys Ala Thr Pro Ala Val Ser Pro Ala Ala
 35 40 45

Ser Asn Pro Asp Gly Gln Val Ile Glu Phe Gly Asn Ile Thr Asp Met
 50 55 60

Glu Val Thr Asp Gly Asp Ile Leu Gly Val Arg Thr Glu Asp Ala Leu
 65 70 75 80

Ala Ile Gly Thr Val Ser Asp Phe Glu Ala Gly Ser Gln Val Glu Leu
 85 90 95

Asp Val Asp Lys Gln Cys Gly Asp Leu Thr Ala Thr Gly Gly Thr Phe
 100 105 110

Val Leu Pro Cys Ala Asp Gly Val Tyr Leu Ile Asp Ala Lys Asp Pro
 115 120 125

Asp Leu Asp Glu Leu Arg Ala Thr Asp Lys Pro Val Thr Val Ala Ala
 130 135 140

Leu Thr Ser Asp Asp Gln Leu Leu Val Gly Asn Gly Glu Asp Glu Glu
 145 150 155 160

Leu Thr Ile Tyr Arg Glu Gly Glu Glu Pro Glu Thr Phe Thr Val Ala
 165 170 175

Gly Pro Asn Thr Gln Leu Ile Ala Val Pro Val Ile Asp Arg His Asp
 180 185 190

Ala Val Val Arg Thr Trp Asn Glu Asn Thr Thr Ile Gln Asp Val Asp
 195 200 205

Tyr Pro Asn Asp Arg Glu Gly Ala Thr Leu Arg Val Gly Leu Gly Val
 210 215 220

Gly Gln Met Ala Gly Gly Glu Asp Gly Leu Leu Val Val Ser Asp Glu
 225 230 235 240

Met Gly Gly Gln Ile Ala Ile Tyr Asn Ala Asp Asp Val Ile Arg Leu
 245 250 255

Gln Asn Asp Arg Pro His Arg Arg Gly Thr
 260 265

<210> 1041

<211> 859

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(859)

<223> FRXA02207

<400> 1041

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gaatcgggtga ctttgccaac accaatcaca caagcccttg atgatgtctc cctgtgactt 60
ggtccaatta cttcactcgg taatctgaaa ccttgtgaat atg cgc cgt cga tcc 115
Met Arg Arg Arg Ser
1 5

cgt gtg tcc cgt ttg ctt ccc gcc aca gct ttg ctg gcc tca act gca 163
Arg Val Ser Arg Leu Leu Pro Ala Thr Ala Leu Leu Ala Ser Thr Ala
10 15 20

ctt ctt tta agt gca tgt acg caa ggg gta acg gac tcc ccg gat atg 211
Leu Leu Leu Ala Cys Thr Gln Gly Val Thr Asp Ser Pro Asp Met
25 30 35

ggc aag gca act ccc gct gtc tcc ccc gca gca agc aac ccg gat ggc 259
Gly Lys Ala Thr Pro Ala Val Ser Pro Ala Ala Ser Asn Pro Asp Gly
40 45 50

caa gta att gag ttc ggc aac atc act gac atg gaa gtc act gat ggt 307
Gln Val Ile Glu Phe Gly Asn Ile Thr Asp Met Glu Val Thr Asp Gly
55 60 65

gac atc ctc ggt gta cgc acc gaa gac gca ctc gct att ggt aca gtc 355
Asp Ile Leu Gly Val Arg Thr Glu Asp Ala Leu Ala Ile Gly Thr Val
70 75 80 85

tcc gac ttc gaa gcg ggt agc cag gtg gaa ctg gac gtc gat aag caa 403
Ser Asp Phe Glu Ala Gly Ser Gln Val Glu Leu Asp Val Asp Lys Gln
90 95 100

tgc ggc gac ctg acc gca acc ggc ggc act ttc gtg ctc ccc tgc gcc 451
Cys Gly Asp Leu Thr Ala Thr Gly Gly Thr Phe Val Leu Pro Cys Ala
105 110 115

gat ggc gtt tat ttg att gat gcc aag gac ccg gat ctg gat gag ttg 499
Asp Gly Val Tyr Leu Ile Asp Ala Lys Asp Pro Asp Leu Asp Glu Leu
120 125 130

cgt gca act gac aag cca gtc acg gtg gca gcc ttg acc agc gat gat 547
Arg Ala Thr Asp Lys Pro Val Thr Val Ala Ala Leu Thr Ser Asp Asp
135 140 145

cag ctt ctg gtg ggc aat ggt gaa gat gaa gaa ctc acc atc tac cgc 595
Gln Leu Leu Val Gly Asn Gly Glu Asp Glu Leu Thr Ile Tyr Arg
150 155 160 165

gag ggc gaa gag cca gaa acc ttc acc gtc gcg ggt ccc aat acc cag 643
Glu Gly Glu Glu Pro Glu Thr Phe Thr Val Ala Gly Pro Asn Thr Gln
170 175 180

ctc atc gcc gtt cct gtc att gat cgc cac gac gcc gtt gtg cgc acc 691
Leu Ile Ala Val Pro Val Ile Asp Arg His Asp Ala Val Val Arg Thr
185 190 195

tgg aac gaa aac acc acg att caa gat gtg gac tac ccc aac gac cgt 739
Trp Asn Glu Asn Thr Thr Ile Gln Asp Val Asp Tyr Pro Asn Asp Arg
200 205 210

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gaa ggc gcg acc ctt cgc gtg gga ctc ggc gtt ggt caa atg gct ggt 787
 Glu Gly Ala Thr Leu Arg Val Gly Leu Gly Val Gly Gln Met Ala Gly
 215 220 225

ggc gaa gac ggc ctg ctg gtg gtc tct gat gaa atg ggt ggc caa att 835
 Gly Glu Asp Gly Leu Val Val Ser Asp Glu Met Gly Gly Gln Ile
 230 235 240 245

gcc atc tac aac gct gat gat gtc 859
 Ala Ile Tyr Asn Ala Asp Asp Val
 250

<210> 1042

<211> 253

<212> PRT

<213> Corynebacterium glutamicum

<400> 1042

Met Arg Arg Arg Ser Arg Val Ser Arg Leu Leu Pro Ala Thr Ala Leu
 1 5 10 15

Leu Ala Ser Thr Ala Leu Leu Leu Ser Ala Cys Thr Gln Gly Val Thr
 20 25 30

Asp Ser Pro Asp Met Gly Lys Ala Thr Pro Ala Val Ser Pro Ala Ala
 35 40 45

Ser Asn Pro Asp Gly Gln Val Ile Glu Phe Gly Asn Ile Thr Asp Met
 50 55 60

Glu Val Thr Asp Gly Asp Ile Leu Gly Val Arg Thr Glu Asp Ala Leu
 65 70 75 80

Ala Ile Gly Thr Val Ser Asp Phe Glu Ala Gly Ser Gln Val Glu Leu
 85 90 95

Asp Val Asp Lys Gln Cys Gly Asp Leu Thr Ala Thr Gly Gly Thr Phe
 100 105 110

Val Leu Pro Cys Ala Asp Gly Val Tyr Leu Ile Asp Ala Lys Asp Pro
 115 120 125

Asp Leu Asp Glu Leu Arg Ala Thr Asp Lys Pro Val Thr Val Ala Ala
 130 135 140

Leu Thr Ser Asp Asp Gln Leu Leu Val Gly Asn Gly Glu Asp Glu Glu
 145 150 155 160

Leu Thr Ile Tyr Arg Glu Gly Glu Glu Pro Glu Thr Phe Thr Val Ala
 165 170 175

Gly Pro Asn Thr Gln Leu Ile Ala Val Pro Val Ile Asp Arg His Asp
 180 185 190

Ala Val Val Arg Thr Trp Asn Glu Asn Thr Thr Ile Gln Asp Val Asp
 195 200 205

Tyr Pro Asn Asp Arg Glu Gly Ala Thr Leu Arg Val Gly Leu Gly Val
 210 215 220

Gly Gln Met Ala Gly Gly Glu Asp Gly Leu Val Val Val Ser Asp Glu
 225 230 235 240
 Met Gly Gly Gln Ile Ala Ile Tyr Asn Ala Asp Asp Val
 245 250

<210> 1043

<211> 601

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(601)

<223> RXN02223

<400> 1043

cttgcttttg agggccgcta cgcgcagctg tatcaacgat ggagtgctca atagttcaaa 60

tccaccacaa actctagaga tttggggtag aaacgaagac atg agc acc tac caa 115
 Met Ser Thr Tyr Gln 5

gac gat cgt ttc cca ggc cca gac ccc tac gca ccg ett ggt gaa aag 163
 Asp Asp Arg Phe Pro Gly Pro Asp Pro Tyr Ala Pro Leu Gly Glu Lys 10 15 20

cca agc ttt acc ctc acc tcc acc gac ttg gaa aac ggt gca aag ctg 211
 Pro Ser Phe Thr Leu Thr Ser Thr Asp Leu Glu Asn Gly Ala Lys Leu 25 30 35

gcc gaa gcc caa ctc ggt ggc acc gat att tcc cca cag ctg tcc tgg 259
 Ala Glu Ala Gln Leu Gly Gly Thr Asp Ile Ser Pro Gln Leu Ser Trp 40 45 50

tca gat ctt cca gaa ggc acc aaa tcc ctc gcg atc acc tgc ctc gac 307
 Ser Asp Leu Pro Glu Gly Thr Lys Ser Leu Ala Ile Thr Cys Leu Asp 55 60 65

cca gat gcc cca acc ggc gct ggt ttc tgg cac tgg gca gtg ttt aac 355
 Pro Asp Ala Pro Thr Gly Ala Gly Phe Trp His Trp Ala Val Phe Asn 70 75 80 85

atc ccc aca act gtc acg gag atc ccc acc ggt gct ggc gat gaa acc 403
 Ile Pro Thr Thr Val Thr Glu Ile Pro Thr Gly Ala Gly Asp Glu Thr 90 95 100

ctc ggc ggc atc gaa ggc gta gtt tcc ctc aag ggt gat tcc ggc aag 451
 Leu Gly Gly Ile Glu Gly Val Val Ser Leu Lys Gly Asp Ser Gly Lys 105 110 115

cgt ggc ttc tac gga gcg caa cct cca gct ggc cac gca ccg cac cgt 499
 Arg Gly Phe Tyr Gly Ala Gln Pro Pro Ala Gly His Ala Pro His Arg 120 125 130

tac ctc ttc gca gtt cat gca ctt gat gtg gaa aaa ctc gac atc gcc 547
 Tyr Leu Phe Ala Val His Ala Leu Asp Val Glu Lys Leu Asp Ile Ala 135 140 145

ccc gac gct acc ccc act ggt cta ggc ttc aac ctg tat ttc cac act 595

Pro Asp Ala Thr Pro Thr Gly Leu Gly Phe Asn Leu Tyr Phe His Thr
 150 155 160 165

ctt ggc
 Leu Gly

601

<210> 1044
 <211> 167
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1044
 Met Ser Thr Tyr Gln Asp Asp Arg Phe Pro Gly Pro Asp Pro Tyr Ala
 1 5 10 15

Pro Leu Gly Glu Lys Pro Ser Phe Thr Leu Thr Ser Thr Asp Leu Glu
 20 25 30

Asn Gly Ala Lys Leu Ala Glu Ala Gln Leu Gly Gly Thr Asp Ile Ser
 35 40 45

Pro Gln Leu Ser Trp Ser Asp Leu Pro Glu Gly Thr Lys Ser Leu Ala
 50 55 60

Ile Thr Cys Leu Asp Pro Asp Ala Pro Thr Gly Ala Gly Phe Trp His
 65 70 75 80

Trp Ala Val Phe Asn Ile Pro Thr Thr Val Thr Glu Ile Pro Thr Gly
 85 90 95

Ala Gly Asp Glu Thr Leu Gly Gly Ile Glu Gly Val Val Ser Leu Lys
 100 105 110

Gly Asp Ser Gly Lys Arg Gly Phe Tyr Gly Ala Gln Pro Pro Ala Gly
 115 120 125

His Ala Pro His Arg Tyr Leu Phe Ala Val His Ala Leu Asp Val Glu
 130 135 140

Lys Leu Asp Ile Ala Pro Asp Ala Thr Pro Thr Gly Leu Gly Phe Asn
 145 150 155 160

Leu Tyr Phe His Thr Leu Gly
 165

<210> 1045
 <211> 520
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(520)
 <223> FRXA02223

<400> 1045
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Met Ser Thr Tyr Gln
1 5

gac gat cgt ttc cca ggc cca gac ccc tac gca ccg ott ggt gaa aag 163
Asp Asp Arg Phe Pro Gly Pro Asp Pro Tyr Ala Pro Leu Gly Glu Lys
10 15 20

cca agc ttt acc ctc acc tcc acc gac ttg gaa aac ggt gca aag ctg 211
Pro Ser Phe Thr Leu Thr Ser Thr Asp Leu Glu Asn Gly Ala Lys Leu
25 30 35

gcc gaa gcc caa ctc ggt ggc acc gat att tcc cca cag ctg tcc tgg 259
Ala Glu Ala Gln Leu Gly Gly Thr Asp Ile Ser Pro Gln Leu Ser Trp
40 45 50

tca gat ctt cca gaa ggc acc aaa tcc ctc gcg atc acc tgc ctc gac 307
Ser Asp Leu Pro Glu Gly Thr Lys Ser Leu Ala Ile Thr Cys Leu Asp
55 60 65

cca gat gcc cca acc ggc gct ggt ttc tgg cac tgg gca gtg ttt aac 355
Pro Asp Ala Pro Thr Gly Ala Gly Phe Trp His Trp Ala Val Phe Asn
70 75 80 85

atc ccc aca act gtc acg gag atc ccc acc ggt gct ggc gat gaa acc 403
Ile Pro Thr Thr Val Thr Glu Ile Pro Thr Gly Ala Gly Asp Glu Thr
90 95 100

ctc ggc ggc atc gaa ggc gta gtt tcc ctc aag ggt gat tcc ggc aag 451
Leu Gly Gly Ile Glu Gly Val Val Ser Leu Lys Gly Asp Ser Gly Lys
105 110 115

cgt ggc ttc tac gga gcg caa cct cca gct ggc cac gca ccg cac cgt 499
Arg Gly Phe Tyr Gly Ala Gln Pro Pro Ala Gly His Ala Pro His Arg
120 125 130

tac ctc ttc gca gtt cat gca 520
Tyr Leu Phe Ala Val His Ala
135 140

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<210> 1046

<211> 140

<212> PRT

<213> Corynebacterium glutamicum

<400> 1046

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Met Ser Thr Tyr Gln Asp Asp Arg Phe Pro Gly Pro Asp Pro Tyr Ala
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Pro Leu Gly Glu Lys Pro Ser Phe Thr Leu Thr Ser Thr Asp Leu Glu
20 25 30

Asn Gly Ala Lys Leu Ala Glu Ala Gln Leu Gly Gly Thr Asp Ile Ser
35 40 45

Pro Gln Leu Ser Trp Ser Asp Leu Pro Glu Gly Thr Lys Ser Leu Ala
50 55 60

Ile Thr Cys Leu Asp Pro Asp Ala Pro Thr Gly Ala Gly Phe Trp His
65 70 75 80

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400> 1047																				
ctgacacctc	ctatggc	cagc	cggtatg	ttt	aataaac	gta	attcgag	ttt	cggcggc	cgt	60									
gtcgcgcggc	caggacg	acc	ctagctt	ta	aggaccc	acc	atg	act	gag	aac	cag	115								
							Met	Thr	Glu	Asn	Gln	5								
act	ccc	agc	tcc	acc	tct	gca	ccg	aag	ccg	gga	cct	cg	ccg	ggy	cca	163				
Thr	Pro	Ser	Ser	Thr	Ser	Ala	Pro	Lys	Pro	Gly	Pro	Arg	Pro	Gly	Pro					
				10					15					20						
cgg	cca	gga	ccc	cga	cct	ggg	gct	cag	gtt	gct	gca	aag	aaa	gct	gcg	211				
Arg	Pro	Gly	Pro	Arg	Pro	Gly	Ala	Gln	Val	Ala	Ala	Lys	Lys	Ala	Ala					
			25					30					35							
gtt	gct	aca	cct	gcg	ccg	atc	gcc	aaa	act	tct	aac	gat	cct	gca	aag	259				
Val	Ala	Thr	Pro	Ala	Pro	Ile	Ala	Lys	Thr	Ser	Asn	Asp	Pro	Ala	Lys					
		40					45					50								
ttt	ggt	cg	gtt	gag	gca	gac	gga	tct	gca	tat	gtc	acc	acc	tct	gct	307				
Phe	Gly	Arg	Val	Glu	Ala	Asp	Gly	Ser	Ala	Tyr	Val	Thr	Thr	Ser	Ala					
	55					60					65									
ggc	gag	cgt	ctg	att	ggt	tct	tgg	cag	gcc	ggc	acc	cct	gag	gaa	ggt	355				
Gly	Glu	Arg	Leu	Ile	Gly	Ser	Trp	Gln	Ala	Gly	Thr	Pro	Glu	Glu	Gly					
	70				75				80					85						
ctt	gct	cac	tac	ggc	gcc	cgt	ttt	gat	gat	gcc	acc	gaa	gtt	gag		403				
Leu	Ala	His	Tyr	Gly	Ala	Arg	Phe	Asp	Asp	Leu	Ala	Thr	Glu	Val	Glu					
				90					95					100						
ctc	atg	gaa	cag	cgc	cta	atc	tcc	cac	cct	gat	gag	gcg	acc	tcc	atc	451				
Leu	Met	Glu	Gln	Arg	Leu	Ile	Ser	His	Pro	Asp	Asp	Ala	Thr	Ser	Ile					
				105				110				115								
cgc	acg	aag	gct	gaa	gaa	cct	aag	gca	acc	ctg	ccc	acc	att	gct	gcg	499				
Arg	Thr	Lys	Ala	Glu	Glu	Leu	Lys	Ala	Thr	Leu	Pro	Thr	Ile	Ala	Ala					

120	125	130	
atc ggt gac ctt gat ggc gtt gaa gct cgc ctg tcc aag atc atc aac Ile Gly Asp Leu Asp Gly Val Glu Ala Arg Leu Ser Lys Ile Ile Asn 135 140 145			547
aac tcc gag gaa gcc aac gag cgc gcc aag gaa caa aag gct aaa aac Asn Ser Glu Glu Ala Asn Glu Arg Ala Lys Glu Gln Lys Ala Lys Asn 150 155 160 165			595
cgt gag cgc gca gta gct cgc aag gaa gag ctc gct gtt gag gct gaa Arg Glu Arg Ala Val Ala Arg Lys Glu Glu Leu Ala Val Glu Ala Glu 170 175 180			643
acc ttg gca gaa aac tcc tcc gac tgg aag gtt gct ggc gac cgc atc Thr Leu Ala Glu Asn Ser Ser Asp Trp Lys Val Ala Gly Asp Arg Ile 185 190 195			691
cgc gcc atc ctg gat gag tgg aag tcc atc cac ggc atc gac cgc aag Arg Ala Ile Leu Asp Glu Trp Lys Ser Ile His Gly Ile Asp Arg Lys 200 205 210			739
acc gat gat gaa ctg tgg aaa cgc tac tcc cgt gcg cgt gac tcc ttc Thr Asp Asp Glu Leu Trp Lys Arg Tyr Ser Arg Ala Arg Asp Ser Phe 215 220 225			787
aac cgt cgc cgc gcc gca cac ttc gca gag ctg gat cgc acc cgc gca Asn Arg Arg Arg Gly Ala His Phe Ala Glu Leu Asp Arg Thr Arg Ala 230 235 240 245			835
tct gca cgc aaa ctc aag gaa gaa ctc gtt gag cgc gcc aat gct ctc Ser Ala Arg Lys Leu Lys Glu Glu Leu Val Glu Arg Ala Asn Ala Leu 250 255 260			883
aag gaa tcc act gag tgg aac gac acc gcc cgc gca ttc cgc gat ctc Lys Glu Ser Thr Glu Trp Asn Asp Thr Ala Arg Ala Phe Arg Asp Leu 265 270 275			931
atg acc gaa tgg aaa gcc gcc ggc cgc gca cca cgc gaa atc gac gac Met Thr Glu Trp Lys Ala Ala Gly Arg Ala Pro Arg Glu Ile Asp Asp 280 285 290			979
aag ctg tgg gca gca ttc aag ggc gcc cag gac tac ttc ttt gat aag Lys Leu Trp Ala Ala Phe Lys Gly Ala Gln Asp Tyr Phe Phe Asp Lys 295 300 305			1027
cgc aac gcc gta gcc aag gaa cgc gac cag gaa ttc gaa gcc aac gca Arg Asn Ala Val Ala Lys Glu Arg Asp Gln Glu Phe Glu Ala Asn Ala 310 315 320 325			1075
acc gca aag cag cag ctc atc gac gaa tac gac gca cag atc aac ccc Thr Ala Lys Gln Gln Leu Ile Asp Glu Tyr Asp Ala Gln Ile Asn Pro 330 335 340			1123
gag cag gcc ctc gat gga gcg cgc agc aag ctc Glu Gln Gly Leu Asp Gly Ala Arg Ser Lys Leu 345 350			1156

<210> 1048

<211> 352

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1048

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Met Thr Glu Asn Gln Thr Pro Ser Ser Thr Ser Ala Pro Lys Pro Gly
 1           5           10           15

Pro Arg Pro Gly Pro Arg Pro Gly Pro Arg Pro Gly Ala Gln Val Ala
          20           25           30

Ala Lys Lys Ala Ala Val Ala Thr Pro Ala Pro Ile Ala Lys Thr Ser
          35           40           45

Asn Asp Pro Ala Lys Phe Gly Arg Val Glu Ala Asp Gly Ser Ala Tyr
          50           55           60

Val Thr Thr Ser Ala Gly Glu Arg Leu Ile Gly Ser Trp Gln Ala Gly
          65           70           75           80

Thr Pro Glu Glu Gly Leu Ala His Tyr Gly Ala Arg Phe Asp Asp Leu
          85           90           95

Ala Thr Glu Val Glu Leu Met Glu Gln Arg Leu Ile Ser His Pro Asp
          100          105          110

Asp Ala Thr Ser Ile Arg Thr Lys Ala Glu Glu Leu Lys Ala Thr Leu
          115          120          125

Pro Thr Ile Ala Ala Ile Gly Asp Leu Asp Gly Val Glu Ala Arg Leu
          130          135          140

Ser Lys Ile Ile Asn Asn Ser Glu Glu Ala Asn Glu Arg Ala Lys Glu
          145          150          155          160

Gln Lys Ala Lys Asn Arg Glu Arg Ala Val Ala Arg Lys Glu Glu Leu
          165          170          175

Ala Val Glu Ala Glu Thr Leu Ala Glu Asn Ser Ser Asp Trp Lys Val
          180          185          190

Ala Gly Asp Arg Ile Arg Ala Ile Leu Asp Glu Trp Lys Ser Ile His
          195          200          205

Gly Ile Asp Arg Lys Thr Asp Asp Glu Leu Trp Lys Arg Tyr Ser Arg
          210          215          220

Ala Arg Asp Ser Phe Asn Arg Arg Arg Gly Ala His Phe Ala Glu Leu
          225          230          235          240

Asp Arg Thr Arg Ala Ser Ala Arg Lys Leu Lys Glu Glu Leu Val Glu
          245          250          255

Arg Ala Asn Ala Leu Lys Glu Ser Thr Glu Trp Asn Asp Thr Ala Arg
          260          265          270

Ala Phe Arg Asp Leu Met Thr Glu Trp Lys Ala Ala Gly Arg Ala Pro
          275          280          285

Arg Glu Ile Asp Asp Lys Leu Trp Ala Ala Phe Lys Gly Ala Gln Asp
          290          295          300

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Tyr Phe Phe Asp Lys Arg Asn Ala Val Ala Lys Glu Arg Asp Gln Glu
 305 310 315 320

Phe Glu Ala Asn Ala Thr Ala Lys Gln Gln Leu Ile Asp Glu Tyr Asp
 325 330 335

Ala Gln Ile Asn Pro Glu Gln Gly Leu Asp Gly Ala Arg Ser Lys Leu
 340 345 350

<210> 1049

<211> 1156

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1156)

<223> FRXA02226

<400> 1049

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gtcgcgcggc caggacgacc ctatctttta aggaccacc atg act gag aac cag 115
 Met Thr Glu Asn Gln
 1 5

act ccc agc tcc acc tct gca cgg aag cgg gga cct cgc cgg ggc cca 163
 Thr Pro Ser Ser Thr Ser Ala Pro Lys Pro Gly Pro Arg Pro Gly Pro
 10 15 20

cgg cca gga ccc cga cct ggg gct cag gtt gct gca aag aaa gct gcg 211
 Arg Pro Gly Pro Arg Pro Gly Ala Gln Val Ala Ala Lys Lys Ala Ala
 25 30 35

gtt gct aca cct gcg cgg atc gcc aaa act tct aac gat cct gca aag 259
 Val Ala Thr Pro Ala Pro Ile Ala Lys Thr Ser Asn Asp Pro Ala Lys
 40 45 50

ttt ggt cgc gtt gag gca gac gga tct gca tat gtc acc acc tct gct 307
 Phe Gly Arg Val Glu Ala Asp Gly Ser Ala Tyr Val Thr Thr Ser Ala
 55 60 65

ggc gag cgt ctg att ggt tct tgg cag gcc ggc acc cct gag gaa ggt 355
 Gly Glu Arg Leu Ile Gly Ser Trp Gln Ala Gly Thr Pro Glu Glu Gly
 70 75 80 85

ctt gct cac tac ggc gcc cgt ttt gat gat ctg gcc acc gaa gtt gag 403
 Leu Ala His Tyr Gly Ala Arg Phe Asp Asp Leu Ala Thr Glu Val Glu
 90 95 100

ctc atg gaa cag cgc cta atc tcc cac cct gat gat gcg acc tcc atc 451
 Leu Met Glu Gln Arg Leu Ile Ser His Pro Asp Asp Ala Thr Ser Ile
 105 110 115

cgc acg aag gct gaa gaa ctc aag gca acc ctg ccc acc atc gct gcg 499
 Arg Thr Lys Ala Glu Glu Leu Lys Ala Thr Leu Pro Thr Ile Ala Ala
 120 125 130

atc ggt gac ctt gat ggc gtt gaa gct cgc ctg tcc aag atc atc aac	547
Ile Gly Asp Leu Asp Gly Val Glu Ala Arg Leu Ser Lys Ile Ile Asn	
135 140 145	
aac tcc gag gaa gcc aac gag cgc gcc aag gaa caa aag gct aaa aac	595
Asn Ser Glu Glu Ala Asn Glu Arg Ala Lys Glu Gln Lys Ala Lys Asn	
150 155 160 165	
cgt gag cgc gca gta gct cgc aag gaa gag ctc gct gtt gag gct gaa	643
Arg Glu Arg Ala Val Ala Arg Lys Glu Glu Leu Ala Val Glu Ala Glu	
170 175 180	
acc ttg gca gaa aac tcc tcc gac tgg aag gtt gct ggc gac cgc atc	691
Thr Leu Ala Glu Asn Ser Ser Asp Trp Lys Val Ala Gly Asp Arg Ile	
185 190 195	
cgc gcc atc ctg gat gag tgg aag tcc atc cac ggc atc gac cgc aag	739
Arg Ala Ile Leu Asp Glu Trp Lys Ser Ile His Gly Ile Asp Arg Lys	
200 205 210	
acc gat gat gaa ctg tgg aaa cgc tac tcc cgt gcg cgt gac tcc ttc	787
Thr Asp Asp Glu Leu Trp Lys Arg Tyr Ser Arg Ala Arg Asp Ser Phe	
215 220 225	
aac cgt cgc cgc ggc gca cac ttc gca gag ctg gat cgc acc cgc gca	835
Asn Arg Arg Arg Gly Ala His Phe Ala Glu Leu Asp Arg Thr Arg Ala	
230 235 240 245	
tct gca cgc aaa ctc aag gaa gaa ctc gtt gag cgc gcc aat gct ctc	883
Ser Ala Arg Lys Leu Lys Glu Glu Leu Val Glu Arg Ala Asn Ala Leu	
250 255 260	
aag gaa tcc act gag tgg aac gac acc gcc cgc gca ttc cgc gat ctc	931
Lys Glu Ser Thr Glu Trp Asn Asp Thr Ala Arg Ala Phe Arg Asp Leu	
265 270 275	
atg acc gaa tgg aaa gcc gcc gcc cgc gca cca cgc gaa atc gac gac	979
Met Thr Glu Trp Lys Ala Ala Gly Arg Ala Pro Arg Glu Ile Asp Asp	
280 285 290	
aag ctg tgg gca gca ttc aag gcc gcc cag gac tac ttc ttt gat aag	1027
Lys Leu Trp Ala Ala Phe Lys Gly Ala Gln Asp Tyr Phe Phe Asp Lys	
295 300 305	
cgc aac gcc gta gcc aag gaa cgc gac cag gaa ttc gaa gcc aac gca	1075
Arg Asn Ala Val Ala Lys Glu Arg Asp Gln Glu Phe Glu Ala Asn Ala	
310 315 320 325	
acc gca aag cag cag ctc atc gac gaa tac gac gca cag atc aac ccc	1123
Thr Ala Lys Gln Gln Leu Ile Asp Glu Tyr Asp Ala Gln Ile Asn Pro	
330 335 340	
gag cag gcc ctc gat gga gcg cgc agc aag ctc	1156
Glu Gln Gly Leu Asp Gly Ala Arg Ser Lys Leu	
345 350	

<210> 1050

<211> 352

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1050

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Met Thr Glu Asn Gln Thr Pro Ser Ser Thr Ser Ala Pro Lys Pro Gly
 1             5             10             15

Pro Arg Pro Gly Pro Arg Pro Gly Pro Arg Pro Gly Ala Gln Val Ala
      20             25             30

Ala Lys Lys Ala Ala Val Ala Thr Pro Ala Pro Ile Ala Lys Thr Ser
      35             40             45

Asn Asp Pro Ala Lys Phe Gly Arg Val Glu Ala Asp Gly Ser Ala Tyr
      50             55             60

Val Thr Thr Ser Ala Gly Glu Arg Leu Ile Gly Ser Trp Gln Ala Gly
      65             70             75             80

Thr Pro Glu Glu Gly Leu Ala His Tyr Gly Ala Arg Phe Asp Asp Leu
      85             90             95

Ala Thr Glu Val Glu Leu Met Glu Gln Arg Leu Ile Ser His Pro Asp
      100            105            110

Asp Ala Thr Ser Ile Arg Thr Lys Ala Glu Glu Leu Lys Ala Thr Leu
      115            120            125

Pro Thr Ile Ala Ala Ile Gly Asp Leu Asp Gly Val Glu Ala Arg Leu
      130            135            140

Ser Lys Ile Ile Asn Asn Ser Glu Glu Ala Asn Glu Arg Ala Lys Glu
      145            150            155            160

Gln Lys Ala Lys Asn Arg Glu Arg Ala Val Ala Arg Lys Glu Glu Leu
      165            170            175

Ala Val Glu Ala Glu Thr Leu Ala Glu Asn Ser Ser Asp Trp Lys Val
      180            185            190

Ala Gly Asp Arg Ile Arg Ala Ile Leu Asp Glu Trp Lys Ser Ile His
      195            200            205

Gly Ile Asp Arg Lys Thr Asp Asp Glu Leu Trp Lys Arg Tyr Ser Arg
      210            215            220

Ala Arg Asp Ser Phe Asn Arg Arg Arg Gly Ala His Phe Ala Glu Leu
      225            230            235            240

Asp Arg Thr Arg Ala Ser Ala Arg Lys Leu Lys Glu Glu Leu Val Glu
      245            250            255

Arg Ala Asn Ala Leu Lys Glu Ser Thr Glu Trp Asn Asp Thr Ala Arg
      260            265            270

Ala Phe Arg Asp Leu Met Thr Glu Trp Lys Ala Ala Gly Arg Ala Pro
      275            280            285

Arg Glu Ile Asp Asp Lys Leu Trp Ala Ala Phe Lys Gly Ala Gln Asp
      290            295            300

Tyr Phe Phe Asp Lys Arg Asn Ala Val Ala Lys Glu Arg Asp Gln Glu

```

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305                      310                      315                      320
Phe Glu Ala Asn Ala Thr Ala Lys Gln Gln Leu Ile Asp Glu Tyr Asp
      325                      330                      335
Ala Gln Ile Asn Pro Glu Gln Gly Leu Asp Gly Ala Arg Ser Lys Leu
      340                      345                      350

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<210> 1051

<211> 408

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(385)

<223> RXN02238

<400> 1051

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ctcttaacac tactgtccat atacttttga aaagggtgtca gtg acc aac gtg agc 115
                                         Val Thr Asn Val Ser
                                         1 5
aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163
Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile
      10                      15                      20
acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211
Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr
      25                      30                      35
gcc ctc gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc 259
Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe
      40                      45                      50
tac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt 307
Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe Ile Gly Pro Leu Val
      55                      60                      65
act ccg cag cca ggc gaa aag cca ett tct att gct ctg cgt gag atc 355
Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile
      70                      75                      80                      85
aat gca ggt ctg ttg gac cac gag gaa ggt taaaagacct tataacttca 405
Asn Ala Gly Leu Leu Asp His Glu Glu Gly
      90                      95
cac 408

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<210> 1052

<211> 95

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1052

Val Thr Asn Val Ser Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp
1 5 10 15

Pro Pro Val Gly Ile Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys
20 25 30

Val Thr Ser Lys Tyr Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg
35 40 45

Gln Ile Asn Ser Phe Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe
50 55 60

Ile Gly Pro Leu Val Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile
65 70 75 80

Ala Leu Arg Glu Ile Asn Ala Gly Leu Leu Asp His Glu Glu Gly
85 90 95

<210> 1053

<211> 408

<212> DNA

<213> Corynebacterium glutamicum

 $\langle 220 \rangle$

<221> CDS

<222> (101) .. (385)

<223> FRXA02238

<400> 1053

ggcgcttagc caaaacatag agcggtaggg tatgcttata cgattgagca acctttcccg 60

ctcttaacac tactgtccat atacttttga aaaggtgtca gtg acc aac gtg agc 115
Val Thr Asn Val Ser
1 5

aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163
Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile
10 15 20

acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211
Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr
25 30 35

gcc ctc gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc 259
Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe
40 45 50

tac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt 307
Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe Ile Gly Pro Leu Val
 55 60 65

act cgc cag cca ggc gaa aag cca ctt tct att gct ctg cgt gag atc 355
Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile
70 75 80 85

aat gca ggt ctg ttg gac cac gag gaa ggt taaaagacct tataacttca 405
Asn Ala Gly Leu Leu Asp His Glu Glu Gly
90 95

$$\begin{aligned} \mathbb{E}[\mathcal{E}_1] &\leq \mathbb{E}[\mathcal{E}_1 | \mathcal{E}_1 \leq \mathcal{E}_2] + \mathbb{E}[\mathcal{E}_1 | \mathcal{E}_1 > \mathcal{E}_2] \\ &\leq \mathbb{E}[\mathcal{E}_1 | \mathcal{E}_1 \leq \mathcal{E}_2] + \mathbb{E}[\mathcal{E}_2 | \mathcal{E}_1 > \mathcal{E}_2] \\ &\leq \mathbb{E}[\mathcal{E}_1 | \mathcal{E}_1 \leq \mathcal{E}_2] + \mathbb{E}[\mathcal{E}_2] \\ &\leq \mathbb{E}[\mathcal{E}_1] + \mathbb{E}[\mathcal{E}_2] \\ &\leq \mathbb{E}[\mathcal{E}_1] + \mathbb{E}[\mathcal{E}_2] \\ &\leq \mathbb{E}[\mathcal{E}_1] + \mathbb{E}[\mathcal{E}_2] \end{aligned}$$

cac

408

<210> 1054

<211> 95

<212> PRT

<213> Corynebacterium glutamicum

<400> 1054

Val Thr Asn Val Ser Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp
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Pro Pro Val Gly Ile Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys
 20 25 30

Val Thr Ser Lys Tyr Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg
 35 40 45

Gln Ile Asn Ser Phe Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe
 50 55 60

Ile Gly Pro Leu Val Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile
 65 70 75 80

Ala Leu Arg Glu Ile Asn Ala Gly Leu Leu Asp His Glu Glu Gly
 85 90 95

<210> 1055

<211> 800

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(777)

<223> RXN02254

<400> 1055

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 Ile Ala Val Ala Glu Glu Gly Gly Leu Trp Glu Asn Leu Leu Gln His
 1 5 10 15

cgc ttc ggt gga cat ggt gcg cta gct ggt cac gcc ttg gga aac ctc 96
 Arg Phe Gly Gly His Gly Ala Leu Ala Gly His Ala Leu Gly Asn Leu
 20 25 30

gtg atc gcg gcg ttg acc gac att ttg ggc acc tcc cag cat gcg ctt 144
 Val Ile Ala Ala Leu Thr Asp Ile Leu Gly Thr Ser Gln His Ala Leu
 35 40 45

gat caa atc gct caa ctc gct gga gcc aaa gga cgc atc atc cgg gta 192
 Asp Gln Ile Ala Gln Leu Ala Gly Ala Lys Gly Arg Ile Ile Pro Val
 50 55 60

tgt gct gaa cct ttg gat ctt gaa gcg gaa gta tca ggt cta gac tct 240
 Cys Ala Glu Pro Leu Asp Leu Glu Ala Glu Val Ser Gly Leu Asp Ser
 65 70 75 80

gat gct cga gtc atg cgt caa gtt cgt ggt caa gtg gcg gta gct gca 288
 Asp Ala Arg Val Met Arg Gln Val Arg Gly Gln Val Ala Val Ala Ala

	85	90	95	
acc ccc ggg cag gtg cga cgc gtt cga atc att ccg gac aat cca gaa	336			
Thr Pro Gly Gln Val Arg Arg Val Arg Ile Ile Pro Asp Asn Pro Glu	100	105	110	
ccg aac ccc gct gcc atc gag gcc att ctc gat gca gat ttg gtc acc	384			
Pro Asn Pro Ala Ala Ile Glu Ala Ile Leu Asp Ala Asp Leu Val Thr	115	120	125	
ctt ggc cca ggt tcc tgg ttc tcc tct gtg att cca cac att ttg gtc	432			
Leu Gly Pro Gly Ser Trp Phe Ser Ser Val Ile Pro His Ile Leu Val	130	135	140	
cca ggg atc gtt gat gcc ttg gcg cag aca aaa gca acc aaa acc gtg	480			
Pro Gly Ile Val Asp Ala Leu Ala Gln Thr Lys Ala Thr Lys Thr Val	145	150	155	160
gtg tta aac ctg acg tcc gag cca ggg gag acc gcg gga ttc tct gca	528			
Val Leu Asn Leu Thr Ser Glu Pro Gly Glu Thr Ala Gly Phe Ser Ala	165	170	175	
gaa cga cac atc cat gtg ctc cgc cag cat gct cga aac ctt cag gtt	576			
Glu Arg His Ile His Val Leu Arg Gln His Ala Arg Asn Leu Gln Val	180	185	190	
gac caa gtc att gtc gat gcc aag aca ctg tcc tca caa acc gaa cgc	624			
Asp Gln Val Ile Val Asp Ala Lys Thr Leu Ser Ser Gln Thr Glu Arg	195	200	205	
aat cat gta gaa cga gct gct cgc acc ctt ggt gca gaa gtc tcc ttc	672			
Asn His Val Glu Arg Ala Ala Arg Thr Leu Gly Ala Glu Val Ser Phe	210	215	220	
cat gat gtc cag gct gaa gat gcc cgt ggt cga ttc acc agt att cac	720			
His Asp Val Gln Ala Glu Asp Gly Arg Gly Arg Phe Thr Ser Ile His	225	230	235	240
gat cca gca aag ctg tgt gca gcg ttg ctg gca agt ttt gct gga gca	768			
Asp Pro Ala Lys Leu Cys Ala Ala Leu Leu Ala Ser Phe Ala Gly Ala	245	250	255	
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Arg Lys Arg				

<210> 1056

<211> 259

<212> PRT

<213> Corynebacterium glutamicum

<400> 1056

Ile	Ala	Val	Ala	Glu	Glu	Gly	Gly	Leu	Trp	Glu	Asn	Leu	Leu	Gln	His
1				5				10						15	

Arg	Phe	Gly	Gly	His	Gly	Ala	Leu	Ala	Gly	His	Ala	Leu	Gly	Asn	Leu
		20					25					30			

Val	Ile	Ala	Ala	Leu	Thr	Asp	Ile	Leu	Gly	Thr	Ser	Gln	His	Ala	Leu
		35					40					45			

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Asp Gln Ile Ala Gln Leu Ala Gly Ala Lys Gly Arg Ile Ile Pro Val
  50                      55                      60

Cys Ala Glu Pro Leu Asp Leu Glu Ala Glu Val Ser Gly Leu Asp Ser
  65                      70                      75                      80

Asp Ala Arg Val Met Arg Gln Val Arg Gly Gln Val Ala Val Ala Ala
          85                      90                      95

Thr Pro Gly Gln Val Arg Arg Val Arg Ile Ile Pro Asp Asn Pro Glu
  100                      105                      110

Pro Asn Pro Ala Ala Ile Glu Ala Ile Leu Asp Ala Asp Leu Val Thr
  115                      120                      125

Leu Gly Pro Gly Ser Trp Phe Ser Ser Val Ile Pro His Ile Leu Val
  130                      135                      140

Pro Gly Ile Val Asp Ala Leu Ala Gln Thr Lys Ala Thr Lys Thr Val
  145                      150                      155                      160

Val Leu Asn Leu Thr Ser Glu Pro Gly Glu Thr Ala Gly Phe Ser Ala
  165                      170                      175

Glu Arg His Ile His Val Leu Arg Gln His Ala Arg Asn Leu Gln Val
  180                      185                      190

Asp Gln Val Ile Val Asp Ala Lys Thr Leu Ser Ser Gln Thr Glu Arg
  195                      200                      205

Asn His Val Glu Arg Ala Ala Arg Thr Leu Gly Ala Glu Val Ser Phe
  210                      215                      220

His Asp Val Gln Ala Glu Asp Gly Arg Gly Arg Phe Thr Ser Ile His
  225                      230                      235                      240

Asp Pro Ala Lys Leu Cys Ala Ala Leu Leu Ala Ser Phe Ala Gly Ala
  245                      250                      255

Arg Lys Arg

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<210> 1057

<211> 804

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(781)

<223> FRXA02254

<400> 1057

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tggacatggt gcgctagctg gtcacgcott gggaaacctc gtc atc gcg gcg ttg 115
                Val Ile Ala Ala Leu
                1                      5

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acc gac att ttg ggc acc tcc cag cat gcg ctt gat caa atc gct caa 163
 Thr Asp Ile Leu Gly Thr Ser Gln His Ala Leu Asp Gln Ile Ala Gln
 10 15 20

ctc gct gga gcc aaa gga cgc atc atc ccg gta tgt gct gaa cct ttg 211
 Leu Ala Gly Ala Lys Gly Arg Ile Ile Pro Val Cys Ala Glu Pro Leu
 25 30 35

gat ctt gaa gcg gaa gta tca ggt cta gac tct gat gct cga gtc atg 259
 Asp Leu Glu Ala Glu Val Ser Gly Leu Asp Ser Asp Ala Arg Val Met
 40 45 50

cgt caa gtt cgt ggt caa gtg gcg gta gct gca acc ccc ggg cag gtg 307
 Arg Gln Val Arg Gly Gln Val Ala Val Ala Ala Thr Pro Gly Gln Val
 55 60 65

cga cgc gtt cga atc att ccg gac aat cca gaa ccg aac ccc gct gcc 355
 Arg Arg Val Arg Ile Ile Pro Asp Asn Pro Glu Pro Asn Pro Ala Ala
 70 75 80 85

atc gag gcc att ctc gat gca gat ttg gtc acc ctt ggc cca ggt tcc 403
 Ile Glu Ala Ile Leu Asp Ala Asp Leu Val Thr Thr Gly Pro Gly Ser
 90 95 100

tggt ttc tcc tct gtg att cca cac att ttg gtc cca ggg atc gtt gat 451
 Trp Phe Ser Ser Val Ile Pro His Ile Leu Val Pro Gly Ile Val Asp
 105 110 115

gcc ttg gcg cag aca aaa gca acc aaa acc gtg gtg tta aac ctg acg 499
 Ala Leu Ala Gln Thr Lys Ala Thr Lys Thr Val Val Leu Asn Leu Thr
 120 125 130

tcc gag cca ggg gag acc gcg gga ttc tct gca gaa cga cac atc cat 547
 Ser Glu Pro Gly Glu Thr Ala Gly Phe Ser Ala Glu Arg His Ile His
 135 140 145

gtg ctc cgc cag cat gct cga aac ctt cag gtt gac caa gtc att gtc 595
 Val Leu Arg Gln His Ala Arg Asn Leu Val Val Asp Gln Val Ile Val
 150 155 160 165

gat gcc aag aca ctg tcc tca caa acc gaa cgc aat cat gta gaa cga 643
 Asp Ala Lys Thr Leu Ser Ser Gln Thr Glu Arg Asn His Val Glu Arg
 170 175 180

gct gct cgc acc ctt ggt gca gaa gtc tcc ttc cat gat gtc cag gct 691
 Ala Ala Arg Thr Leu Gly Ala Glu Val Ser Phe His Asp Val Gln Ala
 185 190 195

gaa gat gcc cgt ggt cga ttc acc agt att cac gat cca gca aag ctg 739
 Glu Asp Gly Arg Gly Arg Phe Thr Ser Ile His Asp Pro Ala Lys Leu
 200 205 210

tgt gca gcg ttg ctg gca agt ttt gct gga gca cga aag cgt 781
 Cys Ala Ala Leu Leu Ala Ser Phe Ala Gly Ala Arg Lys Arg
 215 220 225

taaggagttag gcgtgtcact gac 804

<210> 1058

<211> 227

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1058

Val	Ile	Ala	Ala	Leu	Thr	Asp	Ile	Leu	Gly	Thr	Ser	Gln	His	Ala	Leu
1				5					10					15	

Asp	Gln	Ile	Ala	Gln	Leu	Ala	Gly	Ala	Lys	Gly	Arg	Ile	Ile	Pro	Val
			20					25					30		

Cys	Ala	Glu	Pro	Leu	Asp	Leu	Glu	Ala	Glu	Val	Ser	Gly	Leu	Asp	Ser
		35					40					45			

Asp	Ala	Arg	Val	Met	Arg	Gln	Val	Arg	Gly	Gln	Val	Ala	Val	Ala	Ala
	50					55					60				

Thr	Pro	Gly	Gln	Val	Arg	Arg	Val	Arg	Ile	Ile	Pro	Asp	Asn	Pro	Glu
65				70						75					80

Pro	Asn	Pro	Ala	Ala	Ile	Glu	Ala	Ile	Leu	Asp	Ala	Asp	Leu	Val	Thr
				85					90					95	

Leu	Gly	Pro	Gly	Ser	Trp	Phe	Ser	Ser	Val	Ile	Pro	His	Ile	Leu	Val
			100					105					110		

Pro	Gly	Ile	Val	Asp	Ala	Leu	Ala	Gln	Thr	Lys	Ala	Thr	Lys	Thr	Val
		115						120					125		

Val	Leu	Asn	Leu	Thr	Ser	Glu	Pro	Gly	Glu	Thr	Ala	Gly	Phe	Ser	Ala
		130					135					140			

Glu	Arg	His	Ile	His	Val	Leu	Arg	Gln	His	Ala	Arg	Asn	Leu	Gln	Val
145					150					155					160

Asp	Gln	Val	Ile	Val	Asp	Ala	Lys	Thr	Leu	Ser	Ser	Gln	Thr	Glu	Arg
			165						170					175	

Asn	His	Val	Glu	Arg	Ala	Ala	Arg	Thr	Leu	Gly	Ala	Glu	Val	Ser	Phe
			180					185					190		

His	Asp	Val	Gln	Ala	Glu	Asp	Gly	Arg	Gly	Arg	Phe	Thr	Ser	Ile	His
		195					200					205			

Asp	Pro	Ala	Lys	Leu	Cys	Ala	Ala	Leu	Leu	Ala	Ser	Phe	Ala	Gly	Ala
		210				215						220			

Arg	Lys	Arg
225		

<210> 1059

<211> 681

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(658)

<223> RXN02271

<400> 1059

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<210> 1060
<211> 186
<212> PRT
<213> Corynebacterium glutamicum
<400> 1060
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<400> 1060

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Met Ser Phe Leu Asn Ser Ala Lys Thr Lys Thr Val Ala Leu Thr Ala
 1           5           10           15
Thr Phe Val Gly Ala Ala Thr Leu Ala Thr Pro Ala Ile Ala Ser Ala
           20           25           30
Asp Ile Val Asp Asn Ala Leu Ala Ala Leu Pro Ser Gly Glu Ile Ser
           35           40           45
Cys Ser Gln Ala Glu Lys Tyr Trp Thr Thr Glu Ala Asp Tyr Asn Ser
 50           55           60
Lys Val Ala Gln Ala Asn Ala Leu Ala Met Phe Asp Ser Arg Gly Pro
 65           70           75           80
Gln Ile Gln Ala Ala Leu Ala Arg Val Asp Glu Ala Ala Asn Arg Cys
           85           90           95
Gly Leu Lys Gly Gly Thr Val Ala Ala Gln Ala Glu Ala Thr Glu Ala
 100           105           110
Ala Pro Ala Ala Pro Ala Pro Ala Pro Gln Asp Asn Thr Gly Thr Ser
 115           120           125
Gln Thr Ala Pro Ala Pro Ala Ala Pro Ala Ala Pro Ala Ala Thr Pro
 130           135           140
Val Val Asn Leu Ala Pro Ala Gly Ser Pro Thr Phe Thr Ile Glu Val
 145           150           155           160
Pro Gly Val Gly Gly Val Gln Leu Pro Asp Leu Tyr Gln Ile Val Gln
           165           170           175
Gln Phe Leu Ala Gln Phe Gly Ile Lys Ile
           180           185

```

<210> 1061

<211> 681

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(658)

<223> FRXA02271

<400> 1061

cactccccta tcctaaagcca catctcggtt tattaaactg ttagtgaatt ctccaccgca 60

```

acactgggtg atttcagtta catccgtatg gttattgggt atg agc ttt ctt aac 115
                Met Ser Phe Leu Asn
                        1           5

```

```

tct gca aaa acc aag acc gta gcc ctc acc gca acc ttc ggt gca 163
Ser Ala Lys Thr Lys Thr Val Ala Leu Thr Ala Thr Phe Val Gly Ala
                10           15           20

```

```

gca acc ctt gca act cct gca atc gca tcc gct gac atc gtc gac aac 211
Ala Thr Leu Ala Thr Pro Ala Ile Ala Ser Ala Asp Ile Val Asp Asn
                25           30           35

```

gcc ctc gca gcc ctc cca tcc ggt gag atc agc tgc tcc cag gct gaa 259
Ala Leu Ala Ala Leu Pro Ser Gly Glu Ile Ser Cys Ser Gln Ala Glu
40 45 50

aag tac tgg acc acc gaa gct gat tac aac agc aag gtt gca cag gcc 307
Lys Tyr Trp Thr Thr Glu Ala Asp Tyr Asn Ser Lys Val Ala Gln Ala
55 60 65

aac gcc ttg gca atg ttt gac tcc cgc ggc cca cag atc cag gca gct 355
Asn Ala Leu Ala Met Phe Asp Ser Arg Gly Pro Gln Ile Gln Ala Ala
70 75 80 85

ctc gca cgc gtt gac gaa gca gca aac cgc tgc gga ctc aag ggc ggc 403
Leu Ala Arg Val Asp Glu Ala Ala Asn Arg Cys Gly Leu Lys Gly Gly
90 95 100

acc gta gct gcg cag gct gag gca act gag gct gcg cct gcc gct cca 451
Thr Val Ala Ala Gln Ala Glu Ala Thr Glu Ala Ala Pro Ala Ala Pro
105 110 115

gca cct gca ccg cag gat aac acc ggc act tct cag act gcc cct gcc 499
Ala Pro Ala Pro Gln Asp Asn Thr Thr Ser Gln Thr Ala Pro Ala
120 125 130

cca gca gca cca gca gca cca gca gct acc cct gtg gtt aac ctt gca 547
Pro Ala Ala Pro Ala Ala Pro Ala Ala Thr Pro Val Val Asn Leu Ala
135 140 145

cct gca gga tca cca act ttc acc att gaa gtt cca gga gtt ggc ggc 595
Pro Ala Gly Ser Pro Thr Phe Thr Ile Glu Val Pro Gly Val Gly Gly
150 155 160 165

gtt cag ctg cca gat cta tac caa atc gtc caa cag ttc ttg gca cag 643
Val Gln Leu Pro Asp Leu Tyr Gln Ile Val Gln Gln Phe Leu Ala Gln
170 175 180

ttc gga atc aag atc taaatctatt cacatccctt aac 681
Phe Gly Ile Lys Ile
185

<210> 1062

<211> 186

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1062

Met Ser Phe Leu Asn Ser Ala Lys Thr Lys Thr Val Ala Leu Thr Ala
1 5 10 15

Thr Phe Val Gly Ala Ala Thr Leu Ala Thr Pro Ala Ile Ala Ser Ala
20 25 30

Asp Ile Val Asp Asn Ala Leu Ala Ala Leu Pro Ser Gly Glu Ile Ser
35 40 45

Cys Ser Gln Ala Glu Lys Tyr Trp Thr Thr Glu Ala Asp Tyr Asn Ser
50 55 60

Lys Val Ala Gln Ala Asn Ala Leu Ala Met Phe Asp Ser Arg Gly Pro


```

65              70              75              80
Gln Ile Gln Ala Ala Leu Ala Arg Val Asp Glu Ala Ala Asn Arg Cys
      85              90              95
Gly Leu Lys Gly Gly Thr Val Ala Ala Gln Ala Glu Ala Thr Glu Ala
      100             105             110
Ala Pro Ala Ala Pro Ala Pro Ala Pro Gln Asp Asn Thr Gly Thr Ser
      115             120             125
Gln Thr Ala Pro Ala Pro Ala Ala Pro Ala Ala Pro Ala Ala Thr Pro
      130             135             140
Val Val Asn Leu Ala Pro Ala Gly Ser Pro Thr Phe Thr Ile Glu Val
      145             150             155
Pro Gly Val Gly Gly Val Gln Leu Pro Asp Leu Tyr Gln Ile Val Gln
      165             170             175
Gln Phe Leu Ala Gln Phe Gly Ile Lys Ile
      180             185

```

<210> 1063

<211> 1581

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1558)

<223> RXN02279

<400> 1063

ggtaagagggtg cttttccga tgcgcagcga ttcttgctca acgccgacga gtcgcgggag 60

```

ctttctgatt atgagcgtct ggcttatgcc atcaccttgc ttg atc agc ctg gaa 115
                Leu Ile Ser Leu Glu
                1              5

```

```

aag aag cag aag gac gcg aac ttt ttc ctt tcg gag ctt cgc cgc cag 163
Lys Lys Gln Lys Asp Ala Asn Phe Phe Leu Ser Glu Leu Arg Arg Gln
                10              15              20

```

```

ggc tac cgc gct gtc gat ttc ttg gaa tcc cag act gtt gac cag ctg 211
Gly Tyr Arg Ala Val Asp Phe Leu Glu Ser Gln Thr Val Asp Gln Leu
                25              30              35

```

```

aat aac ccc gat gtc cag act tac ctc acc gaa gcg gaa ctg att cgc 259
Asn Asn Pro Asp Val Gln Thr Tyr Leu Thr Glu Ala Glu Leu Ile Arg
                40              45              50

```

```

gat gac ttg agg tct tgg gca gtc atc aat caa atg gca ttg gac aac 307
Asp Asp Leu Arg Ser Trp Ala Val Ile Asn Gln Met Ala Leu Asp Asn
                55              60              65

```

```

atc gat ctt gtt cca tac ggc gag gaa aac gac gag cca ctt gca atc 355
Ile Asp Leu Val Pro Tyr Gly Glu Glu Asn Asp Glu Pro Leu Ala Ile
                70              75              80              85

```

gcc cgc aag atc atc gag gaa acc gct tcc cat cct gag ctg aga ttc 403
Ala Arg Lys Ile Ile Glu Glu Thr Ala Ser His Pro Glu Leu Arg Phe
90 95 100

gaa aac ctc gag gcc cag ttc tcc gag ttc acc atc ttg ctt gct caa 451
Glu Asn Leu Glu Ala Gln Phe Ser Glu Phe Thr Ile Leu Leu Ala Gln
105 110 115

agc ccg gag aac ctc gac gta gcc cgc tac cag gag ctt cgt aca cag 499
Ser Pro Glu Asn Leu Asp Val Ala Arg Tyr Gln Glu Leu Arg Thr Gln
120 125 130

gga aac ttt gtt caa gaa ctc gcc ttg gac agc att ttc gcc caa cat 547
Gly Asn Phe Val Gln Glu Leu Ala Leu Asp Ser Ile Phe Gly Gln His
135 140 145

gcc gtt gtt caa gac acc gga aac ggc gaa gcc atc cta gat gaa act 595
Ala Val Val Gln Asp Thr Gly Asn Gly Glu Ala Ile Leu Asp Glu Thr
150 155 160 165

atc ggg tac atg atc ggc gcc ggc atg cgt gaa acc act gcc cgc acc 643
Ile Gly Tyr Met Ile Gly Ala Gly Met Arg Glu Thr Thr Ala Arg Thr
170 175 180

gcc agc cag ttc gcg cag ctt tac tca ttt gtg ggc agg cag gaa cgc 691
Ala Ser Gln Phe Ala Gln Leu Tyr Ser Phe Val Gly Arg Gln Glu Arg
185 190 195

tcc att gaa atg gca cga ctc gct ttc gag gaa ctt caa gcg gca gga 739
Ser Ile Glu Met Ala Arg Leu Ala Phe Glu Glu Leu Gln Ala Ala Gly
200 205 210

ctt ccc cac cgt gag gaa gaa ctg cga ttg ggc atg caa ctc gcc cag 787
Leu Pro His Arg Glu Glu Glu Leu Arg Leu Gly Met Gln Leu Ala Gln
215 220 225

gtt gaa cca att gaa gcc cgc gaa atc ctg gaa aag ctg ctg ctg cct 835
Val Glu Pro Ile Glu Ala Arg Glu Ile Leu Glu Lys Phe Leu Leu Leu Pro
230 235 240 245

aaa ttc gag cag aat ctg aca ctt gat gaa ctt gaa act gaa gca ctc 883
Lys Phe Glu Gln Asn Leu Thr Leu Asp Glu Leu Glu Thr Glu Ala Leu
250 255 260

ott cct ttg ggt gct acc gtt gct atc cac gac ccc cag gct gcc gca 931
Leu Pro Leu Gly Ala Thr Val Ala Ile His Asp Pro Gln Ala Ala Ala
265 270 275

gca att ttg cgc cac gct cgc gaa aac gcc gca ggg ttc gcc aac ttc 979
Ala Ile Leu Arg His Ala Arg Glu Asn Ala Ala Gly Phe Gly Asn Phe
280 285 290

gaa ctc gca gtc caa gcg atg acc atg atc acg gat gtc ctc tac acc 1027
Glu Leu Ala Val Gln Ala Met Thr Met Ile Thr Asp Val Leu Tyr Thr
295 300 305

caa aac atg cac gag caa ctg ctg gag gag ctc aac cac tct ctc ccc 1075
Gln Asn Met His Glu Gln Leu Leu Glu Glu Leu Asn His Ser Leu Pro
310 315 320 325

tat gct caa atg ctt gat gat caa cac caa gct gaa ctg aaa ctg ctg 1123

Tyr Ala Gln Met Leu Asp Asp Gln His Gln Ala Glu Leu Lys Leu Leu
 330 335 340
 gac agc atc gcc atc gtc cag gca gac ctc ggt tcc acc gaa gcg ctg 1171
 Asp Ser Ile Ala Ile Val Gln Ala Asp Leu Gly Ser Thr Glu Ala Leu
 345 350 355
 gaa acc ctg ggc acc gca atg gga ctc gca gaa acc aca gct cag aag 1219
 Glu Thr Leu Gly Thr Ala Met Gly Leu Ala Glu Thr Thr Ala Gln Lys
 360 365 370
 cta tac gtg cag gaa tcc ctc aac cgc gca tac ttc act ttt gcc cgc 1267
 Leu Tyr Val Gln Glu Ser Leu Asn Arg Ala Tyr Phe Thr Phe Ala Arg
 375 380 385
 cct gaa gat tgc atc agc gga gca gcc gac gct tct gcc ctg gcc atg 1315
 Pro Glu Asp Cys Ile Ser Gly Ala Ala Asp Ala Ser Ala Leu Ala Met
 390 395 400 405
 caa aac gat gac cct tcc aat gca gct gcc cag ttg gag cag tgt gca 1363
 Gln Asn Asp Asp Pro Ser Asn Ala Ala Gln Leu Glu Gln Cys Ala
 410 415 420
 cag tac ttg ttc caa ttg ggc cac gaa act gac ggc gca agc ctg ctg 1411
 Gln Tyr Leu Phe Gln Leu Gly His Glu Thr Asp Gly Ala Ser Leu Leu
 425 430 435
 gaa tct gca ttc agg gtt gaa ggc atc ccc act gag cag gca ctg tac 1459
 Glu Ser Ala Phe Arg Val Glu Gly Ile Pro Thr Glu Gln Ala Leu Tyr
 440 445 450
 tac gca aat gca ctg tct tcc atc tat gaa gat ttc ggc gat tcc gcg 1507
 Tyr Ala Asn Ala Leu Ser Ser Ile Tyr Glu Asp Phe Gly Asp Ser Ala
 455 460 465
 aag tcg cag tac tgg gag cag cag gcg cag gaa aag cag cag ctt ctg 1555
 Lys Ser Gln Tyr Trp Glu Gln Gln Ala Gln Glu Lys Gln Gln Leu Leu
 470 475 480 485
 gag taacggccgt ttaaagagtc gaa 1581
 Glu

<210> 1064

<211> 486

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1064

Leu Ile Ser Leu Glu Lys Lys Gln Lys Asp Ala Asn Phe Phe Leu Ser
 1 5 10 15

Glu Leu Arg Arg Gln Gly Tyr Arg Ala Val Asp Phe Leu Glu Ser Gln
 20 25 30

Thr Val Asp Gln Leu Asn Asn Pro Asp Val Gln Thr Tyr Leu Thr Glu
 35 40 45

Ala Glu Leu Ile Arg Asp Asp Leu Arg Ser Trp Ala Val Ile Asn Gln
 50 55 60

```

Met Ala Leu Asp Asn Ile Asp Leu Val Pro Tyr Gly Glu Glu Asn Asp
 65              70              75              80

Glu Pro Leu Ala Ile Ala Arg Lys Ile Ile Glu Glu Thr Ala Ser His
              85              90              95

Pro Glu Leu Arg Phe Glu Asn Leu Glu Ala Gln Phe Ser Glu Phe Thr
      100              105              110

Ile Leu Leu Ala Gln Ser Pro Glu Asn Leu Asp Val Ala Arg Tyr Gln
      115              120              125

Glu Leu Arg Thr Gln Gly Asn Phe Val Gln Glu Leu Ala Leu Asp Ser
      130              135              140

Ile Phe Gly Gln His Ala Val Val Gln Asp Thr Gly Asn Gly Glu Ala
      145              150              155              160

Ile Leu Asp Glu Thr Ile Gly Tyr Met Ile Gly Ala Gly Met Arg Glu
      165              170              175

Thr Thr Ala Arg Thr Ala Ser Gln Phe Ala Gln Leu Tyr Ser Phe Val
      180              185              190

Gly Arg Gln Glu Arg Ser Ile Glu Met Ala Arg Leu Ala Phe Glu Glu
      195              200              205

Leu Gln Ala Ala Gly Leu Pro His Arg Glu Glu Glu Leu Arg Leu Gly
      210              215              220

Met Gln Leu Ala Gln Val Glu Pro Ile Glu Ala Arg Glu Ile Leu Glu
      225              230              235              240

Lys Leu Leu Leu Pro Lys Phe Glu Gln Asn Leu Thr Leu Asp Glu Leu
      245              250              255

Glu Thr Glu Ala Leu Leu Pro Leu Gly Ala Thr Val Ala Ile His Asp
      260              265              270

Pro Gln Ala Ala Ala Ala Ile Leu Arg His Ala Arg Glu Asn Ala Ala
      275              280              285

Gly Phe Gly Asn Phe Glu Leu Ala Val Gln Ala Met Thr Met Ile Thr
      290              295              300

Asp Val Leu Tyr Thr Gln Asn Met His Glu Gln Leu Leu Glu Glu Leu
      305              310              315              320

Asn His Ser Leu Pro Tyr Ala Gln Met Leu Asp Asp Gln His Gln Ala
      325              330              335

Glu Leu Lys Leu Leu Asp Ser Ile Ala Ile Val Gln Ala Asp Leu Gly
      340              345              350

Ser Thr Glu Ala Leu Glu Thr Leu Gly Thr Ala Met Gly Leu Ala Glu
      355              360              365

Thr Thr Ala Gln Lys Leu Tyr Val Gln Glu Ser Leu Asn Arg Ala Tyr
      370              375              380

```

Phe Thr Phe Ala Arg Pro Glu Asp Cys Ile Ser Gly Ala Ala Asp Ala
 385 390 395 400
 Ser Ala Leu Ala Met Gln Asn Asp Asp Pro Ser Asn Ala Ala Ala Gln
 405 410 415
 Leu Glu Gln Cys Ala Gln Tyr Leu Phe Gln Leu Gly His Glu Thr Asp
 420 425 430
 Gly Ala Ser Leu Leu Glu Ser Ala Phe Arg Val Glu Gly Ile Pro Thr
 435 440 445
 Glu Gln Ala Leu Tyr Tyr Ala Asn Ala Leu Ser Ser Ile Tyr Glu Asp
 450 455 460
 Phe Gly Asp Ser Ala Lys Ser Gln Tyr Trp Glu Gln Gln Ala Gln Glu
 465 470 475 480
 Lys Gln Gln Leu Leu Glu
 485

<210> 1065
 <211> 1427
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1404)
 <223> FRXA02279

<400> 1065
 ncn gcc agg gct acc gcg ctt gtc gat ttc ttg gaa tcc cag act gtt 48
 Xaa Ala Arg Ala Thr Ala Leu Val Asp Phe Leu Glu Ser Gln Thr Val
 1 5 10 15
 gac cag ctg aat aac ccc gat gtc cag act tac ctc acc gaa gcg gaa 96
 Asp Gln Leu Asn Asn Pro Asp Val Gln Thr Tyr Leu Thr Glu Ala Glu
 20 25 30
 ctg att cgc gat gac ttg agg tct tgg gca gtc atc aaa tca aat ggc 144
 Leu Ile Arg Asp Asp Leu Arg Ser Trp Ala Val Ile Lys Ser Asn Gly
 35 40 45
 att gga caa cat cga tct tgt tcc ata cgg cga gga aac gac gag cca 192
 Ile Gly Gln His Arg Ser Cys Ser Ile Arg Arg Gly Asn Asp Glu Pro
 50 55 60
 ctt gca atc gcc cgc aag atc atc gag gaa acc gct tcc cat cct gag 240
 Leu Ala Ile Ala Arg Lys Ile Ile Glu Glu Thr Ala Ser His Pro Glu
 65 70 75 80
 ctg aga ttc gaa aac ctc gag gcc cag ttc tcc gag ttc acc atc ttg 288
 Leu Arg Phe Glu Asn Leu Glu Ala Gln Phe Ser Glu Phe Thr Ile Leu
 85 90 95
 ctt gct caa agc ccg gag aac ctc gac gta gcc cgc tac cag gag ctt 336
 Leu Ala Gln Ser Pro Glu Asn Leu Asp Val Ala Arg Tyr Gln Glu Leu
 100 105 110

cgt aca cag gga aac ttt gtt caa gaa ctc gcc ttg gac agc att ttc Arg Thr Gln Gly Asn Phe Val Gln Glu Leu Ala Leu Asp Ser Ile Phe 115 120 125	384
ggc caa cat gcc gtt gtt caa gac acc gga aac ggc gaa gcc atc cta Gly Gln His Ala Val Val Gln Asp Thr Gly Asn Gly Glu Ala Ile Leu 130 135 140	432
gat gaa act atc ggg tac atg atc ggc gcc ggc atg cgt gaa acc act Asp Glu Thr Ile Gly Tyr Met Ile Gly Ala Gly Met Arg Glu Thr Thr 145 150 155 160	480
gcc cgc acc gcc agc cag ttc gcg cag ctt tac tca ttt gtg ggc agg Ala Arg Thr Ala Ser Gln Phe Ala Gln Leu Tyr Ser Phe Val Gly Arg 165 170 175	528
cag gaa cgc tcc att gaa atg gca cga ctc gct ttc gag gaa ctt caa Gln Glu Arg Ser Ile Glu Met Ala Arg Leu Ala Phe Glu Leu Gln 180 185 190	576
gcg gca gga ctt ccc cac cgt gag gaa gaa ctg cga ttg ggc atg caa Ala Ala Gly Leu Pro His Arg Glu Glu Glu Leu Arg Leu Gly Met Gln 195 200 205	624
ctc gcc cag gtt gaa cca att gaa gcc cgc gaa atc ctg gaa aag ctg Leu Ala Gln Val Glu Pro Ile Glu Ala Arg Glu Ile Leu Glu Lys Leu 210 215 220	672
ctg ctg cct aaa ttc gag cag aat ctg aca ctt gat gaa ctt gaa act Leu Leu Pro Lys Phe Glu Gln Asn Leu Thr Leu Asp Glu Leu Glu Thr 225 230 235 240	720
gaa gca ctc ctt cct ttg ggt gct acc gtt gct atc cac gac ccc cag Glu Ala Leu Leu Pro Leu Gly Ala Thr Val Ala Ile His Asp Pro Gln 245 250 255	768
gct gcc gca gca att ttg cgc cac gct cgc gaa aac gcc gca ggg ttc Ala Ala Ala Ala Ile Leu Arg His Ala Arg Glu Asn Ala Ala Gly Phe 260 265 270	816
ggc aac ttc gaa ctc gca gtc caa gcg atg acc atg atc acg gat gtc Gly Asn Phe Glu Leu Ala Val Gln Ala Met Thr Met Ile Thr Asp Val 275 280 285	864
ctc tac acc caa aac atg cac gag caa ctg ctg gag gag ctc aac cac Leu Tyr Thr Gln Asn Met His Glu Gln Leu Leu Glu Glu Leu Asn His 290 295 300	912
tct ctc ccc tat gct caa atg ctt gat gat caa cac caa gct gaa ctg Ser Leu Pro Tyr Ala Gln Met Leu Asp Asp Gln His Gln Ala Glu Leu 305 310 315 320	960
aaa ctg ctg gac agc atc gcc atc gtc cag gca gac ctc ggt tcc acc Lys Leu Leu Asp Ser Ile Ala Ile Val Gln Ala Asp Leu Gly Ser Thr 325 330 335	1008
gaa gcg ctg gaa acc ctg ggc acc gca atg gga ctc gca gaa acc aca Glu Ala Leu Glu Thr Leu Gly Thr Ala Met Gly Leu Ala Glu Thr Thr 340 345 350	1056
gct cag aag cta tac gtg cag gaa tcc ctc aac cgc gca tac ttc act	1104

Ala Gln Lys Leu Tyr Val Gln Glu Ser Leu Asn Arg Ala Tyr Phe Thr
 355 360 365

ttt gcc cgc cct gaa gat tgc atc agc gga gca gcc gac gct tct gcc 1152
 Phe Ala Arg Pro Glu Asp Cys Ile Ser Gly Ala Ala Asp Ala Ser Ala
 370 375 380

ctg gcc atg caa aac gat gac cct tcc aat gca gct gcc cag ttg gag 1200
 Leu Ala Met Gln Asn Asp Asp Pro Ser Asn Ala Ala Ala Gln Leu Glu
 385 390 395 400

cag tgt gca cag tac ttg ttc caa ttg ggc cac gaa act gac ggc gca 1248
 Gln Cys Ala Gln Tyr Leu Phe Gln Leu Gly His Glu Thr Asp Gly Ala
 405 410 415

agc ctg ctg gaa tct gca ttc agg gtt gaa ggc atc ccc act gag cag 1296
 Ser Leu Leu Glu Ser Ala Phe Arg Val Glu Gly Ile Pro Thr Glu Gln
 420 425 430

gca ctg tac tac gca aat gca ctg tct tcc atc tat gaa gat ttc ggc 1344
 Ala Leu Tyr Tyr Ala Asn Ala Leu Ser Ser Ile Tyr Glu Asp Phe Gly
 435 440 445

gat tcc gcg aag tcg cag tac tgg gag cag cag gcg cag gaa aag cag 1392
 Asp Ser Ala Lys Ser Gln Tyr Trp Glu Gln Gln Ala Gln Glu Lys Gln
 450 455 460

cag ctt ctg gag taacggcgt ttaaagagtc gaa 1427
 Gln Leu Leu Glu
 465

<210> 1066
 <211> 468
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1066
 Xaa Ala Arg Ala Thr Ala Leu Val Asp Phe Leu Glu Ser Gln Thr Val
 1 5 10 15

Asp Gln Leu Asn Asn Pro Asp Val Gln Thr Tyr Leu Thr Glu Ala Glu
 20 25 30

Leu Ile Arg Asp Asp Leu Arg Ser Trp Ala Val Ile Lys Ser Asn Gly
 35 40 45

Ile Gly Gln His Arg Ser Cys Ser Ile Arg Arg Gly Asn Asp Glu Pro
 50 55 60

Leu Ala Ile Ala Arg Lys Ile Ile Glu Glu Thr Ala Ser His Pro Glu
 65 70 75 80

Leu Arg Phe Glu Asn Leu Glu Ala Gln Phe Ser Glu Phe Thr Ile Leu
 85 90 95

Leu Ala Gln Ser Pro Glu Asn Leu Asp Val Ala Arg Tyr Gln Glu Leu
 100 105 110

Arg Thr Gln Gly Asn Phe Val Gln Glu Leu Ala Leu Asp Ser Ile Phe
 115 120 125

Gly Gln His Ala Val Val Gln Asp Thr Gly Asn Gly Glu Ala Ile Leu
 130 135 140
 Asp Glu Thr Ile Gly Tyr Met Ile Gly Ala Gly Met Arg Glu Thr Thr
 145 150 155 160
 Ala Arg Thr Ala Ser Gln Phe Ala Gln Leu Tyr Ser Phe Val Gly Arg
 165 170 175
 Gln Glu Arg Ser Ile Glu Met Ala Arg Leu Ala Phe Glu Glu Leu Gln
 180 185 190
 Ala Ala Gly Leu Pro His Arg Glu Glu Glu Leu Arg Leu Gly Met Gln
 195 200 205
 Leu Ala Gln Val Glu Pro Ile Glu Ala Arg Glu Ile Leu Glu Lys Leu
 210 215 220
 Leu Leu Pro Lys Phe Glu Gln Asn Leu Thr Leu Asp Glu Leu Glu Thr
 225 230 235 240
 Glu Ala Leu Leu Pro Leu Gly Ala Thr Val Ala Ile His Asp Pro Gln
 245 250 255
 Ala Ala Ala Ala Ile Leu Arg His Ala Arg Glu Asn Ala Ala Gly Phe
 260 265 270
 Gly Asn Phe Glu Leu Ala Val Gln Ala Met Thr Met Ile Thr Asp Val
 275 280 285
 Leu Tyr Thr Gln Asn Met His Glu Gln Leu Leu Glu Glu Leu Asn His
 290 295 300
 Ser Leu Pro Tyr Ala Gln Met Leu Asp Asp Gln His Gln Ala Glu Leu
 305 310 315 320
 Lys Leu Leu Asp Ser Ile Ala Ile Val Gln Ala Asp Leu Gly Ser Thr
 325 330 335
 Glu Ala Leu Glu Thr Leu Gly Thr Ala Met Gly Leu Ala Glu Thr Thr
 340 345 350
 Ala Gln Lys Leu Tyr Val Gln Glu Ser Leu Asn Arg Ala Tyr Phe Thr
 355 360 365
 Phe Ala Arg Pro Glu Asp Cys Ile Ser Gly Ala Ala Asp Ala Ser Ala
 370 375 380
 Leu Ala Met Gln Asn Asp Asp Pro Ser Asn Ala Ala Ala Gln Leu Glu
 385 390 395 400
 Gln Cys Ala Gln Tyr Leu Phe Gln Leu Gly His Glu Thr Asp Gly Ala
 405 410 415
 Ser Leu Leu Glu Ser Ala Phe Arg Val Glu Gly Ile Pro Thr Glu Gln
 420 425 430
 Ala Leu Tyr Tyr Ala Asn Ala Leu Ser Ser Ile Tyr Glu Asp Phe Gly
 435 440 445

Asp Ser Ala Lys Ser Gln Tyr Trp Glu Gln Gln Ala Gln Glu Lys Gln
 450 455 460

Gln Leu Leu Glu
 465

<210> 1067
 <211> 612
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(589)
 <223> RXN02296

<400> 1067
 gcattcatttg tgttggttaa agtatatggc tgttgaagtg ccattttcgc ggattagcat 60

gggaatcacc agtattttctg gacggttaag gatgatcat atg cgt aat caa aca 115
 Met Arg Asn Gln Thr
 1 5

atc gct gcg gtc gca gct ttg gtc ctg ctc acc gcc gcc acg ccc gcg 163
 Ile Ala Ala Val Ala Ala Leu Val Leu Thr Ala Ala Thr Pro Ala
 10 15 20

atc gct gcc acc ccg gcg aca gct gga aac gga ctc tat tcc att gac 211
 Ile Ala Ala Thr Pro Ala Thr Ala Gly Asn Gly Leu Tyr Ser Ile Asp
 25 30 35

atg gcc gac gag caa aag ctt acc tgc gtg ctt ttc gat gag ccc tcc 259
 Met Gly Asp Glu Gln Lys Leu Thr Cys Val Leu Phe Asp Glu Pro Ser
 40 45 50

acc gaa gcg cac gtc gtc gcc agc tgt gct gcg act ttc ccg gtg acc 307
 Thr Glu Ala His Val Val Ala Ser Cys Ala Ala Thr Phe Pro Val Thr
 55 60 65

tgg aag ctt ctc gac gcc gct cac gaa caa gcc gcg aaa ctt gaa atc 355
 Trp Lys Leu Leu Asp Gly Ala His Glu Gln Ala Ala Lys Leu Glu Ile
 70 75 80 85

acc cag gct caa gac ggt gaa ctc tcg gtg aca gcc agc aag cag ccg 403
 Thr Gln Ala Gln Asp Gly Glu Leu Ser Val Thr Ala Ser Lys Gln Pro
 90 95 100

ttg atc acc acg atg att gcg ccc acc agc atc act aag ccc atc act 451
 Leu Ile Thr Thr Met Ile Ala Pro Thr Ser Thr Ile Thr Lys Pro Ile Thr
 105 110 115

gtc aat agg ctt gtg gtt gtt cct ggt gag aat gag gtt cgc ttt tat 499
 Val Asn Arg Leu Val Val Val Pro Gly Glu Asn Glu Val Arg Phe Tyr
 120 125 130

gct acc gat cct gat gtt tta cca gtg ctg atc acg cct gac tcc tat 547
 Ala Thr Asp Pro Asp Val Leu Pro Val Leu Ile Thr Pro Asp Ser Tyr
 135 140 145

gaa gtg ttg acc gat tcc gct gct aaa gtg aaa gcg aca tta 589

Glu Val Leu Thr Asp Ser Ala Ala Lys Val Lys Ala Thr Leu
150 155 160

tgaaataaac gtggatcaag gag

612

<210> 1068

<211> 163

<212> PRT

<213> Corynebacterium glutamicum

<400> 1068

Met Arg Asn Gln Thr Ile Ala Ala Val Ala Ala Leu Val Leu Leu Thr
1 5 10 15

Ala Ala Thr Pro Ala Ile Ala Ala Thr Pro Ala Thr Ala Gly Asn Gly
20 25 30

Leu Tyr Ser Ile Asp Met Gly Asp Glu Gln Lys Leu Thr Cys Val Leu
35 40 45

Phe Asp Glu Pro Ser Thr Glu Ala His Val Val Ala Ser Cys Ala Ala
50 55 60

Thr Phe Pro Val Thr Trp Lys Leu Leu Asp Gly Ala His Glu Gln Ala
65 70 75 80

Ala Lys Leu Glu Ile Thr Gln Ala Gln Asp Gly Glu Leu Ser Val Thr
85 90 95

Ala Ser Lys Gln Pro Leu Ile Thr Thr Met Ile Ala Pro Thr Ser Ile
100 105 110

Thr Lys Pro Ile Thr Val Asn Arg Leu Val Val Val Pro Gly Glu Asn
115 120 125

Glu Val Arg Phe Tyr Ala Thr Asp Pro Asp Val Leu Pro Val Leu Ile
130 135 140

Thr Pro Asp Ser Tyr Glu Val Leu Thr Asp Ser Ala Ala Lys Val Lys
145 150 155 160

Ala Thr Leu

<210> 1069

<211> 612

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(589)

<223> FRXA02296

<400> 1069

gcatacatttg tgtgtgttttaa agtatatggc tgttgaagtg ccatttttcgc ggattagcat 60

gggaatcacc agtattttctg gacgggttaag gatgattcat atg cgt aat caa aca 115
Met Arg Asn Gln Thr

1

5

atc gct gcg gtc gca gct ttg gtc ctg ctc acc gcc gcc acg ccc gcg 163
 Ile Ala Ala Val Ala Ala Leu Val Leu Leu Thr Ala Ala Thr Pro Ala
 10 15 20

atc gct gcc acc ccg gcg aca gct gga aac gga ctc tat tcc att gac 211
 Ile Ala Ala Thr Pro Ala Thr Ala Gly Asn Gly Leu Tyr Ser Ile Asp
 25 30 35

atg ggc gac gag caa aag ctt acc tgc gtg ctt ttc gat gag ccc tcc 259
 Met Gly Asp Glu Gln Lys Leu Thr Cys Val Leu Phe Asp Glu Pro Ser
 40 45 50

acc gaa gcg cac gtc gtc gcc agc tgt gct gcg act ttc ccg gtg acc 307
 Thr Glu Ala His Val Val Ala Ser Cys Ala Ala Thr Phe Pro Val Thr
 55 60 65

tgg aag ctt ctc gac ggc gct cac gaa caa gcc gcg aaa ctt gaa atc 355
 Trp Lys Leu Leu Asp Gly Ala His Glu Gln Ala Ala Lys Leu Glu Ile
 70 75 80 85

acc cag gct caa gac ggt gaa ctc tcg gtg aca gcc agc aag cag ccg 403
 Thr Gln Ala Gln Asp Gly Glu Leu Ser Val Thr Ala Ser Lys Gln Pro
 90 95 100

ttg atc acc acg atg att gcg ccc acc agc atc act aag ccc atc act 451
 Leu Ile Thr Thr Met Ile Ala Pro Thr Ser Thr Ile Thr Lys Pro Ile Thr
 105 110 115

gtc aat agg ctt gtg gtt gtt cct ggt gag aat gag gtt cgc ttt tat 499
 Val Asn Arg Leu Val Val Val Pro Gly Glu Asn Glu Val Arg Phe Tyr
 120 125 130

gct acc gat cct gat gtt tta cca gtg ctg atc acg cct gac tcc tat 547
 Ala Thr Asp Pro Asp Val Leu Pro Val Leu Ile Thr Pro Asp Ser Tyr
 135 140 145

gaa gtg ttg acc gat tcc gct gct aaa gtg aaa gcg aca tta 589
 Glu Val Leu Thr Asp Ser Ala Ala Lys Val Lys Ala Thr Leu
 150 155 160

tgaaataaac gtggatcaag gag 612

<210> 1070

<211> 163

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1070

Met Arg Asn Gln Thr Ile Ala Ala Val Ala Ala Leu Val Leu Leu Thr
 1 5 10 15

Ala Ala Thr Pro Ala Ile Ala Ala Thr Pro Ala Thr Ala Gly Asn Gly
 20 25 30

Leu Tyr Ser Ile Asp Met Gly Asp Glu Gln Lys Leu Thr Cys Val Leu
 35 40 45

Phe Asp Glu Pro Ser Thr Glu Ala His Val Val Ala Ser Cys Ala Ala

```

      50              55              60
Thr Phe Pro Val Thr Trp Lys Leu Leu Asp Gly Ala His Glu Gln Ala
65              70              75              80
Ala Lys Leu Glu Ile Thr Gln Ala Gln Asp Gly Glu Leu Ser Val Thr
85              90              95
Ala Ser Lys Gln Pro Leu Ile Thr Thr Met Ile Ala Pro Thr Ser Ile
100             105             110
Thr Lys Pro Ile Thr Val Asn Arg Leu Val Val Val Pro Gly Glu Asn
115             120             125
Glu Val Arg Phe Tyr Ala Thr Asp Pro Asp Val Leu Pro Val Leu Ile
130             135             140
Thr Pro Asp Ser Tyr Glu Val Leu Thr Asp Ser Ala Ala Lys Val Lys
145             150             155             160
Ala Thr Leu

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<210> 1071
<211> 456
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(433)
<223> RXN02300

```

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<400> 1071
gggtcattcc ggtgaacacg gatttcgcgc cggatgaatct gacggtcagc caattgcggg 60
caatgctgtc caaagcggag cgtaaagata aggatcagaa atg aaa act tat gca 115
Met Lys Thr Tyr Ala
1 5
gta cta att gcg gtg gca ggg ttg gca ctt gct ggg tgt agc tcg tcg 163
Val Leu Ile Ala Val Ala Gly Leu Ala Leu Ala Gly Cys Ser Ser Ser
10 15 20
gct cct gga atc tgg cgt gcc act gaa ccc gca gat gcc tac ctt gaa 211
Ala Pro Gly Ile Trp Arg Ala Thr Glu Pro Ala Asp Ala Tyr Leu Glu
25 30 35
ata gcc gat gac gcc acg ctg tcc gga acc gac ggc tgc aac aga ctt 259
Ile Ala Asp Asp Gly Thr Leu Ser Gly Thr Asp Gly Cys Asn Arg Leu
40 45 50
ttt ggt ggc tgg gaa aaa gac ggc tct acc atc act ttc ggc gcc atc 307
Phe Gly Gly Trp Glu Lys Asp Gly Ser Thr Ile Thr Phe Gly Ala Ile
55 60 65
ggt atg aca gaa atg tac tgc gaa ggc gtc aac gat tgg ctg tcc cag 355
Gly Met Thr Glu Met Tyr Cys Glu Gly Val Asn Asp Trp Leu Ser Gln
70 75 80 85

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aaq 456

<213> *Corynebacterium glutamicum*

Thr Ile Phe Asn Glu Ala Gly Ser Asn Ile Gly Glu Leu Lys Arg
100 105 110

<213> *Corynebacterium glutamicum*

<223> FRXA02300

gct cct gga atc tgg cgt gcc act qaa ccc gca gat gcc tac ctt qaa 211

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Ala Pro Gly Ile Trp Arg Ala Thr Glu Pro Ala Asp Ala Tyr Leu Glu
      25                      30                      35
ata gcc gat gac ggc acg ctg tcc gga acc gac ggc tgc aac aga ctt 259
Ile Ala Asp Asp Gly Thr Leu Ser Gly Thr Asp Gly Cys Asn Arg Leu
      40                      45                      50
ttt ggt ggc tgg gaa aaa gac ggc tct acc atc act ttc ggc gcc atc 307
Phe Gly Thr Trp Glu Lys Asp Gly Ser Thr Ile Thr Phe Gly Ala Ile
      55                      60                      65
ggt atg aca gaa atg tac tgc gaa ggc gtc aac gat tgg ctg tcc cag 355
Gly Met Thr Glu Met Tyr Cys Glu Gly Val Asn Asp Trp Leu Ser Gln
      70                      75                      80                      85
atg cac acc gcc acc gtc acc gat gcc acc atg acc att ttc aac gag 403
Met His Thr Ala Thr Val Thr Asp Ala Thr Met Thr Ile Phe Asn Glu
      90                      95                      100
gcc ggc agc aat att ggc gag cta aaa cgc taaatgcttc tcgacgtcaa 453
Ala Gly Ser Asn Ile Gly Glu Leu Lys Arg
      105                      110
aag 456

```

<210> 1074

<211> 111

<212> PRT

<213> Corynebacterium glutamicum

<400> 1074

```

Met Lys Thr Tyr Ala Val Leu Ile Ala Val Ala Gly Leu Ala Leu Ala
  1              5              10              15

```

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Gly Cys Ser Ser Ser Ala Pro Gly Ile Trp Arg Ala Thr Glu Pro Ala
      20              25              30

```

```

Asp Ala Tyr Leu Glu Ile Ala Asp Asp Gly Thr Leu Ser Gly Thr Asp
      35              40              45

```

```

Gly Cys Asn Arg Leu Phe Gly Gly Trp Glu Lys Asp Gly Ser Thr Ile
      50              55              60

```

```

Thr Phe Gly Ala Ile Gly Met Thr Glu Met Tyr Cys Glu Gly Val Asn
      65              70              75              80

```

```

Asp Trp Leu Ser Gln Met His Thr Ala Thr Val Thr Asp Ala Thr Met
      85              90              95

```

```

Thr Ile Phe Asn Glu Ala Gly Ser Asn Ile Gly Glu Leu Lys Arg
      100              105              110

```

<210> 1075

<211> 840

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(817)

<223> RXN02301

<400> 1075

gtttcgata tgtctggatc ttattggatg tatgagtcag agatcagga gatcgcgac 60

taacgaacc tggccagtgc aacaggatta tgtttaaagc atg gat ctt gca ctg 115
 Met Asp Leu Ala Leu
 1 5

gct cag gtt gat tcc acc gtt tgc ggg ctt tat gac gcc ctc gat ctc 163
 Ala Gln Val Asp Ser Thr Val Ser Gly Leu Tyr Asp Ala Leu Asp Leu
 10 15 20

atc ggc gtg ctg ctg aac gga ata atc atc ggt gga acg atc gcc agg caa 211
 Ile Gly Val Leu Leu Asn Gly Ile Ile Gly Gly Thr Ile Ala Arg Gln
 25 30 35

cga ggc tat gac atc att ggc ttt ctg ttc ctg gcg tta ttt tct gcg 259
 Arg Gly Tyr Asp Ile Ile Gly Phe Leu Phe Leu Ala Leu Phe Ser Ala
 40 45 50

ctg ggt ggc gga atg atc cgt gac atg ctg att cag cag ggg act gtc 307
 Leu Gly Gly Gly Met Ile Arg Asp Met Leu Ile Gln Gln Gly Thr Val
 55 60 65

gcg gcg atc gat aat cag atc tac ctt gcg ctc gcg ttt tct ggc gcg 355
 Ala Ala Ile Asp Asn Gln Ile Tyr Leu Ala Leu Ala Phe Ser Gly Ala
 70 75 80 85

ctg att gcc atg gcg gtg aac ttt aaa ggc agg gtg tgg gag ctg ttt 403
 Leu Ile Ala Met Ala Val Asn Phe Lys Gly Arg Val Trp Glu Leu Phe
 90 95 100

aaa gtt cac ggc gat gcc att gtg ttg ggc gtc tgg gcg gtg acg ggt 451
 Lys Val His Gly Asp Ala Ile Val Leu Gly Val Trp Ala Val Thr Gly
 105 110 115

tcc gtg aag gcg atg aat gcg ggg gtg gct ccg ctg ccg agt att ttc 499
 Ser Val Lys Ala Met Asn Ala Gly Val Ala Pro Leu Pro Ser Ile Phe
 120 125 130

atg ggc gtg ctc acc gcg gtg ggt ggt ggc atg gtg cgt gat gtg gct 547
 Met Gly Val Leu Thr Ala Val Gly Gly Gly Met Val Arg Asp Val Ala
 135 140 145

act ggc cag acg ccg acg att ttt ggt ggc gga act ctt tac gct gtg 595
 Thr Gly Gln Thr Pro Thr Ile Phe Gly Gly Gly Thr Leu Tyr Ala Val
 150 155 160 165

cct gcg acg ctt tct gcc acg tca atg gtt att ttt cat agc ttt gac 643
 Pro Ala Thr Leu Ser Ala Thr Ser Met Val Ile Phe His Ser Phe Asp
 170 175 180

cag gta att ctg ggt atg att att tca ccg ttc ttg ggt atc gcg ttg 691
 Gln Val Ile Leu Gly Met Ile Ile Ser Pro Phe Leu Gly Ile Ala Leu
 185 190 195

gcg gtt act gcg tat tgg tgc ggt tgg gtc att ccg gtg aac acg gat 739
 Ala Val Thr Ala Tyr Trp Cys Gly Trp Val Ile Pro Val Asn Thr Asp
 200 205 210

ttc gcg ccg gtg aat ctg acg gtc agc caa ttg cgg gca atg ctg tcc 787
 Phe Ala Pro Val Asn Leu Thr Val Ser Gln Leu Arg Ala Met Leu Ser
 215 220 225

aaa gcg gag cgt aaa gat aag gat cag aaa tgaaaactta tgcagtacta 837
 Lys Ala Glu Arg Lys Asp Lys Asp Gln Lys
 230 235

att 840

<210> 1076

<211> 239

<212> PRT

<213> Corynebacterium glutamicum

<400> 1076

Met Asp Leu Ala Leu Ala Gln Val Asp Ser Thr Val Ser Gly Leu Tyr
 1 5 10 15

Asp Ala Leu Asp Leu Ile Gly Val Leu Leu Asn Gly Ile Ile Gly Gly
 20 25 30

Thr Ile Ala Arg Gln Arg Gly Tyr Asp Ile Ile Gly Phe Leu Phe Leu
 35 40 45

Ala Leu Phe Ser Ala Leu Gly Gly Met Ile Arg Asp Met Leu Ile
 50 55 60

Gln Gln Gly Thr Val Ala Ala Ile Asp Asn Gln Ile Tyr Leu Ala Leu
 65 70 75 80

Ala Phe Ser Gly Ala Leu Ile Ala Met Ala Val Asn Phe Lys Gly Arg
 85 90 95

Val Trp Glu Leu Phe Lys Val His Gly Asp Ala Ile Val Leu Gly Val
 100 105 110

Trp Ala Val Thr Gly Ser Val Lys Ala Met Asn Ala Gly Val Ala Pro
 115 120 125

Leu Pro Ser Ile Phe Met Gly Val Leu Thr Ala Val Gly Gly Gly Met
 130 135 140

Val Arg Asp Val Ala Thr Gly Gln Thr Pro Thr Ile Phe Gly Gly Gly
 145 150 155 160

Thr Leu Tyr Ala Val Pro Ala Thr Leu Ser Ala Thr Ser Met Val Ile
 165 170 175

Phe His Ser Phe Asp Gln Val Ile Leu Gly Met Ile Ile Ser Pro Phe
 180 185 190

Leu Gly Ile Ala Leu Ala Val Thr Ala Tyr Trp Cys Gly Trp Val Ile
 195 200 205

Pro Val Asn Thr Asp Phe Ala Pro Val Asn Leu Thr Val Ser Gln Leu
 210 215 220

Arg Ala Met Leu Ser Lys Ala Glu Arg Lys Asp Lys Asp Gln Lys

225

230

235

<210> 1077
 <211> 840
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(817)
 <223> FRXA02301

<400> 1077
 gcttcgcata tgtctggatc ttattggatg tatgagtcag agatcaggga gatcgcgac 60
 taaccgaacc tggccagtg aacaggatta tgtttaaacg atg gat ctt gca ctg 115
 Met Asp Leu Ala Leu 5
 1
 gct cag gtt gat tcc acc gtt tcg ggg ctt tat gac gcc ctc gat ctc 163
 Ala Gln Val Asp Ser Thr Val Ser Gly Leu Tyr Asp Ala Leu Asp Leu 20
 10 15
 atc ggc gtg ctg ctg aac gga ata atc ggt gga acg atc gcc agg caa 211
 Ile Gly Val Leu Leu Asn Gly Ile Ile Gly Gly Thr Ile Ala Arg Gln 35
 25 30
 cga ggc tat gac atc att ggc ttt ctg ttc ctg gcg tta ttt tct gcg 259
 Arg Gly Tyr Asp Ile Ile Gly Phe Leu Phe Leu Ala Leu Phe Ser Ala 50
 40 45
 ctg ggt ggc gga atg atc cgt gac atg ctg att cag cag ggg act gtc 307
 Leu Gly Gly Gly Met Ile Arg Asp Met Leu Ile Gln Gln Gly Thr Val 60
 55 60 65
 gcg gcg atc gat aat cag atc tac ctt gcg ctc gcg ttt tct ggc gcg 355
 Ala Ala Ile Asp Asn Gln Ile Tyr Leu Ala Leu Ala Phe Ser Gly Ala 85
 70 75 80
 ctg att gcc atg gcg gtg aac ttt aaa ggc agg gtg tgg gag ctg ttt 403
 Leu Ile Ala Met Ala Val Asn Phe Lys Gly Arg Val Trp Glu Leu Phe 95
 90 95 100
 aaa gtt cac ggc gat gcc att gtg ttg ggc gtc tgg gcg gtg acg ggt 451
 Lys Val His Gly Asp Ala Ile Val Leu Gly Val Trp Ala Val Thr Gly 115
 105 110
 tcc gtg aag gcg atg aat gcg ggg gtg gct cgg ctg cgg agt att ttc 499
 Ser Val Lys Ala Met Asn Ala Gly Val Ala Pro Leu Pro Ser Ile Phe 125
 120 125 130
 atg ggc gtg ctc acc gcg gtg ggt ggt gcc atg gtg cgt gat gtg gct 547
 Met Gly Val Leu Thr Ala Val Gly Gly Gly Met Val Arg Asp Val Ala 145
 135 140 145
 act ggc cag acg cgg acg att ttt ggt ggc gga act ctt tac gct gtg 595
 Thr Gly Gln Thr Pro Thr Ile Phe Gly Gly Gly Thr Leu Tyr Ala Val 165
 150 155 160 165
 cct gcg acg ctt tct gcc acg tca atg gtt att ttt cat agc ttt gac 643

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Pro Ala Thr Leu Ser Ala Thr Ser Met Val Ile Phe His Ser Phe Asp
      170                      175                      180

cag gta att ctg ggt atg att att tca ccg ttc ttg ggt atc gcg ttg   691
Gln Val Ile Leu Gly Met Ile Ile Ser Pro Phe Leu Gly Ile Ala Leu
      185                      190                      195

gcg gtt act gcg tat tgg tgc ggt tgg gtc att ccg gtg aac acg gat   739
Ala Val Thr Ala Tyr Trp Cys Gly Trp Val Ile Pro Val Asn Thr Asp
      200                      205                      210

ttc gcg ccg gtg aat ctg acg gtc agc caa ttg ccg gca atg ctg tcc   787
Phe Ala Pro Val Asn Leu Thr Val Ser Gln Leu Arg Ala Met Leu Ser
      215                      220                      225

aaa gcg gag cgt aaa gat aag gat cag aaa tgaaaaactta tgcagtacta   837
Lys Ala Glu Arg Lys Asp Lys Asp Gln Lys
      230                      235

att                                                                    840

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<210> 1078
<211> 239
<212> PRT
<213> Corynebacterium glutamicum

<400> 1078
Met Asp Leu Ala Leu Ala Gln Val Asp Ser Thr Val Ser Gly Leu Tyr
  1              5              10              15

Asp Ala Leu Asp Leu Ile Gly Val Leu Leu Asn Gly Ile Ile Gly Gly
      20              25              30

Thr Ile Ala Arg Gln Arg Gly Tyr Asp Ile Ile Gly Phe Leu Phe Leu
      35              40              45

Ala Leu Phe Ser Ala Leu Gly Gly Gly Met Ile Arg Asp Met Leu Ile
      50              55              60

Gln Gln Gly Thr Val Ala Ala Ile Asp Asn Gln Ile Tyr Leu Ala Leu
      65              70              75              80

Ala Phe Ser Gly Ala Leu Ile Ala Met Ala Val Asn Phe Lys Gly Arg
      85              90              95

Val Trp Glu Leu Phe Lys Val His Gly Asp Ala Ile Val Leu Gly Val
      100             105             110

Trp Ala Val Thr Gly Ser Val Lys Ala Met Asn Ala Gly Val Ala Pro
      115             120             125

Leu Pro Ser Ile Phe Met Gly Val Leu Thr Ala Val Gly Gly Gly Met
      130             135             140

Val Arg Asp Val Ala Thr Gly Gln Thr Pro Thr Ile Phe Gly Gly Gly
      145             150             155             160

Thr Leu Tyr Ala Val Pro Ala Thr Leu Ser Ala Thr Ser Met Val Ile
      165             170             175

```

Phe His Ser Phe Asp Gln Val Ile Leu Gly Met Ile Ile Ser Pro Phe
 180 185 190

Leu Gly Ile Ala Leu Ala Val Thr Ala Tyr Trp Cys Gly Trp Val Ile
 195 200 205

Pro Val Asn Thr Asp Phe Ala Pro Val Asn Leu Thr Val Ser Gln Leu
 210 215 220

Arg Ala Met Leu Ser Lys Ala Glu Arg Lys Asp Lys Asp Gln Lys
 225 230 235

<210> 1079
 <211> 1002
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(979)
 <223> RXN02302

<400> 1079
 ggccaggttc ggtagtgcg cgaatccct gatctctgac tcatacatcc aataagatcc 60

agacatatgc gaagctaag aaggaaacga ggagctgata gtg gca aca aat cgt 115
 Val Ala Thr Asn Arg
 1 5

aca tct tcc gct ggt gtc atc acg tct gtt ctc gca tcc gct ttg ttc 163
 Thr Ser Ser Ala Gly Val Ile Thr Ser Val Leu Ala Ser Ala Leu Phe
 10 15 20

gga gcg atc ttt ttc atc tct ggg gcg att gag gca aag gcg gaa aca 211
 Gly Ala Ile Phe Phe Ile Ser Gly Ala Ile Glu Ala Lys Ala Glu Thr
 25 30 35

ctt gtt gct tgg cgt gtc ctt cta aca gcg gca tgc tat ttg ctt gcc 259
 Leu Val Ala Trp Arg Val Leu Leu Thr Ala Ala Cys Tyr Leu Leu Ala
 40 45 50

ctt ctg cac cct gct ggt cgg aag gtg ttt aag gaa ttt tgg gac aca 307
 Leu Leu His Pro Ala Gly Arg Lys Val Phe Lys Glu Phe Trp Asp Thr
 55 60 65

cta agg tcc caa cct cgt caa att ctg tac ttt atc ttc ctc gtt gta 355
 Leu Arg Ser Gln Pro Arg Gln Ile Leu Tyr Phe Ile Phe Leu Val Val
 70 75 80 85

ctc atc acg ctt cag ctg tgg ctg ttt tct tgg tgg cct aag agt cat 403
 Leu Ile Thr Leu Gln Leu Trp Leu Phe Ser Trp Ser Pro Lys Ser His
 90 95 100

gct tta gat gcc tca ctt ggt tac ctg tta ctg ccc att ttc cta gta 451
 Ala Leu Asp Ala Ser Leu Gly Tyr Leu Leu Leu Pro Ile Phe Leu Val
 105 110 115

att gtg ggg cgg ttt ttc ttc gct gat tac atc acc agg ctg cag tgg 499
 Ile Val Gly Arg Phe Phe Phe Ala Asp Tyr Ile Thr Arg Leu Gln Trp
 120 125 130

att gcg gtg gga atc gcg ctg atc gca gta acc ttg aaa ttt gtc att 547
 Ile Ala Val Gly Ile Ala Leu Ile Ala Val Thr Leu Lys Phe Val Ile
 135 140 145

agt gcg caa tta tgg gta act ttt gcc atc gct gcg ggt tat gca 595
 Ser Ala Gln Leu Ser Trp Val Thr Phe Ala Ile Ala Ala Gly Tyr Ala
 150 155 160 165

ctg tat ttt gcg ctt cgt aaa tac tgg ggg ctg aac aac gct ttt gct 643
 Leu Tyr Phe Ala Leu Arg Lys Tyr Ser Gly Leu Asn Asn Ala Phe Ala
 170 175 180

tac ggc gca gaa gtt tta gcg tta agt ccc ctg gca ttt ttc atg ctc 691
 Tyr Gly Ala Glu Val Leu Ala Leu Ser Pro Leu Ala Phe Phe Met Leu
 185 190 195

gcc act gtc gag gat ccg ctg tct aac gcc atg ttg tca atg gtt att 739
 Ala Thr Val Glu Asp Pro Leu Ser Asn Ala Met Leu Ser Met Val Ile
 200 205 210

ctg gcg ggc ctc gct ggc gca tta gct atg gcg ttg tat cta gcc gcc 787
 Leu Ala Gly Leu Ala Gly Ala Leu Ala Met Ala Leu Tyr Leu Ala Ala
 215 220 225

tca act ctg ctt agt atg ccg atg ttt ggc ctg ctc agt tat ggt gaa 835
 Ser Thr Leu Leu Ser Met Pro Met Phe Gly Leu Leu Ser Tyr Gly Glu
 230 235 240 245

cca atc ttg ctg ttt gtt gca gca cta tta ctt ggt gaa acg ttg aat 883
 Pro Ile Leu Leu Phe Val Ala Ala Leu Leu Gly Glu Thr Leu Asn
 250 255 260

ctc agc gac gcc att gtc tac tca cta ctg gcg tgc gcc ctg gcg tta 931
 Leu Ser Asp Ala Ile Val Tyr Ser Leu Leu Ala Cys Ala Leu Ala Leu
 265 270 275

ctg gga ttt gat ggg ata cga agg tct cga aaa aac ctc gag acc gat 979
 Leu Gly Phe Asp Gly Ile Arg Arg Ser Arg Lys Asn Leu Glu Thr Asp
 280 285 290

taacttctgc tcaacttccc acc 1002

<210> 1080

<211> 293

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1080

Val Ala Thr Asn Arg Thr Ser Ser Ala Gly Val Ile Thr Ser Val Leu
 1 5 10 15

Ala Ser Ala Leu Phe Gly Ala Ile Phe Phe Ile Ser Gly Ala Ile Glu
 20 25 30

Ala Lys Ala Glu Thr Leu Val Ala Trp Arg Val Leu Leu Thr Ala Ala
 35 40 45

Cys Tyr Leu Leu Ala Leu Leu His Pro Ala Gly Arg Lys Val Phe Lys
 50 55 60

Glu Phe Trp Asp Thr Leu Arg Ser Gln Pro Arg Gln Ile Leu Tyr Phe
65 70 75 80

Ile Phe Leu Val Val Leu Ile Thr Leu Gln Leu Trp Leu Phe Ser Trp
85 90 95

Ser Pro Lys Ser His Ala Leu Asp Ala Ser Leu Gly Tyr Leu Leu Leu
100 105 110

Pro Ile Phe Leu Val Ile Val Gly Arg Phe Phe Phe Ala Asp Tyr Ile
115 120 125

Thr Arg Leu Gln Trp Ile Ala Val Gly Ile Ala Leu Ile Ala Val Thr
130 135 140

Leu Lys Phe Val Ile Ser Ala Gln Leu Ser Trp Val Thr Phe Ala Ile
145 150 155 160

Ala Ala Gly Tyr Ala Leu Tyr Phe Ala Leu Arg Lys Tyr Ser Gly Leu
165 170 175

Asn Asn Ala Phe Ala Tyr Gly Ala Glu Val Leu Ala Leu Ser Pro Leu
180 185 190

Ala Phe Phe Met Leu Ala Thr Val Glu Asp Pro Leu Ser Asn Ala Met
195 200 205

Leu Ser Met Val Ile Leu Ala Gly Leu Ala Gly Ala Leu Ala Met Ala
210 215 220

Leu Tyr Leu Ala Ala Ser Thr Leu Leu Ser Met Pro Met Phe Gly Leu
225 230 235 240

Leu Ser Tyr Gly Glu Pro Ile Leu Leu Phe Val Ala Ala Leu Leu Leu
245 250 255

Gly Glu Thr Leu Asn Leu Ser Asp Ala Ile Val Tyr Ser Leu Leu Ala
260 265 270

Cys Ala Leu Ala Leu Leu Gly Phe Asp Gly Ile Arg Arg Ser Arg Lys
275 280

Asn Leu Glu Thr Asp
290

<210> 1081

<211> 865

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)...(865)

<223> FRXA02302

<400> 1081

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agacatatgc gaagctaataa aagaaaacga ggagctgata gtg gca aca aat cgt 115

	Val	Ala	Thr	Asn	Arg	
	1				5	
aca tct tcc gct ggt gtc atc acg tct gtt ctc gca tcc gct ttg ttc						163
Thr Ser Ser Ala Gly Val Ile Thr Ser Val Leu Ala Ser Ala Leu Phe	10				20	
gga gcg atc ttt ttc atc tct ggg gcg att gag gca aag gcg gaa aca						211
Gly Ala Ile Phe Phe Ile Ser Gly Ala Ile Glu Ala Lys Ala Glu Thr	25		30		35	
ctt gtt gct tgg cgt gtc ctt cta aca gcg gca tgc tat ttg ctt gcc						259
Leu Val Ala Trp Arg Val Leu Thr Ala Ala Cys Tyr Leu Leu Ala	40		45		50	
ctt ctg cac cct gct ggt cgg aag gtg ttt aag gaa ttt tgg gac aca						307
Leu Leu His Pro Ala Gly Arg Lys Val Phe Lys Glu Phe Trp Asp Thr	55		60		65	
cta agg tcc caa cct cgt caa att ctg tac ttt atc ttc ctc gtt gta						355
Leu Arg Ser Gln Pro Arg Gln Ile Leu Tyr Phe Ile Phe Leu Val Val	70		75		80	85
ctc atc acg ctt cag ctg tgg ctg ttt tct tgg tcg cct aag agt cat						403
Leu Ile Thr Leu Gln Leu Trp Leu Phe Ser Trp Ser Pro Lys Ser His	90			95		100
gct tta gat gcc tca ctt ggt tac ctg tta ctg ccc att ttc cta gta						451
Ala Leu Asp Ala Ser Leu Gly Tyr Leu Leu Leu Pro Ile Phe Leu Val	105		110		115	
att gtg ggg cgg ttt ttc ttc gct gat tac atc acc agg ctg cag tgg						499
Ile Val Ala Arg Phe Phe Phe Ala Asp Tyr Ile Thr Arg Leu Gln Trp	120		125		130	
att gcg gtg gga atc gcg ctg atc gca gta acc ttg aaa ttt gtc att						547
Ile Ala Val Gly Ile Ala Leu Ile Ala Val Thr Leu Lys Phe Val Ile	135		140		145	
agt gcg caa tta tcg tgg gta act ttt gcc atc gct gcg ggt tat gca						595
Ser Ala Gln Leu Ser Trp Val Thr Phe Ala Ile Ala Ala Gly Tyr Ala	150		155		160	165
ctg tat ttt gcg ctt cgt aaa tac tcg ggg ctg aac aac gct ttt gct						643
Leu Tyr Phe Ala Leu Arg Lys Tyr Ser Gly Leu Asn Asn Ala Phe Ala	170		175		180	
tac ggc gca gaa gtt tta gcg tta agt ccc ctg gca ttt ttc atg ctc						691
Tyr Gly Ala Glu Val Leu Ala Leu Ser Pro Leu Ala Phe Phe Met Leu	185		190		195	
gcc act gtc gag gat ccg ctg tot aac gcc atg ttg tca atg gtt att						739
Ala Thr Val Glu Asp Pro Leu Ser Asn Ala Met Leu Ser Met Val Ile	200		205		210	
ctg gcg ggc ctc gct ggc gca tta gct atg gcg ttg tat cta gcc gcc						787
Leu Ala Gly Leu Ala Gly Ala Leu Ala Met Ala Leu Tyr Leu Ala Ala	215		220		225	
tca act ctg ctt agt atg ccg atg ttt ggc ctg ctc agt tat ggt gaa						835
Ser Thr Leu Leu Ser Met Pro Met Phe Gly Leu Leu Ser Tyr Gly Glu						

230 235 240 245

cca atc ttg ctg ttt gtt gca gca cta tta 865
 Pro Ile Leu Leu Phe Val Ala Ala Leu Leu
 250 255

<210> 1082
 <211> 255
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 1082
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 Ala Ser Ala Leu Phe Gly Ala Ile Phe Phe Ile Ser Gly Ala Ile Glu
 20 25 30
 Ala Lys Ala Glu Thr Leu Val Ala Trp Arg Val Leu Leu Thr Ala Ala
 35 40 45
 Cys Tyr Leu Leu Ala Leu Leu His Pro Ala Gly Arg Lys Val Phe Lys
 50 55 60
 Glu Phe Trp Asp Thr Leu Arg Ser Gln Pro Arg Gln Ile Leu Tyr Phe
 65 70 75 80
 Ile Phe Leu Val Val Leu Ile Thr Leu Gln Leu Trp Leu Phe Ser Trp
 85 90 95
 Ser Pro Lys Ser His Ala Leu Asp Ala Ser Leu Gly Tyr Leu Leu Leu
 100 105 110
 Pro Ile Phe Leu Val Ile Val Gly Arg Phe Phe Phe Ala Asp Tyr Ile
 115 120 125
 Thr Arg Leu Gln Trp Ile Ala Val Gly Ile Ala Leu Ile Ala Val Thr
 130 135 140
 Leu Lys Phe Val Ile Ser Ala Gln Leu Ser Trp Val Thr Phe Ala Ile
 145 150 155 160
 Ala Ala Gly Tyr Ala Leu Tyr Phe Ala Leu Arg Lys Tyr Ser Gly Leu
 165 170 175
 Asn Asn Ala Phe Ala Tyr Gly Ala Glu Val Leu Ala Leu Ser Pro Leu
 180 185 190
 Ala Phe Phe Met Leu Ala Thr Val Glu Asp Pro Leu Ser Asn Ala Met
 195 200 205
 Leu Ser Met Val Ile Leu Ala Gly Leu Ala Gly Ala Leu Ala Met Ala
 210 215 220
 Leu Tyr Leu Ala Ala Ser Thr Leu Leu Ser Met Pro Met Phe Gly Leu
 225 230 235 240
 Leu Ser Tyr Gly Glu Pro Ile Leu Leu Phe Val Ala Ala Leu Leu
 245 250 255

<210> 1083
 <211> 1029
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1006)
 <223> RXN02303

<400> 1083
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 Met Ala Glu Asn Asn
 1 5
 acc cca caa gaa act gaa caa gat cag gaa gca cgc ttc cgt gag gag 163
 Thr Pro Gln Glu Thr Glu Gln Asp Gln Glu Ala Arg Phe Arg Glu Glu
 10 15 20
 ttc gag gtt ggc ggt aag gat cgt cag ctt tct gaa gaa gaa cag ctg 211
 Phe Glu Val Gly Gly Lys Asp Arg Gln Leu Ser Glu Glu Glu Gln Leu
 25 30 35
 gag cag ctg gga tgc tat att gat gcg cac tac cct gtt cca gat ttc 259
 Glu Gln Leu Gly Ser Tyr Ile Asp Ala His Tyr Pro Val Pro Asp Phe
 40 45 50
 acg ccc cct tgg gca ggt ggc gcc ggc gat cct gat cca gca gac cgc 307
 Thr Pro Pro Trp Ala Gly Gly Ala Gly Asp Pro Asp Pro Ala Asp Arg
 55 60 65
 tat att gca cat ctt ccc gat cgc acc acg cat act gcg atg atc atg 355
 Tyr Ile Ala His Leu Pro Asp Arg Thr Thr His Thr Ala Met Ile Met
 70 75 80 85
 ttg ggt tct ggc ctt gat cat tcc atg ccg ggt gtc gca ttt atc ggt 403
 Leu Gly Ser Gly Leu Asp His Ser Met Pro Gly Val Ala Phe Ile Gly
 90 95 100
 ggt gtg agc gtc gat gac gtc ccg gag gtc gga ggc gcg att ttc cac 451
 Gly Val Ser Val Asp Asp Val Pro Glu Val Gly Gly Ala Ile Phe His
 105 110 115
 ccg tgc aat ccg acg ggc cgc tgg gct gta tgc ttc cac agc ggt ggt 499
 Pro Ser Asn Pro Thr Gly Arg Trp Ala Val Ser Phe His Ser Gly Gly
 120 125 130
 tgg tgg cgc ggt tcc ggt gat gcg ttg gag ttc cag tgg cgt cca gag 547
 Trp Trp Arg Gly Ser Gly Asp Ala Leu Glu Phe Gln Trp Arg Pro Glu
 135 140 145
 gtc gcg gca get gcg gaa ttg tcc ggc aca acc atc ctt gac ctg gac 595
 Val Ala Ala Ala Ala Glu Leu Ser Gly Thr Thr Ile Leu Asp Leu Asp
 150 155 160 165
 tat ccg ctg gcc cca ggc cat aac ctc cac gat atg aat gag gtt gtg 643
 Tyr Pro Leu Ala Pro Gly His Asn Leu His Asp Met Asn Glu Val Val
 170 175 180

ggc aag gcg gtc ggt tac gcc cgc cac cat aat ccg gtg tgg atc acg 691
 Gly Lys Ala Val Gly Tyr Ala Arg His His Asn Pro Val Ser Ile Thr
 185 190 195

ggt tgg ggt tat tcc tgg gcc gcg gcg tta gcc gcg att aat gca tgg 739
 Gly Trp Gly Tyr Ser Ser Gly Ala Ala Leu Ala Ala Ile Asn Ala Ser
 200 205 210

ctt ttc gac gcc ctg gtc ctc acc ttt ccg gac ctg ggt agc gtc gag 787
 Leu Phe Asp Ala Leu Val Leu Thr Phe Pro Asp Leu Gly Ser Val Glu
 215 220 225

aag ctc cct gcc gaa att cgt gga gac gct gta gtg ccc gcg gcg gct 835
 Lys Leu Pro Ala Glu Ile Arg Gly Asp Ala Val Val Pro Ala Ala Ala
 230 235 240 245

gcg tgg ccg acg acc ttt gtg cag atc gcg gcg cag gat gag atc gcg 883
 Ala Trp Pro Thr Phe Val Gln Ile Ala Ala Gln Asp Glu Ile Ala
 250 255 260

gag cgg cca gga gag ctt gcc gac gcg acc gtg aag gaa tac gtt tcc 931
 Glu Arg Pro Gly Glu Leu Gly Asp Ala Thr Val Lys Glu Tyr Val Ser
 265 270 275

cgc cac cgt att tcc aca ccg aag gtc gcg cgc gaa aaa atc acc gac 979
 Arg His Arg Ile Ser Thr Pro Lys Val Ala Arg Glu Lys Ile Thr Asp
 280 285 290

gtg gcg gag ttc ctt aaa act gtt tgc taatgtgccca gcaggttgta 1026
 Val Ala Glu Phe Leu Lys Thr Val Cys
 295 300

aat 1029

<210> 1084
 <211> 302
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 1084
 Met Ala Glu Asn Asn Thr Pro Gln Glu Thr Glu Gln Asp Gln Glu Ala
 1 5 10 15

Arg Phe Arg Glu Glu Phe Glu Val Gly Gly Lys Asp Arg Gln Leu Ser
 20 25 30

Glu Glu Glu Gln Leu Glu Gln Leu Gly Ser Tyr Ile Asp Ala His Tyr
 35 40 45

Pro Val Pro Asp Phe Thr Pro Pro Trp Ala Gly Gly Ala Gly Asp Pro
 50 55 60

Asp Pro Ala Asp Arg Tyr Ile Ala His Leu Pro Asp Arg Thr Thr His
 65 70 75 80

Thr Ala Met Ile Met Leu Gly Ser Gly Leu Asp His Ser Met Pro Gly
 85 90 95

Val Ala Phe Ile Gly Gly Val Ser Val Asp Asp Val Pro Glu Val Gly

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100              105              110
Gly Ala Ile Phe His Pro Ser Asn Pro Thr Gly Arg Trp Ala Val Ser
115              120
Phe His Ser Gly Gly Trp Trp Arg Gly Ser Gly Asp Ala Leu Glu Phe
130              135              140
Gln Trp Arg Pro Glu Val Ala Ala Ala Glu Leu Ser Gly Thr Thr
145              150              155              160
Ile Leu Asp Leu Asp Tyr Pro Leu Ala Pro Gly His Asn Leu His Asp
165              170              175
Met Asn Glu Val Val Gly Lys Ala Val Gly Tyr Ala Arg His His Asn
180              185              190
Pro Val Ser Ile Thr Gly Trp Gly Tyr Ser Ser Gly Ala Ala Leu Ala
195              200              205
Ala Ile Asn Ala Ser Leu Phe Asp Ala Leu Val Leu Thr Phe Pro Asp
210              215              220
Leu Gly Ser Val Glu Lys Leu Pro Ala Glu Ile Arg Gly Asp Ala Val
225              230              235              240
Val Pro Ala Ala Ala Ala Trp Pro Thr Thr Phe Val Gln Ile Ala Ala
245              250              255
Gln Asp Glu Ile Ala Glu Arg Pro Gly Glu Leu Gly Asp Ala Thr Val
260              265              270
Lys Glu Tyr Val Ser Arg His Arg Ile Ser Thr Pro Lys Val Ala Arg
275              280              285
Glu Lys Ile Thr Asp Val Ala Glu Phe Leu Lys Thr Val Cys
290              295              300

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<210> 1085

<211> 743

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(720)

<223> FRXA02303

<400> 1085

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gat cct gat cca gca gac cgc tat att gca cat ctt ccc gat cgc acc 48
Asp Pro Asp Pro Ala Asp Arg Tyr Ile Ala His Leu Pro Asp Arg Thr
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acg cat act gcg atg atc atg ttg ggt tct ggc ctt gat cat tcc atg 96
Thr His Thr Ala Met Ile Met Leu Gly Ser Gly Leu Asp His Ser Met
20      25      30

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ccg ggt gtc gca ttt atc ggt ggt gtg agc gtc gat gac gtc ccg gag 144
Pro Gly Val Ala Phe Ile Gly Gly Val Ser Val Asp Asp Val Pro Glu
35      40      45

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gtc gga ggc gcg att ttc cac ccg tcg aat ccg acg ggc cgc tgg gct 192
 Val Gly Gly Ala Ile Phe His Pro Ser Asn Pro Thr Gly Arg Trp Ala
 50 55 60
 gta tcg ttc cac agc ggt tgg tgg cgc ggt tcc ggt gat gcg ttg 240
 Val Ser Phe His Ser Ser Gly Gly Trp Trp Arg Gly Ser Gly Asp Ala Leu
 65 70 75 80
 gag ttc cag tgg cgt cca gag gtc gcg gca gct gcg gaa ttg tcc ggc 288
 Glu Phe Gln Trp Arg Pro Glu Val Ala Ala Ala Glu Leu Ser Gly
 85 90 95
 aca acc atc ctt gac ctg gac tat ccg ctg gcc cca ggc cat aac ctc 336
 Thr Thr Ile Leu Asp Leu Asp Tyr Pro Leu Ala Pro Gly His Asn Leu
 100 105 110
 cac gat atg aat gag gtt gtg ggc aag gcg gtc ggt tac gcc cgc cac 384
 His Asp Met Asn Glu Val Val Gly Lys Ala Val Gly Tyr Ala Arg His
 115 120 125
 cat aat ccg gtg tcg atc acg ggt tgg ggt tat tcc tcg gcc gcg gcg 432
 His Asn Pro Val Ser Ile Thr Gly Trp Gly Tyr Ser Ser Gly Ala Ala
 130 135 140
 tta gcc gcg att aat gca tcg ctt ttc gac gcc ctg gtc ctc acc ttt 480
 Leu Ala Ala Ile Asn Ala Ser Leu Phe Asp Ala Leu Val Leu Thr Phe
 145 150 155 160
 ccg gac ctg ggt agc gtc gag aag ctc cct gcc gaa att cgt gga gac 528
 Pro Asp Leu Gly Ser Val Glu Lys Leu Pro Ala Glu Ile Arg Gly Asp
 165 170 175
 gct gta gtg ccc gcg gcg gct gcg tgg ccg acg acc ttt gtg cag atc 576
 Ala Val Val Pro Ala Ala Ala Ala Trp Pro Thr Thr Phe Val Gln Ile
 180 185 190
 gcg gcg cag gat gag atc gcg gag cgg cca gga gag ctt gcc gac gcg 624
 Ala Ala Gln Asp Glu Ile Ala Glu Arg Pro Gly Glu Leu Gly Asp Ala
 195 200 205
 acc gtg aag gaa tac gtt tcc cgc cac cgt att tcc aca ccg aag gtc 672
 Thr Val Lys Glu Tyr Val Ser Arg His Arg Ile Ser Thr Pro Lys Val
 210 215 220
 gcg cgc gaa aaa atc acc gac gtg gcg gag ttc ctt aaa act gtt tgc 720
 Ala Arg Glu Lys Ile Thr Asp Val Ala Glu Phe Leu Lys Thr Val Cys
 225 230 235 240
 taatgtgcc gtaggttgta aat 743

<210> 1086

<211> 240

<212> PRT

<213> Corynebacterium glutamicum

<400> 1086

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Thr His Thr Ala Met Ile Met Leu Gly Ser Gly Leu Asp His Ser Met
 20 25 30
 Pro Gly Val Ala Phe Ile Gly Gly Val Ser Val Asp Asp Val Pro Glu
 35 40 45
 Val Gly Gly Ala Ile Phe His Pro Ser Asn Pro Thr Gly Arg Trp Ala
 50 55 60
 Val Ser Phe His Ser Gly Gly Trp Trp Arg Gly Ser Gly Asp Ala Leu
 65 70 75 80
 Glu Phe Gln Trp Arg Pro Glu Val Ala Ala Ala Glu Leu Ser Gly
 85 90 95
 Thr Thr Ile Leu Asp Leu Asp Tyr Pro Leu Ala Pro Gly His Asn Leu
 100 105 110
 His Asp Met Asn Glu Val Val Gly Lys Ala Val Gly Tyr Ala Arg His
 115 120 125
 His Asn Pro Val Ser Ile Thr Gly Trp Gly Tyr Ser Ser Gly Ala Ala
 130 135 140
 Leu Ala Ala Ile Asn Ala Ser Leu Phe Asp Ala Leu Val Leu Thr Phe
 145 150 155 160
 Pro Asp Leu Gly Ser Val Glu Lys Leu Pro Ala Glu Ile Arg Gly Asp
 165 170 175
 Ala Val Val Pro Ala Ala Ala Ala Trp Pro Thr Thr Phe Val Gln Ile
 180 185 190
 Ala Ala Gln Asp Glu Ile Ala Glu Arg Pro Gly Glu Leu Gly Asp Ala
 195 200 205
 Thr Val Lys Glu Tyr Val Ser Arg His Arg Ile Ser Thr Pro Lys Val
 210 215 220
 Ala Arg Glu Lys Ile Thr Asp Val Ala Glu Phe Leu Lys Thr Val Cys
 225 230 235 240

<210> 1087

<211> 744

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(721)

<223> RXN02307

<400> 1087

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 Met Ser Gly Thr Ala

1

5

atc atg tac gac acg aca gtt gtt cca tcg aag aaa gaa atc gcg cag 163
 Ile Met Tyr Asp Thr Thr Val Val Pro Ser Lys Lys Glu Ile Ala Gln
 10 15 20

gct tgg act ggt tat gtg gat ctt cag gga agc tac cgc ctg gta gat 211
 Ala Trp Thr Gly Tyr Val Asp Leu Gln Gly Ser Tyr Arg Leu Val Asp
 25 30 35

acg gtg gat ggg gaa gtt ggc gtt gag gtg ctg att tcc aag gat cgg 259
 Thr Val Asp Gly Glu Val Gly Val Glu Val Leu Ile Ser Lys Asp Arg
 40 45 50

gag ggg cgt tta ctc cag att ttt agt tat cgt tcg gca gag att 307
 Glu Gly Arg Leu Leu Gln Ile Pro Phe Ser Tyr Arg Ser Ala Glu Ile
 55 60 65

aac cca gag cag aca ctt tcc aca ttg gag cat ggt gtg ttg ggc aag 355
 Asn Pro Glu Gln Thr Leu Ser Thr Leu Glu His Gly Val Leu Gly Lys
 70 75 80 85

cgt tgg gtg act aat gcg ttg ggt gac cgg gtg gca gtg cgg gag ttt 403
 Arg Trp Val Thr Asn Ala Leu Gly Asp Pro Val Ala Val Arg Glu Phe
 90 95 100

att cgc act att ttg acg ggc gat gat ggt gca gct cgt agc gat ggc 451
 Ile Arg Thr Ile Leu Thr Gly Asp Asp Gly Ala Ala Arg Ser Asp Gly
 105 110 115

gtg aag ggc tat ctg gat att aaa ggt tcc ggc gat gct gag tcg gtg 499
 Val Lys Gly Tyr Leu Asp Ile Lys Gly Ser Gly Asp Ala Glu Ser Val
 120 125 130

gat tta cag gat gta aag ctt act gag gtt aca agg cag cgt gcg att 547
 Asp Leu Gln Asp Val Lys Leu Thr Glu Val Thr Arg Gln Arg Ala Ile
 135 140 145

ggt tcg gta acc atc aac ggt gag cga aag caa ttc tcg ctg cgg ttg 595
 Gly Ser Val Thr Ile Asn Gly Glu Arg Lys Gln Phe Ser Leu Arg Leu
 150 155 160 165

cct cag ttg ctg aag aat ttc agg gag aca gcc gcg ggc cat aca gct 643
 Pro Gln Leu Leu Lys Asn Phe Arg Glu Thr Ala Ala Gly His Thr Ala
 170 175 180

acg act ctt cgt att gtg gcg act cat cgg gaa aag gac gat gtt gag 691
 Thr Thr Leu Arg Ile Val Ala Thr His Pro Glu Lys Asp Asp Val Glu
 185 190 195

ctg ctg gtc gct gag ttc aac tgg atg gaa taatccgaga cagctcctga 741
 Leu Leu Val Ala Glu Phe Asn Trp Met Glu
 200 205

aag 744

<210> 1088

<211> 207

<212> PRT

<213> Corynebacterium glutamicum

<400> 1088

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Met Ser Gly Thr Ala Ile Met Tyr Asp Thr Thr Val Val Pro Ser Lys
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Lys Glu Ile Ala Gln Ala Trp Thr Gly Tyr Val Asp Leu Gln Gly Ser
      20           25           30

Tyr Arg Leu Val Asp Thr Val Asp Gly Glu Val Gly Val Glu Val Leu
      35           40           45

Ile Ser Lys Asp Arg Glu Gly Arg Leu Leu Gln Ile Pro Phe Ser Tyr
      50           55           60

Arg Ser Ala Glu Ile Asn Pro Glu Gln Thr Leu Ser Thr Leu Glu His
      65           70           75           80

Gly Val Leu Gly Lys Arg Trp Val Thr Asn Ala Leu Gly Asp Pro Val
      85           90           95

Ala Val Arg Glu Phe Ile Arg Thr Ile Leu Thr Gly Asp Asp Gly Ala
      100          105          110

Ala Arg Ser Asp Gly Val Lys Gly Tyr Leu Asp Ile Lys Gly Ser Gly
      115          120          125

Asp Ala Glu Ser Val Asp Leu Gln Asp Val Lys Leu Thr Glu Val Thr
      130          135          140

Arg Gln Arg Ala Ile Gly Ser Val Thr Ile Asn Gly Glu Arg Lys Gln
      145          150          155          160

Phe Ser Leu Arg Leu Pro Gln Leu Leu Lys Asn Phe Arg Glu Thr Ala
      165          170          175

Ala Gly His Thr Ala Thr Thr Leu Arg Ile Val Ala Thr His Pro Glu
      180          185          190

Lys Asp Asp Val Glu Leu Leu Val Ala Glu Phe Asn Trp Met Glu
      195          200          205

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<210> 1089

<211> 490

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(490)

<223> FRXA02307

<400> 1089

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                Met Ser Gly Thr Ala
                1           5

atc atg tac gac acg aca gtt gtt cca tcg aag aaa gaa atc gcg cag 163
Ile Met Tyr Asp Thr Thr Val Val Pro Ser Lys Lys Glu Ile Ala Gln

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	10	15	20	
	gct tgg act ggt tat gtg gat ctt cag gga agc tac cgc ctg gta gat			211
	Ala Trp Thr Gly Tyr Val Asp Leu Gln Gly Ser Tyr Arg Leu Val Asp			
	25	30	35	
	acg gtg gat ggg gaa gtt ggc gtt gag gtg ctg att tcc aag gat cgg			259
	Thr Val Asp Gly Glu Val Gly Val Glu Val Leu Ile Ser Lys Asp Arg			
	40	45	50	
	gag ggg cgt tta ctc cag att ccg ttt agt tat cgt tcg gca gag att			307
	Glu Gly Arg Leu Leu Gln Ile Pro Phe Ser Tyr Arg Ser Ala Glu Ile			
	55	60	65	
	aac cca gag cag aca ctt tcc aca ttg gag cat ggt gtg ttg ggc aag			355
	Asn Pro Glu Gln Thr Leu Ser Thr Leu Glu His Gly Val Leu Gly Lys			
	70	75	80	85
	cgt tgg gtg act aat gcg ttg ggt gac ccg gtg gca gtg cgg gag ttt			403
	Arg Trp Val Thr Asn Ala Leu Gly Asp Pro Val Ala Val Arg Glu Phe			
	90	95	100	
	att cgc act att ttg acg ggc gat gat ggt gca gct cgt agc gat ggc			451
	Ile Arg Thr Ile Leu Thr Gly Asp Asp Gly Ala Ala Arg Ser Asp Gly			
	105	110	115	
	gtg aag ggc tat ctg gat att aaa ggt tcc ggc gat gct			490
	Val Lys Gly Tyr Leu Asp Ile Lys Gly Ser Gly Asp Ala			
	120	125	130	
	<210> 1090			
	<211> 130			
	<212> PRT			
	<213> Corynebacterium glutamicum			
	<400> 1090			
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	Lys Glu Ile Ala Gln Ala Trp Thr Gly Tyr Val Asp Leu Gln Gly Ser			
	20	25	30	
	Tyr Arg Leu Val Asp Thr Val Asp Gly Glu Val Gly Val Glu Val Leu			
	35	40	45	
	Ile Ser Lys Asp Arg Glu Gly Arg Leu Leu Gln Ile Pro Phe Ser Tyr			
	50	55	60	
	Arg Ser Ala Glu Ile Asn Pro Glu Gln Thr Leu Ser Thr Leu Glu His			
	65	70	75	80
	Gly Val Leu Gly Lys Arg Trp Val Thr Asn Ala Leu Gly Asp Pro Val			
	85	90	95	
	Ala Val Arg Glu Phe Ile Arg Thr Ile Leu Thr Gly Asp Asp Gly Ala			
	100	105	110	
	Ala Arg Ser Asp Gly Val Lys Gly Tyr Leu Asp Ile Lys Gly Ser Gly			
	115	120	125	

Asp Ala
130

<210> 1091
<211> 564
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (101)..(541)
<223> RXN02314

<400> 1091
tgataccacc gaagtatccg gattcaccat tattgaagct tcgaccgtcc gagatacccg 60

ccgtgcacaa cagcaagctc tcatggacac ggtgcactaa atg gag tgg tac caa 115
Met Glu Trp Tyr Gln
1 5

gtg cgc cga cgg gcc cga caa ctg ctc att gtc ctt ttt ata gca gcg 163
Val Arg Arg Arg Ala Arg Gln Leu Leu Ile Val Leu Phe Ile Ala Ala
10 15 20

atg ctc gga gca gcc tcc atg gtg atc ggg cca ttc ctt aac gac cgc 211
Met Leu Gly Ala Ala Ser Met Val Ile Gly Pro Phe Leu Asn Asp Arg
25 30 35

act atc gaa ggc aac tcc ggg cgc gcc ttg gca caa gta acc aac gtc 259
Thr Ile Glu Gly Asn Ser Gly Arg Ala Leu Ala Gln Val Thr Asn Val
40 45 50

ggc agc tac cgc aca acg gtg gat ttc caa gat gaa aac ggc atc tat 307
Gly Ser Tyr Arg Thr Thr Val Asp Phe Gln Asp Glu Asn Gly Ile Tyr
55 60 65

cac tca cca gcc acc ggc ctg ttg ttc ccc acg gga ctg ggc gag ggg 355
His Ser Pro Ala Thr Gly Leu Leu Phe Pro Thr Gly Leu Gly Glu Gly
70 75 80 85

caa cgc gtg tgg gtg aac tac gcc aaa tca gat cca gac ctg gtc aaa 403
Gln Arg Val Trp Val Asn Tyr Ala Lys Ser Asp Pro Asp Leu Val Lys
90 95 100

gta gaa ggc cgc aag tgg aca ctg tcc atc atc cca gcg ctt agt gtc 451
Val Glu Gly Arg Lys Trp Thr Leu Ser Ile Ile Pro Ala Leu Ser Val
105 110 115

gca gct gtc gcc acc gct acc tgg tca gta cta tgg ctg gga gtg ggc 499
Ala Ala Val Ala Thr Ala Thr Trp Ser Val Leu Trp Leu Gly Val Gly
120 125 130

aga ttc gga aga cga tcc gac gac gcc aac gaa acc aca gtg 541
Arg Phe Gly Arg Arg Ser Asp Asp Ala Asn Glu Thr Thr Val
135 140 145

taaagctcta tgccgggagc att 564

<210> 1092

<211> 147

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1092

Met Glu Trp Tyr Gln Val Arg Arg Arg Ala Arg Gln Leu Leu Ile Val
 1 5 10 15

Leu Phe Ile Ala Ala Met Leu Gly Ala Ala Ser Met Val Ile Gly Pro
 20 25 30

Phe Leu Asn Asp Arg Thr Ile Glu Gly Asn Ser Gly Arg Ala Leu Ala
 35 40 45

Gln Val Thr Asn Val Gly Ser Tyr Arg Thr Thr Val Asp Phe Gln Asp
 50 55 60

Glu Asn Gly Ile Tyr His Ser Pro Ala Thr Gly Leu Leu Phe Pro Thr
 65 70 75 80

Gly Leu Gly Glu Gly Gln Arg Val Trp Val Asn Tyr Ala Lys Ser Asp
 85 90 95

Pro Asp Leu Val Lys Val Glu Gly Arg Lys Trp Thr Leu Ser Ile Ile
 100 105 110

Pro Ala Leu Ser Val Ala Ala Val Ala Thr Ala Thr Trp Ser Val Leu
 115 120 125

Trp Leu Gly Val Gly Arg Phe Gly Arg Arg Ser Asp Asp Ala Asn Glu
 130 135 140

Thr Thr Val
 145

<210> 1093

<211> 564

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(541)

<223> FRXA02314

<400> 1093

tgataccacc gaagtatccg gattcaccat tattgaagct tcgaccgtcc gagatacccg 60

ccgtgcacaa cagcaagctc tcatggacac ggtgcactaa atg gag tgg tac caa 115
 Met Glu Trp Tyr Gln
 1 5

gtg cgc cga cgg gcc cga caa ctg ctc att gtc ctt ttt ata gca gcg 163
 Val Arg Arg Arg Ala Arg Gln Leu Leu Ile Val Leu Phe Ile Ala Ala
 10 15 20

atg ctc gga gca gcc tcc atg gtg atc ggg cca ttc ctt aac gac cgc 211
 Met Leu Gly Ala Ala Ser Met Val Ile Gly Pro Phe Leu Asn Asp Arg
 25 30 35

act atc gaa ggc aac tcc ggg cgc gcc ttg gca caa gta acc aac gtc 259
 Thr Ile Glu Gly Asn Ser Gly Arg Ala Leu Ala Gln Val Thr Asn Val
 40 45 50

ggc agc tac cgc aca acg gtg gat ttc caa gat gaa aac ggc atc tat 307
 Gly Ser Tyr Arg Thr Thr Val Asp Phe Gln Asp Glu Asn Gly Ile Tyr
 55 60 65

cac tca cca gcc acc ggc ctg ttg ttc ccc acg gga ctg ggc gag ggg 355
 His Ser Pro Ala Thr Gly Leu Leu Phe Pro Thr Gly Leu Gly Glu Gly
 70 75 80 85

caa cgc gtg tgg gtg aac tac gcc aaa tca gat cca gac ctg gtc aaa 403
 Gln Arg Val Trp Val Asn Tyr Ala Lys Ser Asp Pro Asp Leu Val Lys
 90 95 100

gta gaa ggc cgc aag tgg aca ctg tcc atc atc cca gcg ctt agt gtc 451
 Val Glu Gly Arg Lys Trp Thr Leu Ser Ile Ile Pro Ala Leu Ser Val
 105 110 115

gca gct gtc gcc acc gct acc tgg tca gta cta tgg ctg gga gtg ggc 499
 Ala Ala Val Ala Thr Ala Thr Trp Ser Val Leu Trp Leu Gly Val Gly
 120 125 130

aga ttc gga aga cga tcc gac gac gcc aac gaa acc aca gtg 541
 Arg Phe Gly Arg Arg Ser Asp Asp Ala Asn Glu Thr Thr Val
 135 140 145

taaagctcta tgccggggagc att 564

<210> 1094
 <211> 147
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 1094
 Met Glu Trp Tyr Gln Val Arg Arg Arg Ala Arg Gln Leu Leu Ile Val
 1 5 10 15

Leu Phe Ile Ala Ala Met Leu Gly Ala Ala Ser Met Val Ile Gly Pro
 20 25 30

Phe Leu Asn Asp Arg Thr Ile Glu Gly Asn Ser Gly Arg Ala Leu Ala
 35 40 45

Gln Val Thr Asn Val Gly Ser Tyr Arg Thr Thr Val Asp Phe Gln Asp
 50 55 60

Glu Asn Gly Ile Tyr His Ser Pro Ala Thr Gly Leu Leu Phe Pro Thr
 65 70 75 80

Gly Leu Gly Glu Gly Gln Arg Val Trp Val Asn Tyr Ala Lys Ser Asp
 85 90 95

Pro Asp Leu Val Lys Val Glu Gly Arg Lys Trp Thr Leu Ser Ile Ile
 100 105 110

Pro Ala Leu Ser Val Ala Ala Val Ala Thr Ala Thr Trp Ser Val Leu
 115 120 125

Trp Leu Gly Val Gly Arg Phe Gly Arg Arg Ser Asp Asp Ala Asn Glu
130 135 140

Thr Thr Val
145

<210> 1095

<211> 1446

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1423)

<223> RXN02337

<400> 1095

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aaatcatgag gtcataagct ttctgggagg ttgtcaaagg atg tcg aag ctt tac 115
Met Ser Lys Leu Tyr
1 5

gcg ggg gca agg atc aat gca ctg cgc cga acc cat cag ctc acc caa 163
Ala Gly Ala Arg Ile Asn Ala Leu Arg Arg Thr His Gln Leu Thr Gln
10 15 20

tca gca ttg gcc gac aag ctt gat ctc tcc acc agc tat ctc aac cag 211
Ser Ala Leu Ala Asp Lys Leu Asp Leu Ser Thr Ser Tyr Leu Asn Gln
25 30 35

ttg gaa aat gac gga cgg cca ctc act gcc acg gtg ctt ctg cag ctg 259
Leu Glu Asn Asp Gly Arg Pro Leu Thr Ala Thr Val Leu Leu Gln Leu
40 45 50

atg aaa gtg ttc gat gtt gag gcc agt tac ttc tcc cct gac cgg ggt 307
Met Lys Val Phe Asp Val Glu Ala Ser Tyr Phe Ser Pro Asp Arg Gly
55 60 65

acg gcc act gct acc cga ctg gct gaa acc ttg gcg atg aat cag ggt 355
Thr Ala Thr Ala Thr Arg Leu Ala Glu Thr Leu Ala Met Asn Gln Gly
70 75 80 85

cgg acg atg tcg atg gat gat ctt tta gat ttc gcg gat cgt ttc cct 403
Pro Thr Met Ser Met Asp Asp Leu Leu Asp Phe Ala Asp Arg Phe Pro
90 95 100

cag tta gcg cag cat att atc cag cct gct gag gtt gat ccc acg cat 451
Gln Leu Ala Gln His Ile Ile Gln Pro Ala Glu Val Asp Pro Thr His
105 110 115

agt tct gcg cat gat ttt gtt cgg gat tat ttt gcc acc cac aaa aac 499
Ser Ser Ala His Asp Phe Val Arg Asp Tyr Phe Ala Thr His Lys Asn
120 125 130

tac att gat tcg ctc gat cgc ctt gga gag gag ttg gca act gcc att 547
Tyr Ile Asp Ser Leu Asp Arg Leu Gly Glu Leu Ala Thr Ala Ile
135 140 145

ggg cag ccg gga ctt cgg gtt act agg ctc gcg cag ttg ctt gat gcg 595

Gly	Gln	Pro	Gly	Leu	Arg	Val	Thr	Arg	Leu	Ala	Gln	Leu	Leu	Asp	Ala	
150					155					160					165	
gag	tac	aac	atc	acg	gtg	cgt	ttc	cgg	gcg	ccg	gat	att	act	ggc	cgg	643
Glu	Tyr	Asn	Ile	Thr	Val	Arg	Phe	Arg	Ala	Pro	Asp	Ile	Thr	Gly	Arg	
			170						175					180		
agg	cac	ttt	gat	ccc	caa	tcg	cgt	cag	att	ctg	ctg	cgg	caa	gat	ctc	691
Arg	His	Phe	Asp	Pro	Gln	Ser	Arg	Gln	Ile	Leu	Leu	Arg	Gln	Asp	Leu	
			185						190					195		
agc	gag	gcg	cag	cag	tgt	ttc	cag	ttg	gcg	gag	gaa	ttg	acg	ttt	ctt	739
Ser	Glu	Ala	Gln	Gln	Cys	Phe	Gln	Leu	Ala	Glu	Glu	Leu	Thr	Phe	Leu	
			200					205					210			
gct	cat	gca	gag	ctc	ttg	gat	acc	ctg	acc	aca	gat	caa	ccg	gat	ctc	787
Ala	His	Ala	Glu	Leu	Leu	Asp	Thr	Leu	Thr	Thr	Asp	Gln	Pro	Asp	Leu	
			215				220							225		
cct	tct	gag	gca	gct	atc	cgc	ctg	gct	aag	gtg	ggc	ctc	tcc	caa	tat	835
Pro	Ser	Glu	Ala	Ala	Ile	Arg	Leu	Ala	Lys	Val	Gly	Leu	Ser	Gln	Tyr	
			230			235				240					245	
ttc	gcg	gct	gct	gtt	gtc	atg	ccg	tac	acc	cgc	ttt	ttg	gaa	ttc	gcc	883
Phe	Ala	Ala	Ala	Val	Val	Met	Pro	Tyr	Thr	Arg	Phe	Leu	Glu	Phe	Ala	
				250						255					260	
cag	gat	aag	cac	tat	gac	atc	gag	ttg	atc	tct	gag	gcg	ttt	gga	gtg	931
Gln	Asp	Lys	His	Tyr	Asp	Ile	Glu	Leu	Ile	Ser	Glu	Ala	Phe	Gly	Val	
			265					270						275		
tct	ttc	gag	tct	gca	tgc	cac	cgc	ctg	tct	act	ctg	cag	cgt	tgc	ggg	979
Ser	Phe	Glu	Ser	Ala	Cys	His	Arg	Leu	Ser	Thr	Leu	Gln	Arg	Ser	Gly	
			280					285						290		
gcg	tca	ggg	gtg	ccg	ttt	ttc	ttt	gtg	cgc	tgc	gat	cgt	gca	gga	aat	1027
Ala	Ser	Gly	Val	Pro	Phe	Phe	Phe	Val	Arg	Ser	Asp	Arg	Ala	Gly	Asn	
			295				300					305				
atc	tcc	aag	cgg	caa	tct	gca	gct	acg	ttc	cac	ttc	tgc	cga	aca	gac	1075
Ile	Ser	Lys	Arg	Gln	Ser	Ala	Ala	Thr	Phe	His	Phe	Ser	Arg	Thr	Asp	
						315					320				325	
ggc	act	tgt	cct	ttg	tgg	gcg	ctg	cat	cgt	gct	ttt	gaa	cgt	cag	gga	1123
Gly	Thr	Cys	Pro	Leu	Trp	Ala	Leu	His	Arg	Ala	Phe	Glu	Arg	Gln	Gly	
				330					335						340	
aac	atc	acc	cgc	cag	gtt	gct	cgc	atg	ccg	gat	ggc	cgg	acc	tat	ttg	1171
Asn	Ile	Thr	Arg	Gln	Val	Ala	Arg	Met	Pro	Asp	Gly	Arg	Thr	Tyr	Leu	
			345					350						355		
tgg	ctc	gca	cgc	gcg	gtg	aaa	ggc	cga	act	cat	ggc	ttc	ggg	tat	cct	1219
Trp	Leu	Ala	Arg	Ala	Val	Lys	Gly	Arg	Thr	His	Gly	Phe	Gly	Tyr	Pro	
			360					365						370		
gct	gcg	gaa	ttc	gcc	atc	ggc	ctg	ggc	tgc	gat	atc	agc	gag	gca	cca	1267
Ala	Ala	Glu	Phe	Ala	Ile	Gly	Leu	Gly	Cys	Asp	Ile	Ser	Glu	Ala	Pro	
			375				380									
ggc	ttg	gtg	tat	tcc	caa	ggc	ctt	aat	ttg	gat	ccc	gag	tcc	gcc	gca	1315
Gly	Leu	Val	Tyr	Ser	Gln	Gly	Leu	Asn	Leu	Asp	Pro	Glu	Ser	Ala	Ala	

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<210> 1096
<211> 441
<212> PRT
<213> Corynebacterium glutamicum
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Met Ser Lys Leu Tyr Ala Gly Ala Arg Ile Asn Ala Leu Arg Arg Thr
1 5 10 15

His Gln Leu Thr Gln Ser Ala Leu Ala Asp Lys Leu Asp Leu Ser Thr
20 25 30

Ser Tyr Leu Asn Gln Leu Glu Asn Asp Gly Arg Pro Leu Thr Ala Thr
35 40 45

Val Leu Leu Gln Leu Met Lys Val Phe Asp Val Glu Ala Ser Tyr Phe
50 55 60

Ser Pro Asp Arg Gly Thr Ala Thr Ala Thr Arg Leu Ala Glu Thr Leu
65 70 75 80

Ala Met Asn Gln Gly Pro Thr Met Ser Met Asp Asp Leu Leu Asp Phe
85 90 95

Ala Asp Arg Phe Pro Gln Leu Ala Gln His Ile Ile Gln Pro Ala Glu
100 105 110

Val Asp Pro Thr His Ser Ser Ala His Asp Phe Val Arg Asp Tyr Phe
115 120 125

Ala Thr His Lys Asn Tyr Ile Asp Ser Leu Asp Arg Leu Gly Glu Glu
130 135 140

Leu Ala Thr Ala Ile Gly Gln Pro Gly Leu Arg Val Thr Arg Leu Ala
145 150 155 160

Gln Leu Leu Asp Ala Glu Tyr Asn Ile Thr Val Arg Phe Arg Ala Pro
165 170 175

Asp Ile Thr Gly Arg Arg His Phe Asp Pro Gln Ser Arg Gln Ile Leu
180 185 190

Leu Arg Gln Asp Leu Ser Glu Ala Gln Gln Cys Phe Gln Leu Ala Glu
195 200 205

Glu Leu Thr Phe Leu Ala His Ala Glu Leu Leu Asp Thr Leu Thr Thr

gcg ggg gca agg atc aat gca ctg cgc cga acc cat cag ctc acc caa 163
 Ala Gly Ala Arg Ile Asn Ala Leu Arg Arg Thr His Gln Leu Thr Gln
 10 15 20

tca gca ttg gcc gac aag ctt gat ctc tcc acc agc tat ctc aac cag 211
 Ser Ala Leu Asn Asp Lys Leu Asp Leu Ser Thr Ser Tyr Leu Leu Asn Gln
 25 30 35

ttg gaa aat gac gga cgg cca ctc act gcc acg gtg ctt ctg cag ctg 259
 Leu Glu Asn Asp Gly Arg Pro Leu Thr Ala Thr Val Leu Leu Gln Leu
 40 45 50

atg aaa gtg ttc gat gtt gag gcc agt tac ttc tcc cct gac cgg ggt 307
 Met Lys Val Phe Asp Val Glu Ala Ser Tyr Phe Ser Pro Asp Arg Gly
 55 60 65

acg gcc act gct acc cga ctg gct gaa acc ttg gcg atg aat cag ggt 355
 Thr Ala Thr Ala Thr Arg Leu Ala Glu Thr Leu Ala Met Asn Gln Gly
 70 75 80 85

ccg acg atg tcg atg gat gat ctt tta gat ttc gcg gat cgt ttc cct 403
 Pro Thr Met Ser Met Asp Asp Leu Leu Asp Phe Ala Asp Arg Phe Pro
 90 95 100

cag tta gcg cag cat att atc cag cct gct gag gtt gat ccc acg cat 451
 Gln Leu Ala Gln His Ile Ile Gln Pro Ala Glu Val Asp Thr Thr His
 105 110 115

agt tct gcg cat gat ttt gtt cgg gat tat ttt gcc acc cac aaa aac 499
 Ser Ser Ala His Asp Phe Val Arg Asp Tyr Phe Ala Thr His Lys Asn
 120 125 130

tac att gat tcg ctc gat cgc ctt gga gag gag ttg gca act gcc att 547
 Tyr Ile Asp Ser Leu Asp Arg Leu Gly Glu Glu Leu Ala Thr Ala Ile
 135 140 145

ggt cag ccg gga ctt cgg gtt act agg ctc gcg cag ttg ctt gat gcg 595
 Gly Gln Pro Gly Leu Arg Val Thr Arg Leu Ala Gln Leu Leu Asp Ala
 150 155 160 165

gag tac aac atc acg gtg cgt ttc cgg gcg ccg gat att act ggc cgg 643
 Glu Tyr Asn Ile Thr Val Arg Phe Arg Ala Pro Asp Ile Thr Gly Arg
 170 175 180

agg cac ttt gat ccc caa tcg cgt cag att ctg ctg ccg caa gat ctc 691
 Arg His Phe Asp Pro Gln Ser Arg Gln Ile Leu Leu Arg Gln Asp Leu
 185 190 195

agc gag gcg cag cag tgt ttc cag ttg gcg gag gaa ttg acg ttt ctt 739
 Ser Glu Ala Gln Gln Cys Phe Gln Leu Ala Glu Glu Leu Thr Phe Leu
 200 205 210

gct cat gca gag ctc ttg gat acc ctg acc aca gat caa ccg gat ctc 787
 Ala His Ala Glu Leu Leu Asp Thr Leu Thr Thr Asp Gln Pro Asp Leu
 215 220 225

cct tct gag gca gct atc cgc ctg gct aag gtg ggt ctc tcc caa tat 835
 Pro Ser Glu Ala Ala Ile Arg Leu Ala Lys Val Gly Leu Ser Gln Tyr
 230 235 240 245

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ttc gcg gct gct gtt gtc atg ccg tac acc cgc ttt ttg gaa ttc gcc 883
Phe Ala Ala Ala Val Met Pro Tyr Thr Arg Phe Leu Glu Phe Ala
      250      255      260

cag gat aag cac tat gac atc gag ttg atc tct gag gcg ttt gga gtg 931
Gln Asp Lys His Tyr Asp Ile Glu Leu Ile Ser Glu Ala Phe Gly Val
      265      270      275

tct ttc gag tct gca tgc cac cgc ctg tct act ctg cag cgt tcg ggg 979
Ser Phe Glu Ser Ala Cys His Arg Leu Ser Thr Leu Gln Arg Ser Gly
      280      285      290

gcg tca ggg gtg ccg ttt ttc ttt gtg cgc tcg gat cgt gca gga 1024
Ala Ser Gly Val Pro Phe Phe Phe Val Arg Ser Asp Arg Ala Gly
      295      300      305

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<210> 1098

<211> 308

<212> PRT

<213> Corynebacterium glutamicum

<400> 1098

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Met Ser Lys Leu Tyr Ala Gly Ala Arg Ile Asn Ala Leu Arg Arg Thr
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His Gln Leu Thr Gln Ser Ala Leu Ala Asp Lys Leu Asp Leu Ser Thr
      20           25           30

Ser Tyr Leu Asn Gln Leu Glu Asn Asp Gly Arg Pro Leu Thr Ala Thr
      35           40           45

Val Leu Leu Gln Leu Met Lys Val Phe Asp Val Glu Ala Ser Tyr Phe
      50           55           60

Ser Pro Asp Arg Gly Thr Ala Thr Ala Thr Arg Leu Ala Glu Thr Leu
      65           70           75           80

Ala Met Asn Gln Gly Pro Thr Met Ser Met Asp Asp Leu Leu Asp Phe
      85           90           95

Ala Asp Arg Phe Pro Gln Leu Ala Gln His Ile Ile Gln Pro Ala Glu
      100          105          110

Val Asp Pro Thr His Ser Ser Ala His Asp Phe Val Arg Asp Tyr Phe
      115          120          125

Ala Thr His Lys Asn Tyr Ile Asp Ser Leu Asp Arg Leu Gly Glu Glu
      130          135          140

Leu Ala Thr Ala Ile Gly Gln Pro Gly Leu Arg Val Thr Arg Leu Ala
      145          150          155          160

Gln Leu Leu Asp Ala Glu Tyr Asn Ile Thr Val Arg Phe Arg Ala Pro
      165          170          175

Asp Ile Thr Gly Arg Arg His Phe Asp Pro Gln Ser Arg Gln Ile Leu
      180          185          190

Leu Arg Gln Asp Leu Ser Glu Ala Gln Gln Cys Phe Gln Leu Ala Glu
      195          200          205

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Glu Leu Thr Phe Leu Ala His Ala Glu Leu Leu Asp Thr Leu Thr Thr
 210 215 220

Asp Gln Pro Asp Leu Pro Ser Glu Ala Ala Ile Arg Leu Ala Lys Val
 225 230 235 240

Gly Leu Ser Gln Tyr Phe Ala Ala Val Val Met Pro Tyr Thr Arg
 245 250 255

Phe Leu Glu Phe Ala Gln Asp Lys His Tyr Asp Ile Glu Leu Ile Ser
 260 265 270

Glu Ala Phe Gly Val Ser Phe Glu Ser Ala Cys His Arg Leu Ser Thr
 275 280 285

Leu Gln Arg Ser Gly Ala Ser Gly Val Pro Phe Phe Phe Val Arg Ser
 290 295 300

Asp Arg Ala Gly
 305

<210> 1099
 <211> 515
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(492)
 <223> RXN02339

<400> 1099
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 Pro Thr Asp Asn Leu Phe Ser Tyr Pro Ala Gln Arg Tyr Asp Leu Leu
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aca ctt gcc ttt gaa gtt agg att ggg gac atg gtt caa att aat gac 96
 Thr Leu Ala Phe Glu Val Arg Ile Gly Asp Met Val Gln Ile Asn Asp
 20 25 30

atg ctt gcc cct cct cca gta aaa ctt ccg gaa gat cct gcc ctc ggc 144
 Met Leu Ala Pro Pro Pro Val Lys Leu Pro Glu Asp Pro Ala Leu Gly
 35 40 45

gcc gat cca act ttg acc tcg aca gcg att gcg cat cct gac agc cca 192
 Ala Asp Pro Thr Leu Thr Ser Thr Ala Ile Ala His Pro Asp Ser Pro
 50 55 60

ttg gtg tgg gcg tac cga gct gaa aat ctt atc aaa tct gca tca aat 240
 Leu Val Trp Ala Tyr Arg Ala Glu Asn Leu Ile Lys Ser Ala Ser Asn
 65 70 75 80

gat gaa gag aag att cag gcc tac gct ttt gcg cgc acg ggt tac cac 288
 Asp Glu Glu Lys Ile Gln Ala Tyr Ala Phe Ala Arg Thr Gly Tyr His
 85 90 95

cgc agt ctc gat cgt ctg cgt gcc aat ggt tgg aag ggt tgg ggt cct 336
 Arg Ser Leu Asp Arg Leu Arg Ala Asn Gly Trp Lys Gly Trp Gly Pro
 100 105 110

gtc ccc ttc tct cat gag cca aac cag gga gtg ttg cgg gct atc gct 384
 Val Pro Phe Ser His Glu Pro Asn Gln Gly Val Leu Arg Ala Ile Ala
 115 120

tcc cta gct ctt gct gcg aag ctg att ggt gag gac aac gaa tac gat 432
 Ser Leu Ala Leu Ala Ala Lys Leu Ile Gly Glu Asp Asn Glu Tyr Asp
 130 135 140

cgt tgc cgc cag atg ctc tct gat gcg gat cca gag tcc gtc gca gtc 480
 Arg Cys Arg Gln Met Leu Ser Asp Ala Asp Pro Glu Ser Val Ala Val
 145 150 155 160

cta ctc gac aaa taaaccacca aaaataaaac aat 515
 Leu Leu Asp Lys

<210> 1100

<211> 164

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1100

Pro Thr Asp Asn Leu Phe Ser Tyr Pro Ala Gln Arg Tyr Asp Leu Leu
 1 5 10 15

Thr Leu Ala Phe Glu Val Arg Ile Gly Asp Met Val Gln Ile Asn Asp
 20 25 30

Met Leu Ala Pro Pro Pro Val Lys Leu Pro Glu Asp Pro Ala Leu Gly
 35 40 45

Ala Asp Pro Thr Leu Thr Ser Thr Ala Ile Ala His Pro Asp Ser Pro
 50 55 60

Leu Val Trp Ala Tyr Arg Ala Glu Asn Leu Ile Lys Ser Ala Ser Asn
 65 70 75 80

Asp Glu Glu Lys Ile Gln Ala Tyr Ala Phe Ala Arg Thr Gly Tyr His
 85 90 95

Arg Ser Leu Asp Arg Leu Arg Ala Asn Gly Trp Lys Gly Trp Gly Pro
 100 105 110

Val Pro Phe Ser His Glu Pro Asn Gln Gly Val Leu Arg Ala Ile Ala
 115 120 125

Ser Leu Ala Leu Ala Ala Lys Leu Ile Gly Glu Asp Asn Glu Tyr Asp
 130 135 140

Arg Cys Arg Gln Met Leu Ser Asp Ala Asp Pro Glu Ser Val Ala Val
 145 150 155 160

Leu Leu Asp Lys

<210> 1101

<211> 515

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(492)

<223> FRXA02339

<400> 1101

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ccc acc gac aac ctc ttt tca tat cct gca caa cgc tat gat ctt ctc 48
Pro Thr Asp Asn Leu Phe Ser Tyr Pro Ala Gln Arg Tyr Asp Leu Leu
      1              5              10              15

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```

aca ctt gcc ttt gaa gtt agg att ggg gac atg gtt caa att aat gac 96
Thr Leu Ala Phe Glu Val Arg Ile Gly Asp Met Val Gln Ile Asn Asp
      20              25              30

```

```

atg ctt gcc cct cct cca gta aaa ctt cgg gaa gat cct gcc ctc ggc 144
Met Leu Ala Pro Pro Pro Val Lys Leu Pro Glu Asp Pro Ala Leu Gly
      35              40              45

```

```

gcc gat cca act ttg acc tcg aca gcg att gcg cat cct gac agc cca 192
Ala Asp Pro Thr Leu Thr Ser Thr Ala Ile Ala His Pro Asp Ser Pro
      50              55              60

```

```

ttg gtg tgg gcg tac cga gct gaa aat ctt atc aaa tct gca tca aat 240
Leu Val Trp Ala Tyr Arg Ala Glu Asn Leu Ile Lys Ser Ala Ser Asn
      65              70              75              80

```

```

gat gaa gag aag att cag gcc tac gct ttt gcg cgc acg ggt tac cac 288
Asp Glu Glu Lys Ile Gln Ala Tyr Ala Phe Ala Arg Thr Gly Tyr His
      85              90              95

```

```

cgc agt ctc gat cgt ctg cgt gcc aat ggt tgg aag ggt tgg ggt cct 336
Arg Ser Leu Asp Arg Leu Arg Ala Asn Gly Trp Lys Gly Trp Gly Pro
      100             105             110

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```

gtc ccc ttc tct cat gag cca aac cag gga gtg ttg cgg gct atc gct 384
Val Pro Phe Ser His Glu Pro Asn Gln Gly Val Leu Arg Ala Ile Ala
      115             120             125

```

```

tcc cta gct ctt gct gcg aag ctg att ggt gag gac aac gaa tac gat 432
Ser Leu Ala Leu Ala Ala Lys Leu Ile Gly Glu Asp Asn Glu Tyr Asp
      130             135             140

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cgt tgc cgc cag atg ctc tct gat gcg gat cca gag tcc gtc gca gtc 480
Arg Cys Arg Gln Met Leu Ser Asp Ala Asp Pro Glu Ser Val Ala Val
      145             150             155             160

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cta ctc gac aaa taaaccacca aaaataaaac aat 515
Leu Leu Asp Lys

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<210> 1102

<211> 164

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1102

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Pro Thr Asp Asn Leu Phe Ser Tyr Pro Ala Gln Arg Tyr Asp Leu Leu
      1              5              10              15

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Thr Leu Ala Phe Glu Val Arg Ile Gly Asp Met Val Gln Ile Asn Asp
20 25 30

Met Leu Ala Pro Pro Pro Val Lys Leu Pro Glu Asp Pro Ala Leu Gly
35 40 45

Ala Asp Pro Thr Leu Thr Ser Thr Ala Ile Ala His Pro Asp Ser Pro
50 55 60

Leu Val Trp Ala Tyr Arg Ala Glu Asn Leu Ile Lys Ser Ala Ser Asn
65 70 75 80

Asp Glu Glu Lys Ile Gln Ala Tyr Ala Phe Ala Arg Thr Gly Tyr His
85 90 95

Arg Ser Leu Asp Arg Leu Arg Ala Asn Gly Trp Lys Gly Trp Gly Pro
100 105 110

Val Pro Phe Ser His Glu Pro Asn Gln Gly Val Leu Arg Ala Ile Ala
115 120 125

Ser Leu Ala Leu Ala Ala Lys Leu Ile Gly Glu Asp Asn Glu Tyr Asp
130 135 140

Arg Cys Arg Gln Met Leu Ser Asp Ala Asp Pro Glu Ser Val Ala Val
145 150 155 160

Leu Leu Asp Lys

<210> 1103

<211> 1188

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1165)

<223> RXN02340

<400> 1103

aaaacgtgtc taaaaattca gttttttattg ctgctgatca cctcttgaag aactcaaccc 60

aaaagtgcct caagttatga gaaagtgaat tccaacaccc atg aaa aag agc atc 115
Met Lys Lys Ser Ile
1 5

ggt gta ttt gaa gtc gaa ggc ggc tcc gac aag cac ttc gac ggt cac 163
Val Val Phe Glu Val Glu Gly Gly Ser Asp Lys His Phe Asp Gly His
10 15 20

cgt aaa gac acc atg cct atc gtc aac tcc ata aat gat gct ggc tgg 211
Arg Lys Asp Thr Met Pro Ile Val Asn Ser Ile Asn Asp Ala Gly Trp
25 30 35

cag gca gag gtt gtg tac tac cgc cca gag tgg acc gaa ggt ctc ttt 259
Gln Ala Glu Val Val Tyr Tyr Arg Pro Glu Trp Thr Glu Gly Leu Phe
40 45 50

gag tac gta tct gaa aac ttc gac ggc tac atc tca cgt gtc aac cca	307
Glu Tyr Val Ser Glu Asn Phe Asp Gly Tyr Ile Ser Arg Val Asn Pro	
55 60 65	
ggc aac atc cca ggc ggc gag cgc ggc tac ttt gac ctg ctc acc cgc	355
Gly Asn Ile Pro Gly Gly Glu Arg Gly Tyr Phe Asp Leu Leu Thr Arg	
70 75 80 85	
ctg tcc gaa gca ggg ctc gtg ggc atg tcc acc cct gag gaa atg atg	403
Leu Ser Glu Ala Gly Leu Val Gly Met Ser Thr Pro Glu Glu Met Met	
90 95 100	
gca tac ggc gcg aaa gat gcg ctg gtc aag cta tcc caa acc gac ctg	451
Ala Tyr Gly Ala Lys Asp Ala Leu Val Lys Leu Ser Gln Thr Asp Leu	
105 110 115	
gtg cca tcc gac acc gag gcg tac tac gac gtg gag acc ttc cac aag	499
Val Pro Ser Asp Thr Glu Ala Tyr Tyr Asp Val Glu Thr Phe His Lys	
120 125 130	
gtt ttc cca acc tcc ctg tcc ttc ggt gag cgc gtg ctc aag caa aac	547
Val Phe Pro Thr Ser Leu Ser Phe Gly Glu Arg Val Leu Lys Gln Asn	
135 140 145	
cgt ggc tcc acc ggc tcc ggc att tgg cgc gtc cag ttg gta gac aag	595
Arg Gly Ser Thr Gly Ser Gly Ile Trp Arg Val Gln Leu Val Asp Lys	
150 155 160 165	
gaa ctg gct gca tcc atc gag cca ggc acc gca ctg cca ttg gac act	643
Glu Leu Ala Ala Ser Ile Glu Pro Gly Thr Ala Leu Pro Leu Asp Thr	
170 175 180	
gaa atc aag tgc acc gaa gca gtc gac aac cac act gaa gtc cgc aag	691
Glu Ile Lys Cys Thr Glu Ala Val Asp Asn His Thr Glu Val Arg Lys	
185 190 195	
ctc ggc gag ttc atg gat ttc tgt gac cag tac atc atc ggc gac aac	739
Leu Gly Glu Phe Met Asp Phe Cys Asp Gln Tyr Ile Ile Gly Asp Asn	
200 205 210	
ggc atg ctc gtt gat atg cgt ttc atg cca cgc atc gtc gaa ggc gaa	787
Gly Met Leu Val Asp Met Arg Phe Met Pro Arg Ile Val Glu Gly Glu	
215 220 225	
atc cgc atc ctt ctc gtc gga cca cac cca gtg ttc gtc gtg cac aag	835
Ile Arg Ile Leu Leu Val Gly Pro His Pro Val Phe Val Val His Lys	
230 235 240 245	
aag cca gca gaa ggc ggc gac aac ttc tcc gca acc ctg ttc tcc ggc	883
Lys Pro Ala Glu Gly Gly Asp Asn Phe Ser Ala Thr Leu Phe Ser Gly	
250 255 260	
gcg aag tac acc tac gac aag cca gag cag tgg cag gaa ctg att gac	931
Ala Lys Tyr Thr Tyr Asp Lys Pro Glu Gln Trp Gln Glu Leu Ile Asp	
265 270 275	
ctc ttc gca gac gct cgc cca gtc atc gca gaa aag ctc ggc ggc gac	979
Leu Phe Ala Asp Ala Arg Pro Val Ile Ala Glu Lys Leu Gly Gly Asp	
280 285 290	
aac atc cca ttg atc tgg acc gca gac ttc atg ctc ggc gat gtc gtt	1027

Asn Ile Pro Leu Ile Trp Thr Ala Asp Phe Met Leu Gly Asp Val Val
 295 300 305
 gac ggc aag gac acc tac gtg ctc ggt gaa atc aac tgc tcc tgc gtc 1075
 Asp Gly Lys Asp Thr Tyr Val Leu Gly Glu Ile Asn Cys Ser Cys Val
 310 315 320 325
 ggc ttc acc tcc gag ctg gac atg ggc atc cag cag ctt gtg gca tca 1123
 Gly Phe Thr Ser Glu Leu Asp Met Gly Ile Gln Gln Leu Val Ala Ser
 330 335 340
 gag gcc atc aag cgc atc gag gaa ttc gcg cag ctt act gtt 1165
 Glu Ala Ile Lys Arg Ile Glu Glu Phe Ala Gln Leu Thr Val
 345 350 355
 taaaactttg cttctcgacg tct 1188

<210> 1104

<211> 355

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1104

Met Lys Lys Ser Ile Val Val Phe Glu Val Glu Gly Gly Ser Asp Lys
 1 5 10 15
 His Phe Asp Gly His Arg Lys Asp Thr Met Pro Ile Val Asn Ser Ile
 20 25 30
 Asn Asp Ala Gly Trp Gln Ala Glu Val Val Tyr Tyr Arg Pro Glu Trp
 35 40 45
 Thr Glu Gly Leu Phe Glu Tyr Val Ser Glu Asn Phe Asp Gly Tyr Ile
 50 55 60
 Ser Arg Val Asn Pro Gly Asn Ile Pro Gly Gly Glu Arg Gly Tyr Phe
 65 70 75 80
 Asp Leu Leu Thr Arg Leu Ser Glu Ala Gly Leu Val Gly Met Ser Thr
 85 90 95
 Pro Glu Glu Met Met Ala Tyr Gly Ala Lys Asp Ala Leu Val Lys Leu
 100 105 110
 Ser Gln Thr Asp Leu Val Pro Ser Asp Thr Glu Ala Tyr Tyr Asp Val
 115 120 125
 Glu Thr Phe His Lys Val Phe Pro Thr Ser Leu Ser Phe Gly Glu Arg
 130 135 140
 Val Leu Lys Gln Asn Arg Gly Ser Thr Gly Ser Gly Ile Trp Arg Val
 145 150 155 160
 Gln Leu Val Asp Lys Glu Leu Ala Ala Ser Ile Glu Pro Gly Thr Ala
 165 170 175
 Leu Pro Leu Asp Thr Glu Ile Lys Cys Thr Glu Ala Val Asp Asn His
 180 185 190
 Thr Glu Val Arg Lys Leu Gly Glu Phe Met Asp Phe Cys Asp Gln Tyr

195 200 205

Ile Ile Gly Asp Asn Gly Met Leu Val Asp Met Arg Phe Met Pro Arg
210 215 220

Ile Val Glu Gly Glu Ile Arg Ile Leu Leu Val Gly Pro His Pro Val
225 230 235 240

Phe Val Val His Lys Lys Pro Ala Glu Gly Gly Asp Asn Phe Ser Ala
245 250 255

Thr Leu Phe Ser Gly Ala Lys Tyr Thr Tyr Asp Lys Pro Glu Gln Trp
260 265 270

Gln Glu Leu Ile Asp Leu Phe Ala Asp Ala Arg Pro Val Ile Ala Glu
275 280 285

Lys Leu Gly Gly Asp Asn Ile Pro Leu Ile Trp Thr Ala Asp Phe Met
290 295 300

Leu Gly Asp Val Val Asp Gly Lys Asp Thr Tyr Val Leu Gly Glu Ile
305 310 315 320

Asn Cys Ser Cys Val Gly Phe Thr Ser Glu Leu Asp Met Gly Ile Gln
325 330 335

Gln Leu Val Ala Ser Glu Ala Ile Lys Arg Ile Glu Glu Phe Ala Gln
340 345 350

Leu Thr Val
355

<210> 1105
<211> 580
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (101)..(580)
<223> FRXA02338

<400> 1105
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aaaagtgcct caagttatga gaaagtgaat tccaacaccc atg aaa aag agc atc 115
Met Lys Lys Ser Ile
1 5
gtt gta ttt gaa gtc gaa ggc ggc tcc gac aag cac ttc gac ggt cac 163
Val Val Phe Glu Val Glu Gly Gly Ser Asp Lys His Phe Asp Gly His
10 15 20
cgt aaa gac acc atg cct atc gtc aac tcc ata aat gat gct ggc tgg 211
Arg Lys Asp Thr Met Pro Ile Val Asn Ser Ile Asn Asp Ala Gly Trp
25 30 35
cag gca gag gtt gtg tac tac cgc cca gag tgg acc gaa ggt ctc ttt 259
Gln Ala Glu Val Val Tyr Tyr Arg Pro Glu Trp Thr Glu Gly Leu Phe
40 45 50

gag tac gta tct gaa aac ttc gac ggc tac atc tca cgt gtc aac cca 307
 Glu Tyr Val Ser Glu Asn Phe Asp Gly Tyr Ile Ser Arg Val Asn Pro
 55 60 65

ggc aac atc cca ggc ggc gag cgc ggc tac ttt gac ctg ctc acc cgc 355
 Gly Asn Ile Pro Gly Gly Glu Arg Gly Tyr Phe Asp Leu Leu Thr Arg
 70 75 80 85

ctg tcc gaa gca ggg ctc gtg ggc atg tcc acc cct gag gaa atg atg 403
 Leu Ser Glu Ala Gly Leu Val Gly Met Ser Thr Pro Glu Glu Met Met
 90 95 100

gca tac ggc gcg aaa gat gcg ctg gtc aag cta tcc caa acc gac ctg 451
 Ala Tyr Gly Ala Lys Asp Ala Leu Val Lys Leu Ser Gln Thr Asp Leu
 105 110 115

gtg cca tcc gac acc gag gcg tac tac gac gtg gag acc ttc cac aag 499
 Val Pro Ser Asp Thr Glu Ala Tyr Tyr Asp Val Glu Thr Phe His Lys
 120 125 130

gtt ttc cca acc tcc ctg tcc ttc ggt gaa gcg cgt gct caa gca aaa 547
 Val Phe Pro Thr Ser Leu Ser Phe Gly Glu Ala Arg Ala Gln Ala Lys
 135 140 145

acc tgg ctt cac cgg ctt cgg cat ttg gcg cgt 580
 Thr Trp Leu His Arg Leu Pro His Leu Ala Arg
 150 155 160

<210> 1106
 <211> 160
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1106
 Met Lys Lys Ser Ile Val Val Phe Glu Val Glu Gly Gly Ser Asp Lys
 1 5 10 15

His Phe Asp Gly His Arg Lys Asp Thr Met Pro Ile Val Asn Ser Ile
 20 25 30

Asn Asp Ala Gly Trp Gln Ala Glu Val Val Tyr Tyr Arg Pro Glu Trp
 35 40 45

Thr Glu Gly Leu Phe Glu Tyr Val Ser Glu Asn Phe Asp Gly Tyr Ile
 50 55 60

Ser Arg Val Asn Pro Gly Asn Ile Pro Gly Gly Glu Arg Gly Tyr Phe
 65 70 75 80

Asp Leu Leu Thr Arg Leu Ser Glu Ala Gly Leu Val Gly Met Ser Thr
 85 90 95

Pro Glu Glu Met Met Ala Tyr Gly Ala Lys Asp Ala Leu Val Lys Leu
 100 105 110

Ser Gln Thr Asp Leu Val Pro Ser Asp Thr Glu Ala Tyr Tyr Asp Val
 115 120 125

Glu Thr Phe His Lys Val Phe Pro Thr Ser Leu Ser Phe Gly Glu Ala

130

135

140

Arg Ala Gln Ala Lys Thr Trp Leu His Arg Leu Pro His Leu Ala Arg
 145 150 155 160

<210> 1107

<211> 662

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(639)

<223> FRXA02340

<400> 1107

gag cgc gtg ctc aag caa aac cgt ggc tcc acc ggc tcc ggc att tgg 48
 Glu Arg Val Leu Lys Gln Asn Arg Gly Ser Thr Gly Ser Gly Ile Trp
 1 5 10 15

cgc gtc cag ttg gta gac aag gaa ctg gct gca tcc atc gag cca ggc 96
 Arg Val Gln Leu Val Asp Lys Glu Leu Ala Ala Ser Ile Glu Pro Gly
 20 25 30

acc gca ctg cca ttg gac act gaa atc aag tgc acc gaa gca gtc gac 144
 Thr Ala Leu Pro Leu Asp Thr Glu Ile Lys Cys Thr Glu Ala Val Asp
 35 40 45

aac cac act gaa gtc cgc aag ctc ggc gag ttc atg gat ttc tgt gac 192
 Asn His Thr Glu Val Arg Lys Leu Gly Glu Phe Met Asp Phe Cys Asp
 50 55 60

cag tac atc atc ggc gac aac ggc atg ctc gtt gat atg cgt ttc atg 240
 Gln Tyr Ile Ile Gly Asp Asn Gly Met Leu Val Asp Met Arg Phe Met
 65 70 75 80

cca cgc atc gtc gaa ggc gaa atc cgc atc ctt ctc gtc gga cca cac 288
 Pro Arg Ile Val Glu Gly Glu Ile Arg Ile Leu Leu Val Gly Pro His
 85 90 95

cca gtg ttc gtc gtg cac aag aag cca gca gaa ggc ggc gac aac ttc 336
 Pro Val Phe Val Val His Lys Lys Pro Ala Glu Gly Gly Asp Asn Phe
 100 105 110

tcc gca acc ctg ttc tcc ggc gcg aag tac acc tac gac aag cca gag 384
 Ser Ala Thr Leu Phe Ser Gly Ala Lys Tyr Thr Tyr Asp Lys Pro Glu
 115 120 125

cag tgg cag gaa ctg att gac ctc ttc gca gac gct cgc cca gtc atc 432
 Gln Trp Gln Glu Leu Ile Asp Leu Phe Ala Asp Ala Arg Pro Val Ile
 130 135 140

gca gaa aag ctc ggc ggc gac aac atc cca ttg atc tgg acc gca gac 480
 Ala Glu Lys Leu Gly Gly Asp Asn Ile Pro Leu Ile Trp Thr Ala Asp
 145 150 155 160

ttc atg ctc ggc gat gtc gtt gac ggc aag gac acc tac gtg etc ggt 528

Phe Met Leu Gly Asp Val Val Asp Gly Lys Asp Thr Tyr Val Leu Gly
 165 170 175
 gaa atc aac tgc tcc tgc gtc ggc ttc acc tcc gag ctg gac atg ggc 576
 Glu Ile Asn Cys Ser Cys Val Gly Phe Thr Ser Glu Leu Asp Met Gly
 180 185 190
 atc cag cag ctt gtg gca tca gag gcc atc aag cgc atc gag gaa ttc 624
 Ile Gln Gln Leu Val Ala Ser Glu Ala Ile Lys Arg Ile Glu Glu Phe
 195 200 205
 gcg cag ctt act gtt taaaactttg cttctcgacg tct 662
 Ala Gln Leu Thr Val
 210

<210> 1108

<211> 213

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1108

Glu Arg Val Leu Lys Gln Asn Arg Gly Ser Thr Gly Ser Gly Ile Trp
 1 5 10 15
 Arg Val Gln Leu Val Asp Lys Glu Leu Ala Ala Ser Ile Glu Pro Gly
 20 25 30
 Thr Ala Leu Pro Leu Asp Thr Glu Ile Lys Cys Thr Glu Ala Val Asp
 35 40 45
 Asn His Thr Glu Val Arg Lys Leu Gly Glu Phe Met Asp Phe Cys Asp
 50 55 60
 Gln Tyr Ile Ile Gly Asp Asn Gly Met Leu Val Asp Met Arg Phe Met
 65 70 75 80
 Pro Arg Ile Val Glu Gly Glu Ile Arg Ile Leu Leu Val Gly Pro His
 85 90 95
 Pro Val Phe Val Val His Lys Lys Pro Ala Glu Gly Gly Asp Asn Phe
 100 105 110
 Ser Ala Thr Leu Phe Ser Gly Ala Lys Tyr Thr Tyr Asp Lys Pro Glu
 115 120 125
 Gln Trp Gln Glu Leu Ile Asp Leu Phe Ala Asp Ala Arg Pro Val Ile
 130 135 140
 Ala Glu Lys Leu Gly Gly Asp Asn Ile Pro Leu Ile Trp Thr Ala Asp
 145 150 155 160
 Phe Met Leu Gly Asp Val Val Asp Gly Lys Asp Thr Tyr Val Leu Gly
 165 170 175
 Glu Ile Asn Cys Ser Cys Val Gly Phe Thr Ser Glu Leu Asp Met Gly
 180 185 190
 Ile Gln Gln Leu Val Ala Ser Glu Ala Ile Lys Arg Ile Glu Glu Phe
 195 200 205

Ala Gln Leu Thr Val
210

<210> 1109

<211> 609

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(586)

<223> RXN02341

<400> 1109

cgcgactggc ggagaaattc gtgttcgcga tgcttcgggc accgttcaca cctcaacgc 60

cggtgaaatt acgcaccttc gcctgcagta aggtgacggt atg ggg aat tca ctt 115
Met Gly Asn Ser Leu
1 5

gag aaa cat att gca gag gga gac cgg atc cac gtc gat ctg aca tct 163
Glu Lys His Ile Ala Glu Gly Asp Arg Ile His Val Asp Leu Thr Ser
10 15 20

cct tta tcc gca atg ttg ttc ccc att ttt gaa ctc att gtg att act 211
Pro Leu Ser Ala Met Leu Phe Pro Ile Phe Glu Leu Ile Val Ile Thr
25 30 35

gga atc tgt tgg atg ggc atc ggc ttt ttg gat cag ctt cca gga atc 259
Gly Ile Cys Trp Met Gly Ile Gly Phe Leu Asp Gln Leu Pro Gly Ile
40 45 50

gat ggc acc aac ccc gcc gat agc ttc ccc gaa ggc acc cgc aat ctt 307
Asp Gly Thr Arg Asn Pro Ala Asp Ser Phe Pro Glu Gly Thr Arg Asn Leu
55 60 65

cta gtg ggt gtg tgg gca gta ctt gct gca tgg cgt ttc ggt ctt cct 355
Leu Val Gly Val Trp Ala Val Leu Ala Ala Trp Arg Phe Gly Leu Pro
70 75 80 85

tta ata agg caa cgt cga ctc cgc gtg atc ttg agc gac cgc aaa ctg 403
Leu Ile Arg Gln Arg Arg Leu Arg Val Ile Leu Ser Asp Arg Lys Leu
90 95 100

ctg gtc cga cgc ggc ggt ctg cgc acc ggg ttc gat tcc att cca ctg 451
Leu Val Arg Arg Ala Gly Leu Arg Thr Gly Phe Asp Ser Ile Pro Leu
105 110 115

agc tac att cag cga gtc caa cgt cgg cga aac acc ctg gtc tta ggt 499
Ser Tyr Ile Gln Arg Val Gln Arg Arg Asn Thr Leu Val Leu Gly
120 125 130

gtt ggt gga cac cac cga ccc tat gta atc aac cag gtt ccc aag gct 547
Val Gly Gly His His Arg Pro Tyr Val Ile Asn Gln Val Pro Lys Ala
135 140 145

cga aaa gtg gaa gcg ctg ctc aaa gat ctt aca ttt tgg tgaagcggt 596
Arg Lys Val Glu Ala Leu Leu Lys Asp Leu Thr Phe Trp
150 155 160

atagtttagga ctt

609

<210> 1110

<211> 162

<212> PRT

<213> Corynebacterium glutamicum

<400> 1110

Met	Gly	Asn	Ser	Leu	Glu	Lys	His	Ile	Ala	Glu	Gly	Asp	Arg	Ile	His
1				5					10					15	

Val	Asp	Leu	Thr	Ser	Pro	Leu	Ser	Ala	Met	Leu	Phe	Pro	Ile	Phe	Glu
			20					25					30		

Leu	Ile	Val	Ile	Thr	Gly	Ile	Cys	Trp	Met	Gly	Ile	Gly	Phe	Leu	Asp
		35					40					45			

Gln	Leu	Pro	Gly	Ile	Asp	Gly	Thr	Asn	Pro	Ala	Asp	Ser	Phe	Pro	Glu
	50					55					60				

Gly	Thr	Arg	Asn	Leu	Leu	Val	Gly	Val	Trp	Ala	Val	Leu	Ala	Ala	Trp
	65				70					75					80

Arg	Phe	Gly	Leu	Pro	Leu	Ile	Arg	Gln	Arg	Arg	Leu	Arg	Val	Ile	Leu
				85					90					95	

Ser	Asp	Arg	Lys	Leu	Leu	Val	Arg	Arg	Ala	Gly	Leu	Arg	Thr	Gly	Phe
			100					105					110		

Asp	Ser	Ile	Pro	Leu	Ser	Tyr	Ile	Gln	Arg	Val	Gln	Arg	Arg	Arg	Asn
		115					120					125			

Thr	Leu	Val	Leu	Gly	Val	Gly	Gly	His	His	Arg	Pro	Tyr	Val	Ile	Asn
	130					135					140				

Gln	Val	Pro	Lys	Ala	Arg	Lys	Val	Glu	Ala	Leu	Leu	Lys	Asp	Leu	Thr
	145				150					155				160	

Phe Trp

<210> 1111

<211> 511

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(511)

<223> FRXA02341

<400> 1111

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cggtgaaatt	acgcaccttc	gcctgcagta	agggtgacgt	atg	ggg	aat	tca	ctt	115
				Met	Gly	Asn	Ser	Leu	
				1				5	

gag aaa cat att gca gag gga gac cgg atc cac gtc gat ctg aca tct 163

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Glu Lys His Ile Ala Glu Gly Asp Arg Ile His Val Asp Leu Thr Ser
      10      15      20
cct tta tcc gca atg ttg ttc ccc att ttt gaa ctc att gtg att act 211
Pro Leu Ser Ala Met Leu Phe Pro Ile Phe Glu Leu Ile Val Ile Thr
      25      30      35

gga atc tgt tgg atg ggc atc ggc ttt ttg gat cag ctt cca gga atc 259
Gly Ile Cys Trp Met Gly Ile Gly Phe Leu Asp Gln Leu Pro Gly Ile
      40      45      50

gat ggc acc aac ccc gcc gat agc ttc ccc gaa ggc acc cgc aat ctt 307
Asp Gly Thr Asn Pro Ala Asp Ser Phe Pro Glu Gly Thr Arg Asn Leu
      55      60      65

cta gtg ggt gtg tgg gca gta ctt gct gca tgg cgt ttc ggt ctt cct 355
Leu Val Gly Val Trp Ala Val Leu Ala Ala Trp Arg Phe Gly Leu Pro
      70      75      80      85

tta ata agg caa cgt cga ctc cgc gtg atc ttg agc gac cgc aaa ctg 403
Leu Ile Arg Gln Arg Arg Leu Arg Val Ile Leu Ser Asp Arg Lys Leu
      90      95      100

ctg gtc cga cgc gcg ggt ctg cgc acc ggg ttc gat tcc att cca ctg 451
Leu Val Arg Arg Ala Gly Leu Arg Thr Gly Phe Asp Ser Ile Pro Leu
      105      110      115

agc tac att cag cga gtc caa cgt cgg cga aac acc ctg gtc tta ggt 499
Ser Tyr Ile Gln Arg Val Gln Arg Arg Asn Thr Leu Val Leu Gly
      120      125      130

gtt ggt gga cac 511
Val Gly Gly His
      135

<210> 1112
<211> 137
<212> PRT
<213> Corynebacterium glutamicum

<400> 1112
Met Gly Asn Ser Leu Glu Lys His Ile Ala Glu Gly Asp Arg Ile His
  1      5      10      15

Val Asp Leu Thr Ser Pro Leu Ser Ala Met Leu Phe Pro Ile Phe Glu
      20      25      30

Leu Ile Val Ile Thr Gly Ile Cys Trp Met Gly Ile Gly Phe Leu Asp
      35      40      45

Gln Leu Pro Gly Ile Asp Gly Thr Asn Pro Ala Asp Ser Phe Pro Glu
      50      55      60

Gly Thr Arg Asn Leu Leu Val Gly Val Trp Ala Val Leu Ala Ala Trp
      65      70      75      80

Arg Phe Gly Leu Pro Leu Ile Arg Gln Arg Arg Leu Arg Val Ile Leu
      85      90      95

Ser Asp Arg Lys Leu Leu Val Arg Arg Ala Gly Leu Arg Thr Gly Phe

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100

105

110

Asp Ser Ile Pro Leu Ser Tyr Ile Gln Arg Val Gln Arg Arg Arg Asn
 115 120 125

Thr Leu Val Leu Gly Val Gly Gly His
 130 135

<210> 1113

<211> 2556

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2533)

<223> RXN02360

<400> 1113

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tttaaagaaa attcttctca attctaaggg tgaatatcca atg cgt ggt gac gtt 115
 Met Arg Gly Asp Val
 1 5

caa aaa ata acc aag gtt tat gac ggc aag cac cga acc ttg gaa atc 163
 Gln Lys Ile Thr Lys Val Tyr Asp Gly Lys His Arg Thr Leu Glu Ile
 10 15 20

cgc gtt tat caa cgc aat tac gac tgg act gaa aag caa tgt tca cgc 211
 Pro Val Tyr Gln Arg Asn Tyr Asp Trp Thr Glu Lys Gln Cys Ser Arg
 25 30 35

ctc ttt gat gac ctc agc gaa gtg gtc aaa gaa aac cac cgt caa cat 259
 Leu Phe Asp Asp Leu Ser Glu Val Val Lys Glu Asn His Arg Gln His
 40 45 50

ttt ttt gga gct gtg gtt ggt aag cct caa ggc agc tgg acc tgg gtt 307
 Phe Phe Gly Ala Val Val Gly Lys Pro Gln Gly Ser Trp Thr Trp Val
 55 60 65

gtc atc gat gga cag cag cgt ctt aca aca atc agc ttg ttc atg ctt 355
 Val Ile Asp Gly Gln Gln Arg Leu Thr Thr Ile Ser Leu Phe Met Leu
 70 75 80 85

gcg ctg gta cat tcc ttg cgc gca tct gaa gtt gaa gaa ggt gag ttt 403
 Ala Leu Val His Ser Leu Arg Ala Ser Glu Val Glu Glu Gly Glu Phe
 90 95 100

aat gct ggc tac aac att gat cta gcc aca ttg att gag gat gac tac 451
 Asn Ala Gly Tyr Asn Ile Asp Leu Ala Thr Leu Ile Glu Asp Asp Tyr
 105 110 115

ctc cga tcc ggc aat gag gga aac ctc aag ttc aag ctc aag cca gtt 499
 Leu Arg Ser Gly Asn Glu Gly Asn Leu Lys Phe Lys Leu Lys Pro Val
 120 125 130

aaa aac gat aat gag gct tat caa aag ctc ttc ggc cca gaa tct gaa 547
 Lys Asn Asp Asn Glu Ala Tyr Gln Lys Leu Phe Gly Pro Glu Ser Glu
 135 140 145

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Phe Ile Glu Ser Ser Asn Leu Thr Ala Asn Tyr Arg Tyr Phe Arg Asn	
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Val Leu Lys Ala Thr Asp Leu Thr Ala Ala Gln Leu Trp Glu Ala Ile	
170 175 180	
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Gln Arg Ile Phe Glu Ser Leu Asn Ser Thr Gly Leu Leu Ser Glu	
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Ala Asp Lys Val Arg Asn Leu Val Leu Met Asp Gln Glu Leu Lys Thr	
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Gln Glu Lys Leu Tyr Glu Gln Arg Trp Asn Pro Ile Glu Val Cys Val	
230 235 240 245	
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Lys Phe Asp Thr Asp Asn Phe Ile Arg Trp Tyr Leu Thr Leu Lys Thr	
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gcg cgc acc cca aga aag caa gat gtt tat gag gaa ttc aag aaa ttc	931
Ala Arg Thr Pro Arg Lys Gln Asp Val Tyr Glu Glu Phe Lys Lys Phe	
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Ile Arg Asn Ser Lys Leu Pro Val Glu Phe Ile Leu Asp Asp Met Tyr	
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Ile Ile Thr Glu Ser Asp Phe Leu Gly Val Leu Lys Val Leu Glu Ser	
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Tyr Leu Phe Arg Arg Phe Ala Val Gly Val Ala Ser Asn Ala Leu Ser	
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Lys Ile Phe Ser Thr Ala Tyr Ser Asp Ile Lys Lys Phe Trp Thr Pro	
375 380 385	

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 Phe Leu Arg Arg Val Phe Thr Gln Leu Gly Leu Glu Gln Glu Ala Leu
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 Val Phe Thr Leu Arg Pro Leu Ala Asn Asp Val Glu Pro Arg Asp Asp
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 Ile Pro Gln Leu Glu Glu Ala Glu Asn Leu Glu Gly Ala Asp Thr Glu
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 Val Ile Pro Leu Leu Ser Lys Leu Lys Glu Gln Leu Thr Ala Phe Ser
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 ccg gag aat cct caa gca gcc cta ggg ggc cta cct gtt cca gaa ttc 2371
 Pro Glu Asn Pro Gln Ala Ala Leu Gly Gly Leu Pro Val Glu Phe
 745 750 755
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 Leu Lys Gln Asn Val Ile Glu Gln Leu Ser Ala Glu His Ile Leu Ala
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 Val Leu Thr Gln His Phe Asn Ile Ala Ser Met Gly Asp Asp Tyr
 775 780 785
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<213> Corynebacterium glutamicum

<400> 1114

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Lys Gln Cys Ser Arg Leu Phe Asp Asp Leu Ser Glu Val Val Lys Glu

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Ser	Trp	Thr	Trp	Val	70		Ile	Asp	Gly	Gln	Gln	Arg	Leu	Thr	Thr
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Ser	Leu	Phe	Met	Leu	Ala	Leu	Val	His	Ser	Leu	Arg	Ala	Ser	Glu	Val
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Glu	Glu	Gly	Glu	Phe	Asn	Ala	Gly	Tyr	Asn	Ile	Asp	Leu	Ala	Thr	Leu
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Glu	Phe	Asp	Asp	Pro	Gln	Arg	Ile	Phe	Glu	Ser	Leu	Asn	Ser	Thr	Gly
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Gln	Glu	Leu	Lys	Thr	Gln	Glu	Lys	Leu	Tyr	Glu	Gln	Arg	Trp	Asn	Pro
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Pro	Val	Met	Gly	Asp	Val	Val	Leu	Pro	Phe	Leu	Leu	Pro	Val	Leu	Lys
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Asp	Ala	Lys	Asp	Gly	Ile	Ile	Thr	Glu	Ser	Asp	Phe	Leu	Gly	Val	Leu
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Lys	Val	Leu	Glu	Ser	Tyr	Leu	Phe	Arg	Arg	Phe	Ala	Val	Gly	Val	Ala
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 Lys Phe Trp Thr Pro Gly Gln Ser Tyr Ser Ser Leu Leu Ala Tyr Ile
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 405 410 415
 Arg Glu Asn Phe Ala Thr Lys Asn Phe Trp Asn Ile His Asn Glu Asn
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 Arg Arg Tyr Leu Phe Asp Cys Leu Glu Asn Ala Asp Ser Asn Asp Val
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 Arg Asp Ile Gln Thr Ser Leu Asp Glu Gly Ser Leu Ser Ile Glu His
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 Ile Met Pro Arg Ser Leu Asn Asp Gln Trp Arg Ala Glu Leu Gly Pro
 465 470 475 480
 Glu Tyr Ala Arg Ile His Glu Thr Trp Ile Asn Arg Ile Gly Asn Leu
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 Thr Ile Thr Gly Tyr Asn Ser Ala Tyr Ser Asn Ser Tyr Glu Arg
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 Lys Arg Thr Met Glu Asn Gly Phe Leu Val Ser Pro Tyr Arg Ile Asn
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 Asn Phe Ile Lys Lys Gln Lys His Trp Ser Glu Glu Gln Leu Ile Glu
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 580 585 590
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 Val Leu Lys Val Leu Asn Gln Ser Phe Arg Gln Glu Leu Ile Ala Leu
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 Ser Val Lys Ile Gly Phe Leu Arg Arg Val Phe Thr Gln Leu Gly Leu
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 675 680 685

Glu Pro Arg Asp Asp Glu Leu Glu Val Glu Val Glu Lys Lys Tyr Ser
 690 695 700
 Asp Leu Thr Lys Phe Ile Pro Gln Leu Glu Glu Ala Glu Asn Leu Glu
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 Gly Ala Asp Thr Glu Val Ile Pro Leu Leu Ser Lys Leu Lys Glu Gln
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 Met Arg Gly Asp Val
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 Gln Lys Ile Thr Lys Val Tyr Asp Gly Lys His Arg Thr Leu Glu Ile
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 Val Ile Asp Gly Gln Gln Arg Leu Thr Thr Ile Ser Leu Phe Met Leu
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Ala Leu Val His Ser Leu Arg Ala Ser Glu Val Glu Glu Gly Glu Phe	
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Asn Ala Gly Tyr Asn Ile Asp Leu Ala Thr Leu Ile Glu Asp Asp Tyr	
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Lys Asn Asp Asn Glu Ala Tyr Gln Lys Leu Phe Gly Pro Glu Ser Glu	
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Phe Ile Glu Ser Ser Asn Leu Thr Ala Asn Tyr Arg Tyr Phe Arg Asn	
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Val Leu Lys Ala Thr Asp Leu Thr Ala Ala Gln Leu Trp Glu Ala Ile	
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Glu Lys Leu Arg Val Met Tyr Leu Asp Leu Glu Glu Phe Asp Asp Pro	
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Ile Arg Asn Ser Lys Leu Pro Val Glu Phe Ile Leu Asp Asp Met Tyr	
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Cys	Leu	Ala	Thr	Ser	Asn	Asn	Ser	Asn	Ser	Ser	Leu	Arg	Glu	Ile	Asp	
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Phe	Leu	Arg	Arg	Val	Phe	Thr	Gln	Leu	Gly	Leu	Glu	Gln	Glu	Ala	Leu	
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Val	Phe	Thr	Leu	Arg	Pro	Leu	Ala	Asn	Asp	Val	Glu	Pro	Arg	Asp	Asp	
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Glu	Leu	Glu	Val	Glu	Val	Glu	Lys	Lys	Tyr	Ser	Asp	Leu	Thr	Lys	Phe	
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Ile	Pro	Gln	Leu	Glu	Glu	Ala	Glu	Asn	Leu	Glu	Gly	Ala	Asp	Thr	Glu	
	710				715					720					725	
gtt	att	cct	ctc	ctc	tca	aag	ctc	aag	gaa	caa	ctg	aca	gcc	ttt	agc	2323
Val	Ile	Pro	Leu	Leu	Ser	Lys	Leu	Lys	Glu	Gln	Leu	Thr	Ala	Phe	Ser	
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cgg	gag	aat	cct	caa	gca	gcc	cta	ggg	ggc	cta	cct	gtt	cca	gaa	ttc	2371
Pro	Glu	Asn	Pro	Gln	Ala	Ala	Leu	Gly	Gly	Leu	Pro	Val	Pro	Glu	Phe	
			745					750					755			
ctc	aaa	caa	aat	gtg	att	gaa	caa	cta	agc	gca	gag	cac	atc	ctt	gct	2419
Leu	Lys	Gln	Asn	Val	Ile	Glu	Gln	Leu	Ser	Ala	Glu	His	Ile	Leu	Ala	
		760					765					770				
gta	ctc	act	caa	cac	ttt	aat	atc	gca	tcc	atg	atg	ggg	gat	gac	tat	2467
Val	Leu	Thr	Gln	His	Phe	Asn	Ile									

810

<210> 1116

<211> 811

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1116

Met Arg Gly Asp Val Gln Lys Ile Thr Lys Val Tyr Asp Gly Lys His
1 5 10 15Arg Thr Leu Glu Ile Pro Val Tyr Gln Arg Asn Tyr Asp Trp Thr Glu
20 25 30Lys Gln Cys Ser Arg Leu Phe Asp Asp Leu Ser Glu Val Val Lys Glu
35 40 45Asn His Arg Gln His Phe Phe Gly Ala Val Val Gly Lys Pro Gln Gly
50 55 60Ser Trp Thr Trp Val Val Ile Asp Gly Gln Gln Arg Leu Thr Thr Ile
65 70 75 80Ser Leu Phe Met Leu Ala Leu Val His Ser Leu Arg Ala Ser Glu Val
85 90 95Glu Glu Gly Glu Phe Asn Ala Gly Tyr Asn Ile Asp Leu Ala Thr Leu
100 105 110Ile Glu Asp Asp Tyr Leu Arg Ser Gly Asn Glu Gly Asn Leu Lys Phe
115 120 125Lys Leu Lys Pro Val Lys Asn Asp Asn Glu Ala Tyr Gln Lys Leu Phe
130 135 140Gly Pro Glu Ser Glu Phe Ile Glu Ser Ser Asn Leu Thr Ala Asn Tyr
145 150 155 160Arg Tyr Phe Arg Asn Val Leu Lys Ala Thr Asp Leu Thr Ala Ala Gln
165 170 175Leu Trp Glu Ala Ile Glu Lys Leu Arg Val Met Tyr Leu Asp Leu Glu
180 185 190Glu Phe Asp Asp Pro Gln Arg Ile Phe Glu Ser Leu Asn Ser Thr Gly
195 200 205Leu Glu Leu Ser Glu Ala Asp Lys Val Arg Asn Leu Val Leu Met Asp
210 215 220Gln Glu Leu Lys Thr Gln Glu Lys Leu Tyr Glu Gln Arg Trp Asn Pro
225 230 235 240Ile Glu Val Cys Val Lys Phe Asp Thr Asp Asn Phe Ile Arg Trp Tyr
245 250 255Leu Thr Leu Lys Thr Ala Arg Thr Pro Arg Lys Gln Asp Val Tyr Glu
260 265 270

Glu Phe Lys Lys Phe Ile Arg Asn Ser Lys Leu Pro Val Glu Phe Ile

275	280	285
Leu Asp Asp Met Tyr Glu Tyr	Ala Lys Leu Tyr Arg Asp Leu Leu Gly	
290	295	300
Ala Thr Thr Gly Phe Ile	Ala Ala Asp Arg Cys Leu Lys Arg Phe Val	
305	310	315
Pro Val Met Gly Asp Val Val	Leu Pro Phe Leu Leu Pro Val Leu Lys	
	325	330
Asp Ala Lys Asp Gly Ile Ile	Thr Glu Ser Asp Phe Leu Gly Val Leu	
	340	345
Lys Val Leu Glu Ser Tyr Leu	Phe Arg Arg Phe Ala Val Gly Val Ala	
	355	360
Ser Asn Ala Leu Ser Lys Ile	Phe Ser Thr Ala Tyr Ser Asp Ile Lys	
	370	375
Lys Phe Trp Thr Pro Gly Gln	Ser Tyr Ser Ser Leu Leu Ala Tyr Ile	
	385	390
Leu Lys Arg Arg Asp Gly Ser	Gly Arg Phe Pro Ser Asp Ser Glu Phe	
	405	410
Arg Glu Asn Phe Ala Thr Lys	Asn Phe Trp Asn Ile His Asn Glu Asn	
	420	425
Arg Arg Tyr Leu Phe Asp Cys	Leu Glu Asn Ala Asp Ser Asn Asp Val	
	435	440
Arg Asp Ile Gln Thr Ser Leu	Asp Glu Gly Ser Leu Ser Ile Glu His	
	450	455
Ile Met Pro Arg Ser Leu Asn	Asp Gln Trp Arg Ala Glu Leu Gly Pro	
	465	470
Glu Tyr Ala Arg Ile His Glu	Thr Trp Ile Asn Arg Ile Gly Asn Leu	
	485	490
Thr Ile Thr Gly Tyr Asn Ser	Ala Tyr Ser Asn Ser Ser Tyr Glu Arg	
	500	505
Lys Arg Thr Met Glu Asn Gly	Phe Leu Val Ser Pro Tyr Arg Ile Asn	
	515	520
Asn Phe Ile Lys Lys Gln Lys	His Trp Ser Glu Glu Gln Leu Ile Glu	
	530	535
Arg Thr Glu Leu Leu Thr Gln	Ala Ala Leu Asp Tyr Trp Pro Leu Pro	
	545	550
Lys Glu Thr Phe Gln Pro Pro	Gln Ala Val Leu Pro Thr Glu Ser Leu	
	565	570
Asp Ser Asp Leu Ser Phe Arg	Gly Arg Glu Ile Val Ala Phe Glu Tyr	
	580	585
Glu Asp Tyr Lys Glu Thr Val	Thr Ser Trp Ala Asp Met Leu Gln Ser	
	595	600
		605

cac ttg ctt gct ctt gat cct gcc tcc cct cgt ttg act gtt tat aac 163
His Leu Leu Ala Leu Asp Pro Ala Ser Pro Arg Leu Thr Val Tyr Asn

10 15 20

gag tcc acg ggt gcg cgt ttg gat ttc tcc gcc atc act ctt gat aac 211
 Glu Ser Thr Gly Ala Arg Leu Asp Phe Ser Ala Ile Thr Leu Asp Asn
 25 30 35
 tgg gcg tcc aag gtt ggc aat atg ctc ctt gag gaa ttg gat ctg gag 259
 Trp Ala Ser Lys Val Gly Asn Met Leu Leu Glu Glu Leu Asp Leu Glu
 40 45 50
 gaa ggc tgc ctc atc act att gat ttg ccg gtg agc tgg cag gcc gca 307
 Glu Gly Ser Leu Ile Thr Ile Asp Leu Pro Val Ser Trp Gln Ala Ala
 55 60 65
 atg att atg ctc ggc gct tta gca act agt gtt gag gtc tct ttt gat 355
 Met Ile Met Leu Gly Ala Leu Ala Thr Ser Val Glu Val Ser Phe Asp
 70 75 80 85
 gat ccc gag gca gat gcc atc ttt acc tcc ctc gat aga ttt tcc cac 403
 Asp Pro Glu Ala Asp Ala Ile Phe Thr Ser Leu Asp Arg Phe Ser His
 90 95 100
 tac aag ggc cat agt gat gtg ctg att gtc agc gag gat cct ttt ggt 451
 Tyr Lys Gly His Ser Asp Val Leu Ile Val Ser Glu Asp Pro Phe Gly
 105 110 115
 cgt gga gtt gtt gaa ggt ggc ggt gaa ctg cct aat ggt gcc atc gat 499
 Arg Gly Val Val Glu Gly Gly Glu Leu Pro Asn Gly Ala Ile Asp
 120 125 130
 ttt ggc ccc aca gtg cgt ttt tat ggc gat caa ttc ttc cag cct acc 547
 Phe Gly Pro Thr Val Arg Phe Tyr Gly Asp Gln Phe Phe Gln Pro Thr
 135 140 145
 cgc aca ttg ccg gaa atc atc cag cat tct gat gtt ccg gtt ggc gcc 595
 Arg Thr Leu Pro Glu Ile Ile Gln His Ser Asp Val Pro Val Gly Ala
 150 155 160 165
 aga gtt ctt gca act ggt tgg tca gat atc gag tcc ttc aat cac cag 643
 Arg Val Leu Ala Thr Gly Trp Ser Asp Ile Glu Ser Phe Asn His Gln
 170 175 180
 gtt tta gaa cca ctc gca gtg ggt ggc tct gca gta att gtg acc gga 691
 Val Leu Glu Pro Leu Ala Val Gly Gly Ser Ala Val Ile Val Thr Gly
 185 190 195
 ctg gct gat att gag cgt tta aac cag att gca acc aat gag aag aca 739
 Leu Ala Asp Ile Glu Arg Leu Asn Gln Ile Ala Thr Asn Glu Lys Thr
 200 205 210
 acc cac cgt atc taggcaaatt tcggttacta cta 774
 Thr His Arg Ile
 215

<210> 1118

<211> 217

<212> PRT

<213> Corynebacterium glutamicum

<400> 1118

Met Glu Leu Leu Ser His Leu Leu Ala Leu Asp Pro Ala Ser Pro Arg

```

      1             5             10             15
Leu Thr Val Tyr Asn Glu Ser Thr Gly Ala Arg Leu Asp Phe Ser Ala
      20             25             30
Ile Thr Leu Asp Asn Trp Ala Ser Lys Val Gly Asn Met Leu Leu Glu
      35             40             45
Glu Leu Asp Leu Glu Glu Gly Ser Leu Ile Thr Ile Asp Leu Pro Val
      50             55             60
Ser Trp Gln Ala Ala Met Ile Met Leu Gly Ala Leu Ala Thr Ser Val
      65             70             75             80
Glu Val Ser Phe Asp Asp Pro Glu Ala Asp Ala Ile Phe Thr Ser Leu
      85             90             95
Asp Arg Phe Ser His Tyr Lys Gly His Ser Asp Val Leu Ile Val Ser
      100            105            110
Glu Asp Pro Phe Gly Arg Gly Val Val Glu Gly Gly Gly Glu Leu Pro
      115            120            125
Asn Gly Ala Ile Asp Phe Gly Pro Thr Val Arg Phe Tyr Gly Asp Gln
      130            135            140
Phe Phe Gln Pro Thr Arg Thr Leu Pro Glu Ile Ile Gln His Ser Asp
      145            150            155            160
Val Pro Val Gly Ala Arg Val Leu Ala Thr Gly Trp Ser Asp Ile Glu
      165            170            175
Ser Phe Asn His Gln Val Leu Glu Pro Leu Ala Val Gly Gly Ser Ala
      180            185            190
Val Ile Val Thr Gly Leu Ala Asp Ile Glu Arg Leu Asn Gln Ile Ala
      195            200            205
Thr Asn Glu Lys Thr Thr His Arg Ile
      210            215

<210> 1119
<211> 774
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(751)
<223> FRXA02361

<400> 1119
tagagggaatt ggatagctaa tagccgtagt cggtggtcaa actttgacca cgggactccc 60
ctttaagcac aatctctagc ttttatttag gcttggagtt atg gaa ctt ctc tcc 115
Met Glu Leu Leu Ser
      1             5
cac ttg ctt gct ctt gat cct gcc tcc cct cgt ttg act gtt tat aac 163
His Leu Leu Ala Leu Asp Pro Ala Ser Pro Arg Leu Thr Val Tyr Asn

```

	10	15	20	
	gag tcc acg ggt gcg cgt ttg gat ttc tcc gcc atc act ctt gat aac	211		
	Glu Ser Thr Gly 25	Ala Arg Leu Asp Phe Ser Ala Ile Thr Leu Asp Asn 30		
	tgg gcg tcc aag gtt ggc aat atg ctc ctt gag gaa ttg gat ctg gag	259		
	Trp Ala Ser Lys Val Gly Asn Met 40	Leu Leu Glu Glu 45	Leu Asp Leu Glu 50	
	gaa ggc tcg ctc atc act att gat ttg ccg gtg agc tgg cag gcc gca	307		
	Glu Gly Ser Leu Ile Thr Ile 55	Asp Leu Pro Val Ser 60	Trp Gln Ala Ala 65	
	atg att atg ctc ggc gct tta gca act agt gtt gag gtc tct ttt gat	355		
	Met Ile Met Leu Gly 70	Ala Leu Ala Thr Ser 75	Val Glu Val Ser Phe Asp 80 85	
	gat ccc gag gca gat gcc atc ttt acc tcc ctc gat aga ttt tcc cac	403		
	Asp Pro Glu Ala Asp 90	Ala Ile Phe Thr Ser 95	Leu Asp Arg Phe Ser His 100	
	tac aag ggc cat agt gat gtg ctg att gtc agc gag gat cct ttt ggt	451		
	Tyr Lys Gly His 105	Ser Asp Val Leu Ile Val Ser Glu Asp 110	Pro Phe Gly 115	
	cgt gga gtt gtt gaa ggt ggc ggt gaa ctg cct aat ggt gcc atc gat	499		
	Arg Gly Val Val Glu Gly Gly 120	Gly Glu Leu Pro Asn 125	Gly Ala Ile Asp 130	
	ttt ggc ccc aca gtg cgt ttt tat ggc gat caa ttc ttc cag cct acc	547		
	Phe Gly Pro Thr Val Arg Phe 135	Tyr Gly Asp Gln Phe 140	Phe Gln Pro Thr 145	
	cgc aca ttg ccg gaa atc atc cag cat tct gat gtt ccg gtt ggc gcc	595		
	Arg Thr Leu Pro Glu Ile 150	Ile Gln His Ser 155	Asp Val Pro Val Gly Ala 160 165	
	aga gtt ctt gca act ggt tgg tca gat atc gag tcc ttc aat cac cag	643		
	Arg Val Leu Ala Thr Gly 170	Trp Ser Asp Ile Glu Ser 175	Phe Asn His Gln 180	
	ggt tta gaa cca ctc gca gtg ggt ggc tct gca gta att gtg acc gga	691		
	Val Leu Glu Pro Leu Ala Val Gly 185	Gly Ser Ala Val Ile Val Thr Gly 190		
	ctg gct gat att gag cgt tta aac cag att gca acc aat gag aag aca	739		
	Leu Ala Asp Ile Glu Arg Leu 200	Asn Gln Ile Ala Thr 205	Asn Glu Lys Thr 210	
	acc cac cgt atc taggcaaaatt tcggttacta cta	774		
	Thr His Arg Ile 215			

<210> 1120

<211> 217

<212> PRT

<213> Corynebacterium glutamicum

<400> 1120

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Met Glu Leu Leu Ser His Leu Leu Ala Leu Asp Pro Ala Ser Pro Arg
 1          5          10          15
Leu Thr Val Tyr Asn Glu Ser Thr Gly Ala Arg Leu Asp Phe Ser Ala
          20          25          30
Ile Thr Leu Asp Asn Trp Ala Ser Lys Val Gly Asn Met Leu Leu Glu
          35          40          45
Glu Leu Asp Leu Glu Glu Gly Ser Leu Ile Thr Ile Asp Leu Pro Val
          50          55          60
Ser Trp Gln Ala Ala Met Ile Met Leu Gly Ala Leu Ala Thr Ser Val
          65          70          75          80
Glu Val Ser Phe Asp Asp Pro Glu Ala Asp Ala Ile Phe Thr Ser Leu
          85          90          95
Asp Arg Phe Ser His Tyr Lys Gly His Ser Asp Val Leu Ile Val Ser
          100          105          110
Glu Asp Pro Phe Gly Arg Gly Val Val Glu Gly Gly Gly Glu Leu Pro
          115          120          125
Asn Gly Ala Ile Asp Phe Gly Pro Thr Val Arg Phe Tyr Gly Asp Gln
          130          135          140
Phe Phe Gln Pro Thr Arg Thr Leu Pro Glu Ile Ile Gln His Ser Asp
          145          150          155          160
Val Pro Val Gly Ala Arg Val Leu Ala Thr Gly Trp Ser Asp Ile Glu
          165          170          175
Ser Phe Asn His Gln Val Leu Glu Pro Leu Ala Val Gly Gly Ser Ala
          180          185          190
Val Ile Val Thr Gly Leu Ala Asp Ile Glu Arg Leu Asn Gln Ile Ala
          195          200          205
Thr Asn Glu Lys Thr Thr His Arg Ile
          210          215

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<210> 1121

<211> 732

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(709)

<223> RXN02367

<400> 1121

ggcacttgaa tccggacgct aagtgttgga tacatcaact tatttcttggt ctatacttga 60

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gtgcacgttt ctcagctca ggagaagttc ggagaagttc atg tca aac gca gaa 115
                                     Met Ser Asn Ala Glu
                                     1          5

```

att aat ccc gtt gaa tat gaa atc aac aac cac gcc cct ggt acc gcg 163

Ile Asn Pro Val Glu Tyr Glu Ile Asn Asn His Ala Pro Gly Thr Ala
 10 15 20
 cta aac cca cag tgc gaa gac ggc gcc aac gta gaa atc atc acc tcc 211
 Leu Asn Pro Gln Cys Glu Asp Gly Ala Asn Val Glu Ile Ile Thr Ser
 25 30 35
 cgt gaa gtc ccc ctc ggc gga cca cgc gcc atg acc gtg cac cgc aca 259
 Arg Glu Val Pro Leu Gly Gly Pro Arg Ala Met Thr Val His Arg Thr
 40 45 50
 ctc ccc caa cgc cag cgc tcc ctc atc ggt gcc tgg tgt ttt gtg gat 307
 Leu Pro Gln Arg Gln Arg Ser Trp Cys Phe Val Asp
 55 60 65
 cat tac ggc ccc gat gat gtc tca cta acc ggt ggc atg gat atg gcc 355
 His Tyr Gly Pro Asp Val Ser Leu Thr Gly Met Asp Met Ala
 70 75 80 85
 tcc cac ccg cac acc gga ttg caa aca gtc acg tgg ctt ttt gaa ggc 403
 Ser His Pro His Thr Gly Leu Gln Thr Val Thr Trp Leu Phe Glu Gly
 90 95 100
 gaa gtc acc cac cat gat tcc ggc gga aat cac gca gtc gtg ctt cct 451
 Glu Val Thr His His Asp Ser Gly Gly Asn His Ala Val Val Leu Pro
 105 110 115
 ggc gaa gtc aac ctc atg acc gcc ggc gca ggc atc tgt cac acc gaa 499
 Gly Glu Val Asn Leu Met Thr Ala Gly Ala Gly Ile Cys His Thr Glu
 120 125 130
 gtt tcc gcc acc tcc acc acg att ctg cat ggt ctg cag ttg tgg aca 547
 Val Ser Ala Thr Ser Thr Thr Ile Leu His Gly Leu Gln Leu Trp Thr
 135 140 145
 gtt ctt ccc gac aaa gac cgc gaa gga cca cgc cgc ttt gat cac tac 595
 Val Leu Pro Asp Lys Asp Arg Glu Gly Pro Arg Arg Phe Asp His Tyr
 150 155 160 165
 gct cca gaa gaa atc aca ctc gaa ggc gga agt gca cgc gtt ttc cta 643
 Ala Pro Glu Glu Ile Thr Leu Glu Gly Gly Ser Ala Arg Val Phe Leu
 170 175 180
 ggt tcg cta ttt ggt caa acc tcc cct gtt cat acg ttt act ggc tct 691
 Gly Ser Leu Phe Gly Gln Thr Ser Pro Val His Thr Phe Thr Gly Ser
 185 190 195
 tcc tgt ttt aga gtg cat tgatcttatg gaccaactgc cct 732
 Ser Cys Phe Arg Val His
 200

<210> 1122

<211> 203

<212> PRT

<213> Corynebacterium glutamicum

<400> 1122

Met Ser Asn Ala Glu Ile Asn Pro Val Glu Tyr Glu Ile Asn His
 1 5 10 15

```

Ala Pro Gly Thr Ala Leu Asn Pro Gln Cys Glu Asp Gly Ala Asn Val
      20                      25                      30

Glu Ile Ile Thr Ser Arg Glu Val Pro Leu Gly Gly Pro Arg Ala Met
      35                      40                      45

Thr Val His Arg Thr Leu Pro Gln Arg Gln Arg Ser Leu Ile Gly Ala
      50                      55                      60

Trp Cys Phe Val Asp His Tyr Gly Pro Asp Asp Val Ser Leu Thr Gly
      65                      70                      75                      80

Gly Met Asp Met Ala Ser His Pro His Thr Gly Leu Gln Thr Val Thr
      85                      90                      95

Trp Leu Phe Glu Gly Glu Val Thr His His Asp Ser Gly Gly Asn His
      100                     105                     110

Ala Val Val Leu Pro Gly Glu Val Asn Leu Met Thr Ala Gly Ala Gly
      115                     120                     125

Ile Cys His Thr Glu Val Ser Ala Thr Ser Thr Thr Ile Leu His Gly
      130                     135                     140

Leu Gln Leu Trp Thr Val Leu Pro Asp Lys Asp Arg Glu Gly Pro Arg
      145                     150                     155                     160

Arg Phe Asp His Tyr Ala Pro Glu Glu Ile Thr Leu Glu Gly Gly Ser
      165                     170                     175

Ala Arg Val Phe Leu Gly Ser Leu Phe Gly Gln Thr Ser Pro Val His
      180                     185                     190

Thr Phe Thr Gly Ser Ser Cys Phe Arg Val His
      195                     200

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<210> 1123

<211> 732

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(709)

<223> FRXA02367

<400> 1123

ggcacttgaa tccggacgct aagttgttga tacatcaact tattttcttgg ctatacttga 60

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ggtcacggtt cctcagctca ggagaagttc ggagaagttc atg tca aac gca gaa 115
              Met Ser Asn Ala Glu
              1                      5

```

```

att aat ccc gtt gaa tat gaa atc aac aac cac gcc cct ggt acc gcg 163
Ile Asn Pro Val Glu Tyr Glu Ile Asn Asn His Ala Pro Gly Thr Ala
              10                      15                      20

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```

cta aac cca cag tgc gaa gac ggc gcc aac gta gaa atc atc acc tcc 211
Leu Asn Pro Gln Cys Glu Asp Gly Ala Asn Val Glu Ile Ile Thr Ser
              25                      30                      35

```


cgt gaa gtc ccc ctc ggc gga cca cgc gcc atg acc gtg cac cgc aca 259
 Arg Glu Val Pro Leu Gly Gly Pro Arg Ala Met Thr Val His Arg Thr
 40 45 50

ctc ccc caa cgc cag cgc tcc ctc atc ggt gcc tgg tgt ttt gtg gat 307
 Leu Pro Gln Arg Gln Arg Ser Leu Ile Gly Ala Trp Cys Phe Val Asp
 55 60 65

cat tac ggc ccc gat gat gtc tca cta acc ggt ggc atg gat atg gcc 355
 His Tyr Gly Pro Asp Asp Val Ser Leu Thr Gly Met Asp Met Ala
 70 75 80 85

tcc cac ccg cac acc gga ttg caa aca gtc acg tgg ctt ttt gaa ggc 403
 Ser His Pro His Thr Gly Leu Gln Thr Val Thr Trp Leu Phe Glu Gly
 90 95 100

gaa gtc acc cac cat gat tcc ggc gga aat cac gca gtc gtg ctt cct 451
 Glu Val Thr His His Asp Ser Gly Gly Asn His Ala Val Val Leu Pro
 105 110 115

ggc gaa gtc aac ctc atg acc gcc ggc gca ggc atc tgt cac acc gaa 499
 Gly Glu Val Asn Leu Met Thr Ala Gly Ala Gly Ile Cys His Thr Glu
 120 125 130

gtt tcc gcc acc tcc acc acg att ctg cat ggt ctg cag ttg tgg aca 547
 Val Ser Ala Thr Ser Thr Thr Ile Leu His Gly Leu Gln Leu Trp Thr
 135 140 145

gtt ctt ccc gac aaa gac cgc gaa gga cca cgc cgc ttt gat cac tac 595
 Val Leu Pro Asp Lys Asp Arg Glu Gly Pro Arg Phe Asp His Tyr
 150 155 160 165

gct cca gaa gaa atc aca ctc gaa ggc gga agt gca cgc gtt ttc cta 643
 Ala Pro Glu Glu Ile Thr Leu Leu Gly Gly Ser Ala Arg Val Phe Leu
 170 175 180

ggt tcg cta ttt ggt caa acc tcc cct gtt cat acg ttt act ggc tct 691
 Gly Ser Leu Phe Gly Gln Thr Ser Pro Val His Thr Phe Thr Gly Ser
 185 190 195

tcc tgt ttt aga gtg cat tgatottatg gaccaactgc cct 732
 Ser Cys Phe Arg Val His
 200

<210> 1124

<211> 203

<212> PRT

<213> Corynebacterium glutamicum

<400> 1124

Met Ser Asn Ala Glu Ile Asn Pro Val Glu Tyr Glu Ile Asn Asn His
 1 5 10 15

Ala Pro Gly Thr Ala Leu Asn Pro Gln Cys Glu Asp Gly Ala Asn Val
 20 25 30

Glu Ile Ile Thr Ser Arg Glu Val Pro Leu Gly Gly Pro Arg Ala Met
 35 40 45

Thr Val His Arg Thr Leu Pro Gln Arg Gln Arg Ser Leu Ile Gly Ala
50 55 60

Trp Cys Phe Val Asp His Tyr Gly Pro Asp Asp Val Ser Leu Thr Gly
65 70 75 80

Gly Met Asp Met Ala Ser His Pro His Thr Gly Leu Gln Thr Val Thr
85 90 95

Trp Leu Phe Glu Gly Glu Val Thr His His Asp Ser Gly Gly Asn His
100 105 110

Ala Val Val Leu Pro Gly Glu Val Asn Leu Met Thr Ala Gly Ala Gly
115 120 125

Ile Cys His Thr Glu Val Ser Ala Thr Ser Thr Thr Ile Leu His Gly
130 135 140

Leu Gln Leu Trp Thr Val Leu Pro Asp Lys Asp Arg Glu Gly Pro Arg
145 150 155 160

Arg Phe Asp His Tyr Ala Pro Glu Glu Ile Thr Leu Glu Gly Gly Ser
165 170 175

Ala Arg Val Phe Leu Gly Ser Leu Phe Gly Gln Thr Ser Pro Val His
180 185 190

Thr Phe Thr Gly Ser Ser Cys Phe Arg Val His
195 200

<210> 1125

<211> 798

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(775)

<223> RXN02368

<400> 1125

cttaggtcaa gcttgcattt attggctagt gtcggaaatc atgggagatt tagcaaagca 60

catgggcagt gaaccaccag catggtggaa gtttttacgg atg att gtc ctc gct 115
Met Ile Val Leu Ala
1 5

gga gcc act cga gtt acc tat gaa gta gaa cct tgg ctg gcg atc cca 163
Gly Ala Thr Arg Val Thr Tyr Glu Val Glu Pro Trp Leu Ala Ile Pro
10 15 20

tta ttc att ttg gct ttt gca tcg ata ttg atc cca ttc ccg atc tct 211
Leu Phe Ile Leu Ala Phe Ala Ser Ile Leu Ile Pro Phe Pro Ile Ser
25 30 35

aag aca aaa gga ctc cgt gat atc gat gcc tgg aaa atc cac acc acg 259
Lys Thr Lys Gly Leu Arg Asp Ile Asp Ala Trp Lys Ile His Thr Thr
40 45 50

caa ggc gat aaa aag cgt gcc atc cgc caa ctg atc att ccg gct acg 307


```

Lys Ile His Thr Thr Gln Gly Asp Lys Lys Arg Ala Ile Arg Gln Leu
  50                      55                      60
Ile Ile Pro Ala Thr Ala Leu Ala Ile Asp Ile Ile Gly Leu Pro Thr
  65                      70                      75                      80
Leu Phe Asn Ala Pro Pro Leu Ala Ser Ala Ala Leu Phe Gly Gly Val
                      85                      90                      95
Tyr Gly Ala Ser Leu Ala Trp Ala Ala Tyr Arg Ala Asp Gln Leu Pro
          100                      105                      110
Arg Ile Arg Thr Lys Glu Arg Leu Ala Glu Leu Ser Gln Asn Ala Ser
          115                      120                      125
Leu Asp Asp Val Arg Ser Asp Asp Leu Asp Val Leu Glu Gln Pro Glu
          130                      135                      140
Ser Arg Glu Leu Val Arg Cys Leu Leu Ala His Gly Ala Met Asp Gly
          145                      150                      155                      160
Thr Arg Val Met Ala Arg Gln Val Ala Arg Val Leu Asp Thr Glu Val
                      165                      170                      175
Asp Glu Val His Gln Val Ala Arg Ser Leu Glu Gln His Gly Leu Val
                      180                      185                      190
Ser Arg Ser Thr Ile Met Pro Gly Gly Asp Pro Gly Lys Val Phe Ile
          195                      200                      205
Glu Val Ser Leu Lys Gly Ile Ser Ala Ile Lys Ala Leu Glu Ser Gly
          210                      215                      220

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Arg
225

<210> 1127

<211> 798

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(775)

<223> FRXA02368

<400> 1127

cttaggtcaa gcttgcatatt attggctagt gtcggaaatc atgggagatt tagcaaagca 60

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catgggcagt gaaccaccag catggtggaa gtttttacgg  atg att gtc ctc gct  115
                                     Met Ile Val Leu Ala
                                     1                      5

```

```

gga gcc act cga gtt acc tat gaa gta gaa cct tgg ctg gcg atc cca  163
Gly Ala Thr Arg Val Thr Tyr Glu Val Glu Pro Trp Leu Ala Ile Pro
          10                      15                      20

```

```

tta ttc att ttg gct ttt gca tcg ata ttg atc cca ttc ccg atc tct  211
Leu Phe Ile Leu Ala Phe Ala Ser Ile Leu Ile Pro Phe Pro Ile Ser
          25                      30                      35

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aag aca aaa gga ctc cgt gat atc gat gcc tgg aaa atc cac acc acg 259
 Lys Thr Lys Gly Leu Arg Asp Ile Asp Ala Trp Lys Ile His Thr Thr
 40 45 50
 caa ggc gat aaa aag cgt gcc atc cgc caa ctg atc att ccg gct acg 307
 Gln Gly Asp Lys Lys Arg Ala Ile Arg Gln Leu Ile Ile Pro Ala Thr
 55 60 65
 gct ttg gcc atc gac atc att ggg ctg ccg aca tta ttt aat gcc cct 355
 Ala Leu Ala Ile Asp Ile Ile Gly Leu Pro Thr Leu Phe Asn Ala Pro
 70 75 80 85
 ccc ctt gct tcc gct gca ctt ttt ggc ggt gtt tac ggc gct tcc cta 403
 Pro Leu Ala Ser Ala Ala Leu Phe Gly Gly Val Tyr Gly Ala Ser Leu
 90 95 100
 gct tgg gct gcg tac aga gct gat cag ctt cca cgc att cga acg aag 451
 Ala Trp Ala Ala Tyr Arg Ala Asp Gln Leu Pro Arg Ile Arg Thr Lys
 105 110 115
 gaa cgc ctc gca gaa ctt tca caa aat gca tct ctg gat gat gtg cgc 499
 Glu Arg Leu Ala Glu Leu Ser Gln Asn Ala Ser Leu Asp Asp Val Arg
 120 125 130
 tca gat gac tta gat gtt cta gag cag ccg gaa tcc cgt gaa tta gtg 547
 Ser Asp Asp Leu Asp Val Leu Glu Gln Pro Glu Ser Arg Glu Leu Val
 135 140 145
 cgc tgt ctg ctt gcc cac ggt gcg atg gat ggc act ccg gtg atg gcc 595
 Arg Cys Leu Leu Ala His Gly Ala Met Asp Gly Thr Arg Val Met Ala
 150 155 160 165
 aga cag gtc gcg cga gta ctg gat acc gag gta gac gaa gta cat cag 643
 Arg Gln Val Ala Arg Val Leu Asp Thr Glu Val Asp Glu Val His Gln
 170 175 180
 gta gca cgc tca cta gaa cag cat ggt ttg gtt agt cgc tcc acc atc 691
 Val Ala Arg Ser Leu Glu Gln His Gly Leu Val Ser Arg Ser Thr Ile
 185 190 195
 atg ccg ggt ggg gat cca gga aaa gta ttc atc gaa gtt tcc ctg aaa 739
 Met Pro Gly Gly Asp Pro Gly Lys Val Phe Ile Glu Val Ser Leu Lys
 200 205 210
 ggg atc tca gcc atc aag gca ctt gaa tcc gga cgc taagtgttg 785
 Gly Ile Ser Ala Ile Lys Ala Leu Glu Ser Gly Arg
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<210> 1128

<211> 225

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1128

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 Pro Phe Pro Ile Ser Lys Thr Lys Gly Leu Arg Asp Ile Asp Ala Trp
 35 40 45
 Lys Ile His Thr Thr Gln Gly Asp Lys Lys Arg Ala Ile Arg Gln Leu
 50 55 60
 Ile Ile Pro Ala Thr Ala Leu Ala Ile Asp Ile Ile Gly Leu Pro Thr
 65 70 75 80
 Leu Phe Asn Ala Pro Pro Leu Ala Ser Ala Ala Leu Phe Gly Gly Val
 85 90 95
 Tyr Gly Ala Ser Leu Ala Trp Ala Ala Tyr Arg Ala Asp Gln Leu Pro
 100 105 110
 Arg Ile Arg Thr Lys Glu Arg Leu Ala Glu Leu Ser Gln Asn Ala Ser
 115 120 125
 Leu Asp Asp Val Arg Ser Asp Asp Leu Asp Val Leu Glu Gln Pro Glu
 130 135 140
 Ser Arg Glu Leu Val Arg Cys Leu Leu Ala His Gly Ala Met Asp Gly
 145 150 155 160
 Thr Arg Val Met Ala Arg Gln Val Ala Arg Val Leu Asp Thr Glu Val
 165 170 175
 Asp Glu Val His Gln Val Ala Arg Ser Leu Glu Gln His Gly Leu Val
 180 185 190
 Ser Arg Ser Thr Ile Met Pro Gly Gly Asp Pro Gly Lys Val Phe Ile
 195 200 205
 Glu Val Ser Leu Lys Gly Ile Ser Ala Ile Lys Ala Leu Glu Ser Gly
 210 215 220
 Arg
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<210> 1129

<211> 1146

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> {101}..{1123}

<223> RXN02381

<400> 1129

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ataaaagatt tcataccaac ttgtcagcag gggagctttc atg tct gtc aca aac 115
 Met Ser Val Thr Asn
 1 5

ttc cgt cgg ttt ctt gct ggc ata gcg gtc atc gcg gcg tgt gtt gct 163

Phe	Arg	Arg	Phe	Leu	Ala	Gly	Ile	Ala	Val	Ile	Ala	Ala	Cys	Val	Ala	
				10					15					20		
gcg	act	cca	aca	gct	cag	gca	caa	agc	agt	ggc	tct	tct	gga	tcc	tct	211
Ala	Thr	Pro	Thr	Ala	Gln	Ala	Gln	Ser	Ser	Gly	Ser	Ser	Gly	Ser	Ser	
			25					30					35			
ggt	tct	tca	gcg	gga	tct	agc	ggg	ctg	tgg	gat	tta	ctt	ttt	cca	gaa	259
Gly	Ser	Ser	Ala	Gly	Ser	Ser	Gly	Leu	Trp	Asp	Leu	Leu	Phe	Pro	Glu	
			40				45					50				
tcc	cat	gag	tct	ttt	atc	gag	cgg	ctt	ctt	gat	cct	ttg	gat	gac	agc	307
Ser	His	Glu	Ser	Phe	Ile	Glu	Arg	Leu	Leu	Asp	Pro	Leu	Asp	Asp	Ser	
	55					60					65					
cat	ata	tct	att	cac	cct	gac	ctc	acc	cca	gac	ctg	tat	gaa	gag	gtg	355
His	Ile	Ser	Ile	His	Pro	Asp	Leu	Thr	Pro	Asp	Leu	Tyr	Glu	Glu	Val	
	70				75					80					85	
ttt	gat	cca	ccg	caa	att	ggg	gaa	tgc	cca	gcc	gtt	gtt	gct	gtg	gtc	403
Phe	Asp	Pro	Pro	Gln	Ile	Gly	Glu	Cys	Pro	Ala	Val	Val	Ala	Val	Val	
				90					95				100			
gca	cga	ggc	agt	gaa	caa	aac	ctt	caa	atc	cga	ccc	gcg	cga	tac	agc	451
Ala	Arg	Gly	Ser	Glu	Gln	Asn	Leu	Gln	Ile	Arg	Pro	Ala	Arg	Tyr	Ser	
			105				110					115				
gag	gaa	tct	cca	tgg	aca	tcc	aat	gga	ttt	gag	gaa	aaa	aac	ttt	cgt	499
Glu	Glu	Ser	Pro	Trp	Thr	Ser	Asn	Gly	Phe	Glu	Glu	Lys	Asn	Phe	Arg	
			120				125					130				
agt	ttc	ttt	ggc	cga	atg	gaa	aaa	cac	tac	cgt	gaa	tgc	act	ggc	gag	547
Ser	Phe	Phe	Gly	Arg	Met	Glu	Lys	His	Tyr	Arg	Glu	Ser	Thr	Gly	Glu	
	135				140					145						
tcg	ttg	atg	aaa	gac	gtc	tac	gtg	atg	ggg	ctg	aat	aat	atc	gaa	tac	595
Ser	Leu	Met	Lys	Asp	Val	Tyr	Val	Met	Gly	Leu	Asn	Asn	Ile	Glu	Tyr	
	150				155					160				165		
cct	gct	tct	ttg	cca	ctg	tct	tcg	gag	gga	agc	agc	gcc	att	gaa	ttg	643
Pro	Ala	Ser	Leu	Pro	Leu	Ser	Ser	Glu	Gly	Ser	Ser	Ala	Ile	Glu	Leu	
			170					175					180			
ggc	act	tcc	att	tct	agt	ggg	cgc	gac	aat	gtc	atc	agc	gcg	att	gat	691
Gly	Thr	Ser	Ile	Ser	Ser	Gly	Arg	Asp	Asn	Val	Ile	Ser	Ala	Ile	Asp	
			185				190						195			
cgc	ttt	gaa	tca	gcg	aca	ggg	tgc	acg	ccg	aag	tac	ctg	ttg	gcg	ggg	739
Arg	Phe	Glu	Ser	Ala	Thr	Gly	Cys	Thr	Pro	Lys	Tyr	Leu	Leu	Ala	Gly	
		200					205				210					
tat	tct	caa	ggg	gtc	ctc	atc	gtt	gat	ggc	tat	gaa	gag	gag	ttg	att	787
Tyr	Ser	Gln	Gly	Val	Leu	Ile	Val	Asp	Gly	Tyr	Glu	Glu	Glu	Leu	Ile	
	215				220					225						
gcg	agg	gat	cag	tac	ctc	ggc	acc	ctg	cac	atc	gcg	aat	cca	gcg	caa	835
Ala	Arg	Asp	Gln	Tyr	Leu	Gly	Thr	Leu	His	Ile	Ala	Asn	Pro	Ala	Gln	
	230				235					240				245		
caa	gtt	gat	gat	cca	aca	ctt	gtt	ggg	cat	gaa	gta	acc	acg	gga	ggc	883
Gln	Val	Asp	Asp	Pro	Thr	Leu	Val	Gly	His	Glu	Val	Thr	Thr	Gly	Gly	

	250		255		260	
	ttg gct agt tcc gtg gag ccc gtc gag gac aat cct ttc aag gtg agc					931
	Leu Ala Ser Ser Val Glu Pro Val Glu Asp Asn Pro Phe Lys Val Ser					
	265		270		275	
	tac tgc ctg cct gga gac atc gtg tgc gat cgt tct ttt gaa cag ttc					979
	Tyr Cys Leu Pro Gly Asp Ile Val Cys Asp Arg Ser Phe Glu Gln Phe					
	280		285		290	
	tct gct gcg gga tcc tct ata gca gct gcg caa ttg agc acc gga aat					1027
	Ser Ala Ala Gly Ser Ser Ile Ala Ala Ala Gln Leu Ser Thr Gly Asn					
	295		300		305	
	atc cgt cca ggt cga gta cac gtg caa tac ttc gtt acc acc caa ccg					1075
	Ile Arg Pro Gly Arg Val His Val Gln Tyr Phe Val Thr Thr Gln Pro					
	310		315		320	325
	tgg gat gag cag att ttt gac gaa gtc gca tgc tgg att gaa gct gcc					1123
	Trp Asp Glu Gln Ile Phe Asp Glu Val Ala Ser Trp Ile Glu Ala Ala					
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	taaaaaactcg cgaggacgca tgc					1146
	<210> 1130					
	<211> 341					
	<212> PRT					
	<213> Corynebacterium glutamicum					
	<400> 1130					
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	Ser Ser Gly Ser Ser Gly Ser Ser Ala Gly Ser Ser Gly Leu Trp Asp					
	35 40 45					
	Leu Leu Phe Pro Glu Ser His Glu Ser Phe Ile Glu Arg Leu Leu Asp					
	50 55 60					
	Pro Leu Asp Asp Ser His Ile Ser Ile His Pro Asp Leu Thr Pro Asp					
	65 70 75 80					
	Leu Tyr Glu Glu Val Phe Asp Pro Pro Gln Ile Gly Glu Cys Pro Ala					
	85 90 95					
	Val Val Ala Val Val Ala Arg Gly Ser Glu Gln Asn Leu Gln Ile Arg					
	100 105 110					
	Pro Ala Arg Tyr Ser Glu Glu Ser Pro Trp Thr Ser Asn Gly Phe Glu					
	115 120 125					
	Glu Lys Asn Phe Arg Ser Phe Phe Gly Arg Met Glu Lys His Tyr Arg					
	130 135 140					
	Glu Ser Thr Gly Glu Ser Leu Met Lys Asp Val Tyr Val Met Gly Leu					
	145 150 155 160					


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Asn Asn Ile Glu Tyr Pro Ala Ser Leu Pro Leu Ser Ser Glu Gly Ser
      165                      170                      175

Ser Ala Ile Glu Leu Gly Thr Ser Ile Ser Ser Gly Arg Asp Asn Val
      180                      185                      190

Ile Ser Ala Ile Asp Arg Phe Glu Ser Ala Thr Gly Cys Thr Pro Lys
      195                      200                      205

Tyr Leu Leu Ala Gly Tyr Ser Gln Gly Val Leu Ile Val Asp Gly Tyr
      210                      215                      220

Glu Glu Glu Leu Ile Ala Arg Asp Gln Tyr Leu Gly Thr Leu His Ile
      225                      230                      235                      240

Ala Asn Pro Ala Gln Gln Val Asp Asp Pro Thr Leu Val Gly His Glu
      245                      250                      255

Val Thr Thr Gly Gly Leu Ala Ser Ser Val Glu Pro Val Glu Asp Asn
      260                      265                      270

Pro Phe Lys Val Ser Tyr Cys Leu Pro Gly Asp Ile Val Cys Asp Arg
      275                      280                      285

Ser Phe Glu Gln Phe Ser Ala Ala Gly Ser Ser Ile Ala Ala Ala Gln
      290                      295                      300

Leu Ser Thr Gly Asn Ile Arg Pro Gly Arg Val His Val Gln Tyr Phe
      305                      310                      315                      320

Val Thr Thr Gln Pro Trp Asp Glu Gln Ile Phe Asp Glu Val Ala Ser
      325                      330                      335

Trp Ile Glu Ala Ala
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<210> 1131

<211> 1146

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1123)

<223> FRXA02381

<400> 1131

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ataaaagatt tcataccaac ttgtcagcag gggagcttct atg tct gtc aca aac 115
                Met Ser Val Thr Asn
                1                      5

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ttc cgt cgg ttt ctt gct ggc ata gcg gtc atc gcg gcg tgt gtt gct 163
Phe Arg Arg Phe Leu Ala Gly Ile Ala Val Ile Ala Ala Cys Val Ala
                10                      15                      20

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gcg act cca aca gct cag gca caa agc agt ggc tct tct gga tcc tct 211
Ala Thr Pro Thr Ala Gln Ala Gln Ser Ser Gly Ser Ser Gly Ser Ser
                25                      30                      35

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ggt tct tca gcg gga tct agc ggg ctg tgg gat tta ctt ttt cca gaa 259
 Gly Ser Ser Ala Gly Ser Ser Gly Leu Trp Asp Leu Leu Phe Pro Glu
 40 45 50

tcc cat gag tct ttt atc gag cgg ctt ctt gat cct ttg gat gac agc 307
 Ser His Glu Ser Phe Ile Glu Arg Leu Leu Asp Pro Leu Asp Asp Ser
 55 60 65

cat ata tct att cac cct gac ctc acc cca gac ctg tat gaa gag gtg 355
 His Ile Ser Ile His Pro Asp Leu Thr Pro Asp Leu Tyr Glu Glu Val
 70 75 80 85

ttt gat cca ccg caa att ggt gaa tgc cca gcc gtt gtt gct gtg gtc 403
 Phe Asp Pro Pro Gln Ile Gly Glu Cys Pro Ala Val Val Ala Val Val
 90 95 100

gca cga ggc agt gaa caa aac ctt caa atc cga ccc gcg cga tac agc 451
 Ala Arg Gly Ser Glu Gln Asn Leu Gln Ile Arg Pro Ala Arg Tyr Ser
 105 110 115

gag gaa tct cca tgg aca tcc aat gga ttt gag gaa aaa aac ttt cgt 499
 Glu Glu Ser Pro Trp Thr Ser Asn Gly Phe Glu Glu Lys Asn Phe Arg
 120 125 130

agt ttc ttt ggc cga atg gaa aaa cac tac cgt gaa tcg act ggc gag 547
 Ser Phe Phe Gly Arg Met Glu Lys His Tyr Arg Glu Ser Thr Gly Glu
 135 140 145

tcg ttg atg aaa gac gtc tac gtg atg ggt ctg aat aat atc gaa tac 595
 Ser Leu Met Lys Asp Val Tyr Val Met Gly Leu Asn Asn Ile Glu Tyr
 150 155 160 165

cct gct tct ttg cca ctg tct tcg gag gga agc agc gcc att gaa ttg 643
 Pro Ala Ser Leu Pro Leu Ser Ser Glu Gly Ser Ser Ala Ile Glu Leu
 170 175 180

ggc act tcc att tct agt ggt cgc gac aat gtc atc agc gcg att gat 691
 Gly Thr Ser Ile Ser Ser Gly Arg Asp Asn Val Ile Ser Ala Ile Asp
 185 190 195

cgc ttt gaa tca gcg aca ggg tgc acg ccg aag tac ctg ttg gcg ggt 739
 Arg Phe Glu Ser Ala Thr Gly Cys Thr Pro Lys Tyr Leu Leu Ala Gly
 200 205 210

tat tct caa ggt gtc ctc atc gtt gat ggc tat gaa gag gag ttg att 787
 Tyr Ser Gln Gly Val Leu Ile Val Asp Gly Tyr Glu Glu Glu Ile
 215 220 225

gcg agg gat cag tac ctc ggc acc ctg cac atc gcg aat cca gcg caa 835
 Ala Arg Asp Gln Tyr Leu Gly Thr Leu His Ile Ala Asn Pro Ala Gln
 230 235 240 245

caa gtt gat gat cca aca ctt gtt ggg cat gaa gta acc acg gga ggc 883
 Gln Val Asp Asp Pro Thr Leu Val Gly His Glu Val Thr Thr Gly Gly
 250 255 260

ttg gct agt tcc gtg gag ccc gtc gag gac aat cct ttc aag gtg agc 931
 Leu Ala Ser Ser Val Glu Pro Val Glu Asp Asn Pro Phe Lys Val Ser
 265 270 275

tac tgc ctg cct gga gac atc gtg tgc gat cgt tct ttt gaa cag ttc 979
 Tyr Cys Leu Pro Gly Asp Ile Val Cys Asp Arg Ser Phe Glu Gln Phe
 280 285 290

 tct gct gcg gga tcc tct ata gca gct gcg caa ttg agc acc gga aat 1027
 Ser Ala Ala Gly Ser Ser Ile Ala Ala Ala Gln Leu Ser Thr Gly Asn
 295 300 305

 atc cgt cca ggt cga gta cac gtg caa tac ttc gtt acc acc caa ccg 1075
 Ile Arg Pro Gly Arg Val His Val Gln Tyr Phe Val Thr Thr Gln Pro
 310 315 320 325

 tgg gat gag cag att ttt gac gaa gtc gca tcg tgg att gaa gct gcc 1123
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<210> 1132

<211> 341

<212> PRT

<213> Corynebacterium glutamicum

<400> 1132

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 20 25 30

 Ser Ser Gly Ser Ser Gly Ser Ser Ala Gly Ser Ser Gly Leu Trp Asp
 35 40 45

 Leu Leu Phe Pro Glu Ser His Glu Ser Phe Ile Glu Arg Leu Leu Asp
 50 55 60

 Pro Leu Asp Asp Ser His Ile Ser Ile His Pro Asp Leu Thr Pro Asp
 65 70 75 80

 Leu Tyr Glu Glu Val Phe Asp Pro Pro Gln Ile Gly Glu Cys Pro Ala
 85 90 95

 Val Val Ala Val Val Ala Arg Gly Ser Glu Gln Asn Leu Gln Ile Arg
 100 105 110

 Pro Ala Arg Tyr Ser Glu Glu Ser Pro Trp Thr Ser Asn Gly Phe Glu
 115 120 125

 Glu Lys Asn Phe Arg Ser Phe Phe Gly Arg Met Glu Lys His Tyr Arg
 130 135 140

 Glu Ser Thr Gly Glu Ser Leu Met Lys Asp Val Tyr Val Met Gly Leu
 145 150 155 160

 Asn Asn Ile Glu Tyr Pro Ala Ser Leu Pro Leu Ser Ser Glu Gly Ser
 165 170 175

 Ser Ala Ile Glu Leu Gly Thr Ser Ile Ser Ser Gly Arg Asp Asn Val
 180 185 190

Ile Ser Ala Ile Asp Arg Phe Glu Ser Ala Thr Gly Cys Thr Pro Lys
195 200 205

Tyr Leu Leu Ala Gly Tyr Ser Gln Gly Val Leu Ile Val Asp Gly Tyr
210 215 220

Glu Glu Glu Leu Ile Ala Arg Asp Gln Tyr Leu Gly Thr Leu His Ile
225 230 235 240

Ala Asn Pro Ala Gln Val Asp Asp Pro Thr Leu Val Gly His Glu
245 250 255

Val Thr Thr Gly Gly Leu Ala Ser Ser Val Glu Pro Val Glu Asp Asn
260 265 270

Pro Phe Lys Val Ser Tyr Cys Leu Pro Gly Asp Ile Val Cys Asp Arg
275 280 285

Ser Phe Glu Gln Phe Ser Ala Ala Gly Ser Ser Ile Ala Ala Ala Gln
290 295 300

Leu Ser Thr Gly Asn Ile Arg Pro Gly Arg Val His Val Gln Tyr Phe
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Val Thr Thr Gln Pro Trp Asp Glu Gln Ile Phe Asp Glu Val Ala Ser
325 330 335

Trp Ile Glu Ala Ala
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<210> 1133

<211> 736

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(736)

<223> RXN02383

<400> 1133

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gtaaagaaga tggcaataaa aatgtggagg agtaaaggcg atg cca gtt cgg gta 115
Met Pro Val Arg Val
1 5

att gtt gat tcc tcc gca tgc ttg cca acg cat gtg gcc gag gac ctc 163
Ile Val Asp Ser Ser Ala Cys Leu Pro Thr His Val Ala Glu Asp Leu
10 15 20

gac atc acg gtg att aac ttg cac gtg atg aat aac ggt gaa gaa cgc 211
Asp Ile Thr Val Ile Asn Leu His Val Met Asn Asn Gly Glu Glu Arg
25 30 35

agt aca tcc ggg ttg tgc tgc ttg gaa ctt gca gca agt tac gcc cgc 259
Ser Thr Ser Gly Leu Ser Ser Leu Glu Leu Ala Ala Ser Tyr Ala Arg
40 45 50

cag ctt gaa cgc ggt ggc gat gac ggt gtg ctt gcg ctg cat att tct 307

Gln Leu Glu Arg Gly Gly Asp Asp Gly Val Leu Ala Leu His Ile Ser
 55 60 65
 aaa gag ctc tcc tcc acg tgg tcc gca gcg gtg aca gca gcc gct gtg 355
 Lys Glu Leu Ser Ser Thr Trp Ser Ala Ala Val Thr Ala Ala Ala Val
 70 75 80 85
 ttt gat gat gat tct gtg cgc gtg gtg gat acc agt tcc ctc ggt atg 403
 Phe Asp Asp Asp Ser Val Arg Val Val Asp Thr Ser Ser Leu Gly Met
 90 95 100
 gct gtg ggt gct gcc gcg atg gct gct gcc cgc atg gct aaa gat ggc 451
 Ala Val Gly Ala Ala Met Ala Ala Ala Arg Met Ala Lys Asp Gly
 105 110 115
 gcg tct ttg cag gaa tgc tac gac atc gcg gtg gat acc ttg aag cgt 499
 Ala Ser Leu Gln Glu Cys Tyr Asp Ile Ala Val Asp Thr Leu Lys Arg
 120 125 130
 tca gaa acc tgg atc tac ctg cac cgc att gat gaa atc tgg aag tcc 547
 Ser Glu Thr Trp Ile Tyr Leu His Arg Ile Asp Glu Ile Trp Lys Ser
 135 140 145
 gga cgg att tcc act gca acc gcc atg gtg tca acg gct ctg gca acc 595
 Gly Arg Ile Ser Thr Ala Thr Ala Met Val Ser Thr Ala Leu Ala Thr
 150 155 160 165
 cgc ccc atc atg cgt ttc aac ggt ggt cgc atg gag atc gcc gct aag 643
 Arg Pro Ile Met Arg Phe Asn Gly Gly Arg Met Glu Ile Ala Ala Lys
 170 175 180
 acc cgc acc caa tct aaa gcg ttt gcc aaa ttg gtg gaa tta gcc cag 691
 Thr Arg Thr Gln Ser Lys Ala Phe Ala Lys Leu Val Glu Leu Ala Gln
 185 190 195
 atc agg gca gat ggt gaa ccc gta ttc att gcg att ggc caa aac 736
 Ile Arg Ala Asp Gly Glu Pro Val Phe Ile Ala Ile Gly Gln Asn
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<210> 1134

<211> 212

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1134

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 20 25 30
 Asn Gly Glu Glu Arg Ser Thr Ser Gly Leu Ser Ser Leu Glu Leu Ala
 35 40 45
 Ala Ser Tyr Ala Arg Gln Leu Glu Arg Gly Gly Asp Asp Gly Val Leu
 50 55 60
 Ala Leu His Ile Ser Lys Glu Leu Ser Ser Thr Trp Ser Ala Ala Val
 65 70 75 80

Thr Ala Ala Ala Val Phe Asp Asp Asp Ser Val Arg Val Val Asp Thr
 85 90 95
 Ser Ser Leu Gly Met Ala Val Gly Ala Ala Ala Met Ala Ala Arg
 100 105 110
 Met Ala Lys Asp Gly Ala Ser Leu Gln Glu Cys Tyr Asp Ile Ala Val
 115 120 125
 Asp Thr Leu Lys Arg Ser Glu Thr Trp Ile Tyr Leu His Arg Ile Asp
 130 135 140
 Glu Ile Trp Lys Ser Gly Arg Ile Ser Thr Ala Thr Ala Met Val Ser
 145 150 155 160
 Thr Ala Leu Ala Thr Arg Pro Ile Met Arg Phe Asn Gly Gly Arg Met
 165 170 175
 Glu Ile Ala Ala Lys Thr Arg Thr Gln Ser Lys Ala Phe Ala Lys Leu
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 Val Glu Leu Ala Gln Ile Arg Ala Asp Gly Glu Pro Val Phe Ile Ala
 195 200 205
 Ile Gly Gln Asn
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<210> 1135
 <211> 703
 <212> DNA
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<220>
 <221> CDS
 <222> (101)..(703)
 <223> FRXA02383

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 Met Pro Val Arg Val
 1 5
 att gtt gat tcc tcc gca tgc ttg cca acg cat gtg gcc gag gac ctc 163
 Ile Val Asp Ser Ser Ala Cys Leu Pro Thr His Val Ala Glu Asp Leu
 10 15 20
 gac atc acg gtg att aac ttg cac gtg atg aat aac ggt gaa gaa cgc 211
 Asp Ile Thr Val Ile Asn Leu His Val Met Asn Asn Gly Glu Asp Arg
 25 30 35
 agt aca tcc ggg ttg tgg tgg ttg gaa ctt gca gca agt tac gcc cgc 259
 Ser Thr Ser Ser Gly Leu Ser Ser Leu Glu Leu Ala Ala Ser Tyr Ala Arg
 40 45 50
 cag ctt gaa cgc ggt ggc gat gac ggt gtg ctt gcg ctg cat att tct 307
 Gln Leu Glu Arg Gly Gly Asp Asp Gly Val Leu Ala Leu His Ile Ser
 55 60 65

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Lys Glu Leu Ser Ser Thr Trp Ser Ala Ala Val Thr Ala Ala Ala Val
70 75 80 85

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Phe Asp Asp Asp Ser Val Arg Val Val Asp Thr Ser Ser Leu Gly Met
90 95 100

gct gtg ggt gct gcc gcg atg gct gct gcc cgc atg gct aaa gat gcc 451
Ala Val Gly Ala Ala Ala Met Ala Ala Ala Arg Met Ala Lys Asp Gly
105 110 115

gcg tct ttg cag gaa tgc tac gac atc gcg gtg gat acc ttg aag cgt 499
Ala Ser Leu Gln Glu Cys Tyr Asp Ile Ala Val Asp Thr Leu Lys Arg
120 125 130

tca gaa acc tgg atc tac ctg cac cgc att gat gaa atc tgg aag tcg 547
Ser Glu Thr Trp Ile Tyr Leu His Arg Ile Asp Glu Ile Trp Lys Ser
135 140 145

gga cgg att tcc act gca acc gcc atg gtg tca acg gct ctg gca acc 595
Gly Arg Ile Ser Thr Ala Thr Ala Met Val Ser Thr Ala Leu Ala Thr
150 155 160 165

cgc ccc atc atg cgt ttc aac ggt ggt cgc atg gag atc gcc gct aag 643
Arg Pro Ile Met Arg Phe Asn Gly Gly Arg Met Glu Ile Ala Ala Lys
170 175 180

acc cgc acc caa tct aaa gcg ttt gcc aaa ttg gtg gaa tta gcc cag 691
Thr Arg Thr Gln Ser Lys Ala Phe Ala Lys Leu Val Glu Leu Ala Gln
185 190 195

atc agg gca gat 703
Ile Arg Ala Asp
200

<210> 1136
<211> 201
<212> PRT
<213> Corynebacterium glutamicum

<400> 1136
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Val Ala Glu Asp Leu Asp Ile Thr Val Ile Asn Leu His Val Met Asn
20 25 30

Asn Gly Glu Glu Arg Ser Thr Ser Gly Leu Ser Ser Leu Glu Leu Ala
35 40 45

Ala Ser Tyr Ala Arg Gln Leu Glu Arg Gly Gly Asp Asp Gly Val Leu
50 55 60

Ala Leu His Ile Ser Lys Glu Leu Ser Ser Thr Trp Ser Ala Ala Val
65 70 75 80

Thr Ala Ala Ala Val Phe Asp Asp Asp Ser Val Arg Val Val Asp Thr
85 90 95

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Ser Ser Leu Gly Met Ala Val Gly Ala Ala Met Ala Ala Arg
 100 105 110

Met Ala Lys Asp Gly Ala Ser Leu Gln Glu Cys Tyr Asp Ile Ala Val
 115 120 125

Asp Thr Leu Lys Arg Ser Glu Thr Trp Ile Tyr Leu His Arg Ile Asp
 130 135 140

Glu Ile Trp Lys Ser Gly Arg Ile Ser Thr Ala Met Val Ser
 145 150 155 160

Thr Ala Leu Ala Thr Arg Pro Ile Met Arg Phe Asn Gly Gly Arg Met
 165 170 175

Glu Ile Ala Ala Lys Thr Arg Thr Gln Ser Lys Ala Phe Ala Lys Leu
 180 185 190

Val Glu Leu Ala Gln Ile Arg Ala Asp
 195 200

<210> 1137
 <211> 885
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(862)
 <223> RXN02387

<400> 1137
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 Val Trp Trp Cys Leu
 1 5

cca aca tgg atc aaa gca ggc caa gat gct gta gat cta gcc tta tcc 163
 Pro Thr Trp Ile Lys Ala Gly Gln Asp Ala Val Asp Leu Ala Leu Ser
 10 15 20

gca gca gtt gat ccc agc cct ggt acc tac ttg atc gtc atg cac tct 211
 Ala Ala Val Asp Pro Ser Pro Gly Thr Tyr Leu Ile Val Met His Ser
 25 30 35

ggc ggt gga cgc tct aag tcg atg gtg aag aag ctg gaa aaa gtc gcg 259
 Gly Gly Gly Arg Ser Lys Ser Met Val Lys Lys Leu Glu Lys Val Ala
 40 45 50

gtg gtg cac gat gcc gca aag ctg aaa gac cgg gat cgt cca ggt tgg 307
 Val Val His Asp Ala Ala Lys Leu Lys Asp Arg Asp Arg Pro Gly Trp
 55 60 65

gta aaa caa gag ttc aaa aac cac aaa gtc cag gtc acc cca gat gtc 355
 Val Lys Gln Glu Phe Lys Asn His Lys Val Gln Val Thr Pro Asp Val
 70 75 80 85

att cat gct ctt tta gag ggc gtg ggt tca gat ctt aga gag ctg gcg 403
 Ile His Ala Leu Leu Glu Gly Val Gly Ser Asp Leu Arg Glu Leu Ala

	90	95	100	
tcc gcc gta tcc caa ttg gtt gag gac acc caa ggc aac gtg acg gtg				451
Ser Ala Val Ser Gln Leu Val Glu Asp Thr Gln Gly Asn Val Thr Val				
	105	110	115	
gaa aaa gtc cgt gcc tat tac gtg ggt gtt gct gag gta tgc ggt ttc				499
Glu Lys Val Arg Ala Tyr Tyr Val Gly Val Ala Glu Val Ser Gly Phe				
	120	125	130	
gac atc gcc gat tct gca tgc gcc ggt caa atg tca aag gcc gtg gcc				547
Asp Ile Ala Asp Ser Ala Cys Ala Gly Gln Met Ser Lys Ala Val Ala				
	135	140	145	
agc acc aga cgt gcc ctt caa ttg ggt acc agc ccg gtt gca ttg gca				595
Ser Thr Arg Arg Ala Leu Gln Leu Gly Thr Ser Pro Val Ala Leu Ala				
	150	155	160	165
gct gcg ttg agt atg aaa gtt ggc cag atc gcc agg ctg tat tcc acc				643
Ala Ala Leu Ser Met Lys Val Gly Gln Ile Ala Arg Leu Tyr Ser Thr				
	170	175	180	
agg gga cgc atc aac ggt ttt gag ctg gcc aaa gaa ttg ggc atg ccg				691
Arg Gly Arg Ile Asn Gly Phe Glu Leu Ala Lys Glu Leu Gly Met Pro				
	185	190	195	
ccg ttc gtg gtg gag aag act gcg aaa gtg gcc cga aac tgg tgc gga				739
Pro Phe Val Val Glu Lys Thr Ala Lys Val Ala Arg Asn Trp Ser Gly				
	200	205	210	
gat gcg gtc agc gag gcc gtg att ttg atg gcc gat ctg gat gcc gct				787
Asp Ala Val Ser Glu Ala Val Ile Leu Met Ala Asp Leu Asp Ala Ala				
	215	220	225	
gta aaa gga caa agt ggc gat cct gaa ttt gcc atc gaa tct gcc gtg				835
Val Lys Gly Gln Ser Gly Asp Pro Glu Phe Ala Ile Glu Ser Ala Val				
	230	235	240	245
aga aga gtt gca gag ctg gcg agg ccg taacgctgaa cggcggcggg				882
Arg Arg Val Ala Glu Leu Ala Arg Arg				
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taa				885
<210> 1138				
<211> 254				
<212> PRT				
<213> <i>Corynebacterium glutamicum</i>				
<400> 1138				
Val Trp Trp Cys Leu Pro Thr Trp Ile Lys Ala Gly Gln Asp Ala Val				
1 5 10 15				
Asp Leu Ala Leu Ser Ala Ala Val Asp Pro Ser Pro Gly Thr Tyr Leu				
20 25 30				
Ile Val Met His Ser Gly Gly Gly Arg Ser Lys Ser Met Val Lys Lys				
35 40 45				
Leu Glu Lys Val Ala Val Val His Asp Ala Ala Lys Leu Lys Asp Arg				

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      50              55              60
Asp Arg Pro Gly Trp Val Lys Gln Glu Phe Lys Asn His Lys Val Gln
 65              70              75
Val Thr Pro Asp Val Ile His Ala Leu Leu Glu Gly Val Gly Ser Asp
      85              90              95
Leu Arg Glu Leu Ala Ser Ala Val Ser Gln Leu Val Glu Asp Thr Gln
      100             105             110
Gly Asn Val Thr Val Glu Lys Val Arg Ala Tyr Tyr Val Gly Val Ala
      115             120             125
Glu Val Ser Gly Phe Asp Ile Ala Asp Ser Ala Cys Ala Gly Gln Met
      130             135             140
Ser Lys Ala Val Ala Ser Thr Arg Arg Ala Leu Gln Leu Gly Thr Ser
      145             150             155             160
Pro Val Ala Leu Ala Ala Ala Leu Ser Met Lys Val Gly Gln Ile Ala
      165             170             175
Arg Leu Tyr Ser Thr Arg Gly Arg Ile Asn Gly Phe Glu Leu Ala Lys
      180             185             190
Glu Leu Gly Met Pro Pro Phe Val Val Glu Lys Thr Ala Lys Val Ala
      195             200             205
Arg Asn Trp Ser Gly Asp Ala Val Ser Glu Ala Val Ile Leu Met Ala
      210             215             220
Asp Leu Asp Ala Ala Val Lys Gly Gln Ser Gly Asp Pro Glu Phe Ala
      225             230             235             240
Ile Glu Ser Ala Val Arg Arg Val Ala Glu Leu Ala Arg Arg
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<210> 1139

<211> 778

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(778)

<223> FRXA02387

<400> 1139

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              Val Trp Trp Cys Leu
              1              5

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cca aca tgg atc aaa gca ggc caa gat gct gta gat cta gcc tta tcc 163
Pro Thr Trp Ile Lys Ala Gly Gln Asp Ala Val Asp Leu Ala Leu Ser
              10              15              20

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gca gca gtt gat ccc agc cct ggt acc tac ttg atc gtc atg cac tct 211

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Ala	Ala	Val	Asp	Pro	Ser	Pro	Gly	Thr	Tyr	Leu	Ile	Val	Met	His	Ser		
			25					30					35				
ggc	ggt	gga	cgc	tct	aag	tcg	atg	gtg	aag	aag	ctg	gaa	aaa	gtc	gcg	259	
Gly	Gly	Gly	Arg	Ser	Lys	Ser	Met	Val	Lys	Lys	Leu	Glu	Lys	Val	Ala		
		40					45				50						
gtg	gtg	cac	gat	gcc	gca	aag	ctg	aaa	gac	cgg	gat	cgt	cca	ggt	tgg	307	
Val	Val	His	Asp	Ala	Ala	Lys	Leu	Lys	Asp	Arg	Asp	Arg	Pro	Gly	Trp		
		55				60				65							
gta	aaa	caa	gag	ttc	aaa	aac	cac	aaa	gtc	cag	gtc	acc	cca	gat	gtc	355	
Val	Lys	Gln	Glu	Phe	Lys	Asn	His	Lys	Val	Gln	Val	Thr	Pro	Asp	Val		
	70				75				80					85			
att	cat	gct	ctt	tta	gag	ggc	gtg	ggt	tca	gat	ctt	aga	gag	ctg	gcg	403	
Ile	His	Ala	Leu	Leu	Glu	Gly	Val	Gly	Ser	Asp	Leu	Arg	Glu	Leu	Ala		
				90				95					100				
tcc	gcc	gta	tcc	caa	ttg	gtt	gag	gac	acc	caa	ggc	aac	gtg	acg	gtg	451	
Ser	Ala	Val	Ser	Gln	Leu	Val	Glu	Asp	Thr	Gln	Gly	Asn	Val	Thr	Val		
			105					110					115				
gaa	aaa	gtc	cgt	gcc	tat	tac	gtg	ggt	gtt	gct	gag	gta	tcg	ggt	ttc	499	
Glu	Lys	Val	Arg	Ala	Tyr	Tyr	Val	Gly	Val	Ala	Glu	Val	Ser	Gly	Phe		
		120					125					130					
gac	atc	gcc	gat	tct	gca	tcg	gcc	ggt	caa	atg	tca	aag	gcc	gtg	gcc	547	
Asp	Ile	Ala	Asp	Ser	Ala	Cys	Ala	Gly	Gln	Met	Ser	Lys	Ala	Val	Ala		
		135			140					145							
agc	acc	aga	cgt	gcc	ctt	caa	ttg	ggt	acc	agc	ccg	gtt	gca	ttg	gca	595	
Ser	Thr	Arg	Arg	Ala	Leu	Gln	Leu	Gly	Thr	Ser	Pro	Val	Ala	Leu	Ala		
		150			155				160					165			
gct	gcg	ttg	agt	atg	aaa	gtt	ggc	cag	atc	gcc	agg	ctg	tat	tcc	acc	643	
Ala	Ala	Leu	Ser	Met	Lys	Val	Gly	Gln	Ile	Ala	Arg	Leu	Tyr	Ser	Thr		
				170					175					180			
agg	gga	cgc	atc	aac	ggt	ttt	gag	ctg	gcc	aaa	gaa	ttg	ggc	atg	ccg	691	
Arg	Gly	Arg	Ile	Asn	Gly	Phe	Glu	Leu	Ala	Lys	Glu	Leu	Gly	Met	Pro		
		185					190					195					
ccg	ttc	gtg	gag	aag	act	gcg	aaa	gtg	gcc	cga	aac	tcg	tcg	gga		739	
Pro	Phe	Val	Val	Glu	Lys	Thr	Ala	Lys	Val	Ala	Arg	Asn	Trp	Ser	Gly		
		200				205					210						
gat	gcg	gtc	agc	gag	gcc	gtg	att	ttg	atg	gcc	gat	ctg				778	
Asp	Ala	Val	Ser	Glu	Ala	Val	Ile	Leu	Met	Ala	Asp	Leu					
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<210> 1140
 <211> 226
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 1140
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 1 5 10 15

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Asp Leu Ala Leu Ser Ala Ala Val Asp Pro Ser Pro Gly Thr Tyr Leu
      20      25      30
Ile Val Met His Ser Gly Gly Gly Arg Ser Lys Ser Met Val Lys Lys
      35      40      45
Leu Glu Lys Val Ala Val Val His Asp Ala Ala Lys Leu Lys Asp Arg
      50      55      60
Asp Arg Pro Gly Trp Val Lys Gln Glu Phe Lys Asn His Lys Val Gln
      65      70      75      80
Val Thr Pro Asp Val Ile His Ala Leu Leu Glu Gly Val Gly Ser Asp
      85      90      95
Leu Arg Glu Leu Ala Ser Ala Val Ser Gln Leu Val Glu Asp Thr Gln
      100     105     110
Gly Asn Val Thr Val Glu Lys Val Arg Ala Tyr Tyr Val Gly Val Ala
      115     120     125
Glu Val Ser Gly Phe Asp Ile Ala Asp Ser Ala Cys Ala Gly Gln Met
      130     135     140
Ser Lys Ala Val Ala Ser Thr Arg Arg Ala Leu Gln Leu Gly Thr Ser
      145     150     155     160
Pro Val Ala Leu Ala Ala Ala Leu Ser Met Lys Val Gly Gln Ile Ala
      165     170     175
Arg Leu Tyr Ser Thr Arg Gly Arg Ile Asn Gly Phe Glu Leu Ala Lys
      180     185     190
Glu Leu Gly Met Pro Pro Phe Val Val Glu Lys Thr Ala Lys Val Ala
      195     200     205
Arg Asn Trp Ser Gly Asp Ala Val Ser Glu Ala Val Ile Leu Met Ala
      210     215     220
Asp Leu
225

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<210> 1141

<211> 1725

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1702)

<223> RXN02398

<400> 1141

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tacaggcggt aattaaatgc gttcatagaa gaacttgaaa 115
                Val Val Glu Val Lys
                1                5

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aag cgt aat ctc ctc gta gct ccc ctc act gct tcc ctg gtg ttc tgt 163

Lys	Arg	Asn	Leu	Leu	Val	Ala	Pro	Leu	Thr	Ala	Ser	Leu	Val	Phe	Cys	
				10					15					20		
aac	ttg	gct	gtt	gca	gca	aac	gcc	gtt	gaa	gtt	gag	gcc	gaa	tca	cca	211
Asn	Leu	Ala	Val	Ala	Ala	Asn	Ala	Val	Glu	Val	Glu	Ala	Glu	Ser	Pro	
			25					30					35			
gtt	gtc	atc	aat	gaa	gtt	gaa	tcc	aac	agc	gac	cca	gtt	ggg	gac	tg	259
Val	Val	Ile	Asn	Glu	Val	Glu	Ser	Asn	Ser	Asp	Pro	Val	Gly	Asp	Trp	
		40					45					50				
gtg	gag	ttg	gct	aac	acc	gac	aac	aac	aac	tcc	atc	gac	att	tcc	ggg	307
Val	Glu	Leu	Ala	Asn	Thr	Asp	Asn	Asn	Asn	Ser	Ile	Asp	Ile	Ser	Gly	
	55					60				65						
ttg	tcc	tta	gtc	gat	gac	aag	gaa	gac	ctg	gaa	aat	gcc	ctc	gtc	ctt	355
Trp	Ser	Leu	Val	Asp	Asp	Lys	Glu	Asp	Leu	Glu	Asn	Ala	Leu	Val	Leu	
	70				75					80					85	
cct	gaa	ggc	act	gag	att	gag	tcc	ggg	gga	tac	ttt	gtt	atc	tac	acc	403
Pro	Glu	Gly	Thr	Glu	Ile	Glu	Ser	Gly	Gly	Tyr	Phe	Val	Ile	Tyr	Thr	
			90						95					100		
gac	tct	gct	gat	tac	gtg	cct	acc	aac	aac	acc	ttt	ggg	ggc	cag	gaa	451
Asp	Ser	Ala	Asp	Tyr	Val	Pro	Thr	Asn	Asn	Thr	Phe	Gly	Gly	Gln	Glu	
			105						110				115			
tac	ttc	ggc	ctc	ggc	aaa	gat	gac	act	gtt	act	ctg	cgc	aac	gct	gaa	499
Tyr	Phe	Gly	Leu	Gly	Lys	Asp	Asp	Thr	Val	Thr	Leu	Arg	Asn	Ala	Glu	
		120					125					130				
ggc	gaa	gta	gtt	gct	acc	tat	tcc	ttg	aag	gat	ctg	ggc	gag	cac	gca	547
Gly	Glu	Val	Val	Ala	Thr	Tyr	Ser	Trp	Lys	Asp	Leu	Gly	Glu	His	Ala	
	135					140					145					
gaa	aac	acc	tat	ggg	cgc	atc	cca	gat	atg	act	ggg	gat	ttc	gca	aac	595
Glu	Asn	Thr	Tyr	Gly	Arg	Ile	Pro	Asp	Met	Thr	Gly	Asp	Phe	Ala	Asn	
	150				155					160					165	
acc	ggc	gtt	cca	acc	cca	ggg	gca	aag	aat	gtt	gct	gct	gaa	ggc	tcc	643
Thr	Gly	Val	Pro	Thr	Pro	Gly	Ala	Lys	Asn	Val	Ala	Ala	Glu	Gly	Ser	
			170						175					180		
ggc	gaa	gaa	gaa	ggc	gtt	gtt	gca	aac	gcc	cag	ctt	cca	ttc	cac	aac	691
Gly	Glu	Glu	Glu	Gly	Val	Val	Ala	Asn	Ala	Gln	Leu	Pro	Phe	His	Asn	
		185						190					195			
gtt	gaa	atc	acc	cca	att	cac	ctc	ggg	gga	gat	ttc	acc	ggg	gaa	gat	739
Val	Glu	Ile	Thr	Pro	Ile	His	Leu	Gly	Gly	Asp	Phe	Thr	Gly	Glu	Asp	
		200					205					210				
atg	tcc	ggc	gtt	gat	ttc	gat	gca	aac	agc	acc	gca	ttg	atc	gcc	aac	787
Met	Ser	Gly	Val	Asp	Phe	Asp	Ala	Asn	Ser	Thr	Ala	Trp	Ile	Ala	Asn	
	215					220					225					
aat	gac	att	gga	aag	atc	tac	tcc	ctc	gcc	cac	gac	ata	gct	aac	aac	835
Asn	Asp	Ile	Gly	Lys	Ile	Tyr	Ser	Leu	Ala	His	Asp	Ile	Ala	Asn	Asn	
	230				235					240					245	
acc	tac	aag	ctg	act	ggc	gaa	ttg	gaa	acc	ggc	tac	cca	gaa	ggc	ggc	883
Thr	Tyr	Lys	Leu	Thr	Gly	Glu	Trp	Glu	Thr	Gly	Tyr	Pro	Glu	Gly	Gly	

	250	255	260	
	gga gag cca gac gct gaa ggc atc gtc gca gct acc aac ggt gac atc Gly Glu Pro Asp Ala Glu Gly Ile Val Ala Ala Thr Asn Gly Asp Ile	265 270	275	931
	tac ctg tcc acc gag cgc aac aac gct gac aag aac gtc tct cgc cca Tyr Leu Ser Thr Glu Arg Asn Asn Ala Asp Lys Asn Val Ser Arg Pro	280 285	290	979
	tcc atc ctg cgt ttt gct acc cca act ggc aag act ggc gta caa aac Ser Ile Leu Arg Phe Ala Thr Pro Thr Gly Lys Thr Gly Val Gln Asn	295 300	305	1027
	gca gtt cag gaa tgg gac ctg tct gag ttc gtc ggc gac att cag ccc Ala Val Gln Glu Trp Asp Leu Ser Glu Phe Val Gly Asp Ile Gln Pro	310 315	320	1075
	aat ggt ggt ctt gag gca atc gcg cag ctc gag gac aac atc ttc gtt Asn Gly Gly Leu Glu Ala Ile Ala Gln Leu Glu Asp Asn Ile Phe Val	330 335	340	1123
	gtc ggt gtc gaa gag aca ggt gat gtc atc gtt gtt gat ctt tcc gct Val Gly Val Glu Glu Thr Gly Asp Val Ile Val Val Asp Leu Ser Ala	345 350	355	1171
	gac cag cca gtt ctg gtt caa agg tac gaa tct tcc ttc gac ggt gtc Asp Gln Pro Val Leu Val Gln Arg Tyr Glu Ser Ser Phe Asp Gly Val	360 365	370	1219
	atg tgc ctt gat tac aac gca gca acc aag cag ctc agc gtt gtg tgc Met Ser Leu Asp Tyr Asn Ala Ala Thr Lys Gln Leu Ser Val Val Cys	375 380	385	1267
	gac gaa gca tgt gac ggc ttg tct gaa atc ctc gaa tgg gat ggc gag Asp Glu Ala Cys Asp Gly Leu Ser Glu Ile Leu Glu Trp Asp Gly Glu	390 395	400	1315
	aag ctg tac aag tcc gac gac aag atc tac gag cgt cca gca aac ctg Lys Leu Tyr Lys Ser Asp Asp Lys Ile Tyr Glu Arg Pro Ala Asn Leu	410 415	420	1363
	ggc aac tgg gct aac gaa ggc ttc ggc acc tac acc tca gag ctt aaa Gly Asn Trp Ala Asn Glu Gly Phe Gly Thr Tyr Thr Ser Glu Leu Lys	425 430	435	1411
	tgc gag aac ggc aac acc gtt tct gtc acc agc tac ctc tgg gct gac Cys Glu Asn Gly Asn Thr Val Ser Val Thr Ser Tyr Leu Trp Ala Asp	440 445	450	1459
	gat gca gca acc aac gaa ggc acc tcc ctc aac tcc gca cag gtc atc Asp Ala Ala Thr Asn Glu Gly Thr Ser Leu Asn Ser Ala Gln Val Ile	455 460	465	1507
	aac gga gat tgc ggc gac gtc aac atc cct gga gag tcc tct tcc gac Asn Gly Asp Cys Gly Asp Val Asn Ile Pro Gly Glu Ser Ser Ser Asp	470 475	480	1555
	aat tcc tct tct gac ttt gca acc ggc agc atc gca ggc gcc ttt gca Asn Ser Ser Ser Asp Phe Ala Thr Gly Ser Ile Ala Gly Ala Phe Ala	490 495	500	1603

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acc gca gtg ctc gca gtc gta ggc att gcg ggc gca ctg ggt gga ttc 1651
Thr Ala Val Leu Ala Val Val Gly Ile Ala Gly Ala Leu Gly Gly Phe
      505                510                515

ttc cag cag atc ctc gca gcg ttc cca gca ttg cag cag gtc atc cgt 1699
Phe Gln Gln Ile Leu Ala Ala Phe Pro Ala Leu Gln Gln Val Ile Arg
      520                525                530

ttc taaacccact gcttgaaaca ctt 1725
Phe

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<210> 1142

<211> 534

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1142

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Val Val Glu Val Lys Lys Arg Asn Leu Val Ala Pro Leu Thr Ala
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Ser Leu Val Phe Cys Asn Leu Ala Val Ala Asn Ala Val Glu Val
      20                25                30

Glu Ala Glu Ser Pro Val Val Ile Asn Glu Val Glu Ser Asn Ser Asp
      35                40                45

Pro Val Gly Asp Trp Val Glu Leu Ala Asn Thr Asp Asn Asn Asn Ser
      50                55                60

Ile Asp Ile Ser Gly Trp Ser Leu Val Asp Asp Lys Glu Asp Leu Glu
      65                70                75                80

Asn Ala Leu Val Leu Pro Glu Gly Thr Glu Ile Glu Ser Gly Gly Tyr
      85                90                95

Phe Val Ile Tyr Thr Asp Ser Ala Asp Tyr Val Pro Thr Asn Asn Thr
      100                105                110

Phe Gly Gly Gln Glu Tyr Phe Gly Leu Gly Lys Asp Asp Thr Val Thr
      115                120                125

Leu Arg Asn Ala Glu Gly Glu Val Val Ala Thr Tyr Ser Trp Lys Asp
      130                135                140

Leu Gly Glu His Ala Glu Asn Thr Tyr Gly Arg Ile Pro Asp Met Thr
      145                150                155                160

Gly Asp Phe Ala Asn Thr Gly Val Pro Thr Pro Gly Ala Lys Asn Val
      165                170                175

Ala Ala Glu Gly Ser Gly Glu Glu Glu Gly Val Val Ala Asn Ala Gln
      180                185                190

Leu Pro Phe His Asn Val Glu Ile Thr Pro Ile His Leu Gly Gly Asp
      195                200                205

Phe Thr Gly Glu Asp Met Ser Gly Val Asp Phe Asp Ala Asn Ser Thr
      210                215                220

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Ala Trp Ile Ala Asn Asn Asp Ile Gly Lys Ile Tyr Ser Leu Ala His
 225 230 235 240
 Asp Ile Ala Asn Asn Thr Tyr Lys Leu Thr Gly Glu Trp Glu Thr Gly
 245 250 255
 Tyr Pro Glu Gly Gly Gly Glu Pro Asp Ala Glu Gly Ile Val Ala Ala
 260 265 270
 Thr Asn Gly Asp Ile Tyr Leu Ser Thr Glu Arg Asn Asn Ala Asp Lys
 275 280 285
 Asn Val Ser Arg Pro Ser Ile Leu Arg Phe Ala Thr Pro Thr Gly Lys
 290 295 300
 Thr Gly Val Gln Asn Ala Val Gln Glu Trp Asp Leu Ser Glu Phe Val
 305 310 315 320
 Gly Asp Ile Gln Pro Asn Gly Gly Leu Glu Ala Ile Ala Gln Leu Glu
 325 330 335
 Asp Asn Ile Phe Val Val Gly Val Glu Glu Thr Gly Asp Val Ile Val
 340 345 350
 Val Asp Leu Ser Ala Asp Gln Pro Val Leu Val Gln Arg Tyr Glu Ser
 355 360 365
 Ser Phe Asp Gly Val Met Ser Leu Asp Tyr Asn Ala Ala Thr Lys Gln
 370 375 380
 Leu Ser Val Val Cys Asp Glu Ala Cys Asp Gly Leu Ser Glu Ile Leu
 385 390 395 400
 Glu Trp Asp Gly Glu Lys Leu Tyr Lys Ser Asp Asp Lys Ile Tyr Glu
 405 410 415
 Arg Pro Ala Asn Leu Gly Asn Trp Ala Asn Glu Gly Phe Gly Thr Tyr
 420 425 430
 Thr Ser Glu Leu Lys Cys Glu Asn Gly Asn Thr Val Ser Val Thr Ser
 435 440 445
 Tyr Leu Trp Ala Asp Asp Ala Ala Thr Asn Glu Gly Thr Ser Leu Asn
 450 455 460
 Ser Ala Gln Val Ile Asn Gly Asp Cys Gly Asp Val Asn Ile Pro Gly
 465 470 475 480
 Glu Ser Ser Ser Asp Asn Ser Ser Ser Phe Ala Thr Gly Ser Ile
 485 490 495
 Ala Gly Ala Phe Ala Thr Ala Val Leu Ala Val Val Gly Ile Ala Gly
 500 505 510
 Ala Leu Gly Gly Phe Phe Gln Gln Ile Leu Ala Ala Phe Pro Ala Leu
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 Gln Gln Val Ile Arg Phe
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<210> 1143
 <211> 1630
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1630)
 <223> FRXA02398

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 Val Val Glu Val Lys
 1 5
 aag cgt aat ctc ctc gta gct ccc ctc act gct tcc ctg gtg ttc tgt 163
 Lys Arg Asn Leu Val Ala Pro Leu Thr Ala Ser Leu Val Phe Cys
 10 15 20
 aac ttg gct gtt gca gca aac gcc gtt gaa gtt gag gcc gaa tca cca 211
 Asn Leu Ala Val Ala Ala Asn Ala Val Glu Val Glu Ala Glu Ser Pro
 25 30 35
 gtt gtc atc aat gaa gtt gaa tcc aac agc gac cca gtt ggt gac tgg 259
 Val Val Ile Asn Glu Val Glu Ser Asn Ser Asp Pro Val Gly Asp Trp
 40 45 50
 gtg gag ttg gct aac acc gac aac aac aac tcc atc gac att tcc ggt 307
 Val Glu Leu Ala Asn Thr Asp Asn Asn Asn Ser Ile Asp Ile Ser Gly
 55 60 65
 tgg tcc tta gtc gat gac aag gaa gac ctg gaa aat gcc ctc gtc ctt 355
 Trp Ser Leu Val Asp Asp Lys Glu Asp Leu Glu Asn Ala Leu Val Leu
 70 75 80 85
 cct gaa ggc act gag att gag tcc ggt gga tac ttt gtt atc tac acc 403
 Pro Glu Gly Thr Glu Ile Glu Ser Gly Gly Tyr Phe Val Ile Tyr Thr
 90 95 100
 gac tct gct gat tac gtg cct acc aac aac acc ttt ggt ggc cag gaa 451
 Asp Ser Ala Asp Tyr Val Pro Thr Asn Asn Thr Phe Gly Gly Gln Glu
 105 110 115
 tac ttc ggc ctc ggc aaa gat gac act gtt act ctg cgc aac gct gaa 499
 Tyr Phe Gly Leu Gly Lys Asp Thr Val Thr Leu Arg Asn Ala Glu
 120 125 130
 ggc gaa gta gtt gct acc tat tcc tgg aag gat ctg ggc gag cac gca 547
 Gly Glu Val Val Ala Thr Tyr Ser Trp Lys Asp Leu Gly Glu His Ala
 135 140 145
 gaa aac acc tat ggt cgc atc cca gat atg act ggt gat ttc gca aac 595
 Glu Asn Thr Tyr Gly Arg Ile Pro Asp Met Thr Gly Asp Phe Ala Asn
 150 155 160 165
 acc ggc gtt cca acc cca ggt gca aag aat gtt gct gct gaa ggc tcc 643
 Thr Gly Val Pro Thr Pro Gly Ala Lys Asn Val Ala Ala Glu Gly Ser
 170 175 180

ggc gaa gaa gaa ggc gtt gtt gca aac gcc cag ctt cca ttc cac aac	691
Gly Glu Glu Glu Gly Val Val Ala Asn Ala Gln Leu Pro Phe His Asn	
185 190 195	
ggt gaa atc acc cca att cac ctc ggt gga gat ttc acc ggt gaa gat	739
Val Glu Ile Thr Pro Ile His Leu Gly Gly Asp Phe Thr Gly Glu Asp	
200 205 210	
atg tcc ggc gtt gat ttc gat gca aac agc acc gca tgg atc gcc aac	787
Met Ser Gly Val Asp Phe Asp Ala Asn Ser Thr Ala Trp Ile Ala Asn	
215 220 225	
aat gac att gga aag atc tac tcc ctc gcc cac gac ata gct aac aac	835
Asn Asp Ile Gly Lys Ile Tyr Ser Leu Ala His Asp Ile Ala Asn Asn	
230 235 240 245	
acc tac aag ctg act ggc gaa tgg gaa acc ggc tac cca gaa ggc ggc	883
Thr Tyr Lys Leu Thr Gly Glu Trp Glu Thr Gly Tyr Pro Glu Gly Gly	
250 255 260	
gga gag cca gac gct gaa ggc atc gtc gca gct acc aac ggt gac atc	931
Gly Glu Pro Asp Ala Glu Gly Ile Val Ala Ala Thr Asn Gly Asp Ile	
265 270 275	
tac ctg tcc acc gag cgc aac aac gct gac aag aac gtc tct cgc cca	979
Tyr Leu Ser Thr Glu Arg Asn Asn Ala Asp Lys Asn Val Ser Arg Pro	
280 285 290	
tcc atc ctg cgt ttt gct acc cca act ggc aag act ggc gta caa aac	1027
Ser Ile Leu Arg Phe Ala Thr Pro Thr Gly Lys Thr Gly Val Gln Asn	
295 300 305	
gca gtt cag gaa tgg gac ctg tct gag ttc gtc ggc gac att cag ccc	1075
Ala Val Gln Glu Trp Asp Leu Ser Glu Phe Val Gly Asp Ile Gln Pro	
310 315 320 325	
aat ggt ggt ctt gag gca atc gcg cag ctc gag gac aac atc ttc gtt	1123
Asn Gly Gly Leu Glu Ala Ile Ala Gln Leu Glu Asp Asn Ile Phe Val	
330 335 340	
gtc ggt gtc gaa gag aca ggt gat gtc atc gtt gtt gat ctt tcc gct	1171
Val Gly Val Glu Glu Thr Gly Asp Val Ile Val Val Asp Leu Ser Ala	
345 350 355	
gac cag cca gtt ctg gtt caa agg tac gaa tct tcc ttc gac ggt gtc	1219
Asp Gln Pro Val Leu Val Gln Arg Tyr Glu Ser Ser Phe Asp Gly Val	
360 365 370	
atg tcg ctt gat tac aac gca gca acc aag cag ctc agc gtt gtg tgc	1267
Met Ser Leu Asp Tyr Asn Ala Ala Thr Lys Gln Ser Val Val Cys	
375 380 385	
gac gaa gca tgt gac ggc ttg tct gaa atc ctc gaa tgg gat ggc gag	1315
Asp Glu Ala Cys Asp Gly Leu Ser Glu Ile Leu Glu Trp Asp Gly Glu	
390 395 400 405	
aag ctg tac aag tcc gac gac aag atc tac gag cgt cca gca aac ctg	1363
Lys Leu Tyr Lys Ser Asp Asp Lys Ile Tyr Glu Arg Pro Ala Asn Leu	
410 415 420	

ggc aac tgg gct aac gaa ggc ttc ggc acc tac acc tca gag ctt aaa 1411
 Gly Asn Trp Ala Asn Glu Gly Phe Gly Thr Tyr Thr Ser Glu Leu Lys
 425 430 435

tgc gag aac ggc aac acc gtt tct gtc acc agc tac ctc tgg gct gac 1459
 Cys Glu Asn Gly Asn Thr Val Ser Val Thr Ser Tyr Leu Trp Ala Asp
 440 445 450

gat gca gca acc aac gaa ggc acc tcc ctc aac tcc gca cag gtc atc 1507
 Asp Ala Ala Thr Asn Glu Gly Thr Ser Leu Asn Ser Ala Gln Val Ile
 455 460 465

aac gga gat tgc ggc gac gtc aac atc cct gga gag tcc tct tcc gac 1555
 Asn Gly Asp Cys Gly Asp Val Asn Ile Pro Gly Glu Ser Ser Ser Asp
 470 475 480 485

aat tcc tct tct gac ttt gca acc ggc agc atc gca ggc gcc ttt gca 1603
 Asn Ser Ser Ser Asp Phe Ala Thr Gly Ser Ile Ala Gly Ala Phe Ala
 490 495 500

acc gca gtg ctc gca gtc gta ggc att 1630
 Thr Ala Val Leu Ala Val Val Gly Ile
 505 510

<210> 1144

<211> 510

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1144

Val Val Glu Val Lys Lys Arg Asn Leu Leu Val Ala Pro Leu Thr Ala
 1 5 10 15

Ser Leu Val Phe Cys Asn Leu Ala Val Ala Ala Asn Ala Val Glu Val
 20 25 30

Glu Ala Glu Ser Pro Val Val Ile Asn Glu Val Glu Ser Asn Ser Asp
 35 40 45

Pro Val Gly Asp Trp Val Glu Leu Ala Asn Thr Asp Asn Asn Asn Ser
 50 55 60

Ile Asp Ile Ser Gly Trp Ser Leu Val Asp Asp Lys Glu Asp Leu Glu
 65 70 75 80

Asn Ala Leu Val Leu Pro Glu Gly Thr Glu Ile Glu Ser Gly Gly Tyr
 85 90 95

Phe Val Ile Tyr Thr Asp Ser Ala Asp Tyr Val Pro Thr Asn Asn Thr
 100 105 110

Phe Gly Gly Gln Glu Tyr Phe Gly Leu Gly Lys Asp Asp Thr Val Thr
 115 120 125

Leu Arg Asn Ala Glu Gly Glu Val Val Ala Thr Tyr Ser Trp Lys Asp
 130 135 140

Leu Gly Glu His Ala Glu Asn Thr Tyr Gly Arg Ile Pro Asp Met Thr
 145 150 155 160

Gly Asp Phe Ala Asn Thr Gly Val Pro Thr Pro Gly Ala Lys Asn Val
 165 170
 Ala Ala Glu Gly Ser Gly Glu Glu Glu Gly Val Val Ala Asn Ala Gln
 180 185 190
 Leu Pro Phe His Asn Val Glu Ile Thr Pro Ile His Leu Gly Gly Asp
 195 200 205
 Phe Thr Gly Glu Asp Met Ser Gly Val Asp Phe Asp Ala Asn Ser Thr
 210 215 220
 Ala Trp Ile Ala Asn Asn Asp Ile Gly Lys Ile Tyr Ser Leu Ala His
 225 230 235 240
 Asp Ile Ala Asn Asn Thr Tyr Lys Leu Thr Gly Glu Trp Glu Thr Gly
 245 250 255
 Tyr Pro Glu Gly Gly Glu Glu Pro Asp Ala Glu Gly Ile Val Ala Ala
 260 265 270
 Thr Asn Gly Asp Ile Tyr Leu Ser Thr Glu Arg Asn Asn Ala Asp Lys
 275 280 285
 Asn Val Ser Arg Pro Ser Ile Leu Arg Phe Ala Thr Pro Thr Gly Lys
 290 295 300
 Thr Gly Val Gln Asn Ala Val Gln Glu Trp Asp Leu Ser Glu Phe Val
 305 310 315 320
 Gly Asp Ile Gln Pro Asn Gly Gly Leu Glu Ala Ile Ala Gln Leu Glu
 325 330 335
 Asp Asn Ile Phe Val Val Gly Val Glu Glu Thr Gly Asp Val Ile Val
 340 345 350
 Val Asp Leu Ser Ala Asp Gln Pro Val Leu Val Gln Arg Tyr Glu Ser
 355 360 365
 Ser Phe Asp Gly Val Met Ser Leu Asp Tyr Asn Ala Ala Thr Lys Gln
 370 375 380
 Leu Ser Val Val Cys Asp Glu Ala Cys Asp Gly Leu Ser Glu Ile Leu
 385 390 395 400
 Glu Trp Asp Gly Glu Lys Leu Tyr Lys Ser Asp Asp Lys Ile Tyr Glu
 405 410 415
 Arg Pro Ala Asn Leu Gly Asn Trp Ala Asn Glu Gly Phe Gly Thr Tyr
 420 425 430
 Thr Ser Glu Leu Lys Cys Glu Asn Gly Asn Thr Val Ser Val Thr Ser
 435 440 445
 Tyr Leu Trp Ala Asp Asp Ala Ala Thr Asn Glu Gly Thr Ser Leu Asn
 450 455 460
 Ser Ala Gln Val Ile Asn Gly Asp Cys Gly Asp Val Asn Ile Pro Gly
 465 470 475 480
 Glu Ser Ser Ser Asp Asn Ser Ser Ser Asp Phe Ala Thr Gly Ser Ile

485

490

495

Ala Gly Ala Phe Ala Thr Ala Val Leu Ala Val Val Gly Ile
 500 505 510

<210> 1145

<211> 672

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(649)

<223> RXN02406

<400> 1145

cactctgata gcctttttctc tgaaattgta ccgagcattt gattttgttc cccatcaat 60

gctgggtttg gtgacaaaaa ctgcggcgaa ggaccaccga atg gaa acc ctt gca 115
 Met Glu Thr Leu Ala
 1 5

gca caa gcg cgc acc ctg cta gaa aaa tgg ggc gtc gcg ccg acg cac 163
 Ala Gln Ala Arg Thr Leu Leu Glu Lys Trp Gly Val Ala Pro Thr His
 10 15 20

gca tct ttc gtc gaa tcc att gca aag gcc atc ccg att ctg tcg atc 211
 Ala Ser Phe Val Glu Ser Ile Ala Lys Ala Ile Pro Ile Leu Ser Ile
 25 30 35

ctg ctg acg ctg att gtc acc gtg aat gga att tca agc gga aat ccg 259
 Leu Leu Thr Leu Ile Val Thr Val Asn Gly Ile Ser Ser Gly Asn Pro
 40 45 50

gtc cag cca cca gca ctg gaa cag gta cgg acc gat gta gtg aac aag 307
 Val Gln Pro Pro Ala Leu Glu Gln Val Arg Thr Asp Val Val Asn Lys
 55 60 65

atc aac tac gaa cgc aac cta aag gcc ctc gtc tcg atc agc ccg gag 355
 Ile Asn Tyr Glu Arg Asn Leu Lys Gly Leu Val Ser Ile Ser Pro Glu
 70 75 80 85

ctt gaa tta cac acg gca gcc caa aca att gcg cag cga aat gca gac 403
 Leu Glu Leu His Thr Ala Ala Gln Thr Ile Ala Gln Arg Asn Ala Asp
 90 95 100

tca gat tcc gaa gaa aaa gta ccg gat cca gag ggc aac ctg gtg gtt 451
 Ser Asp Ser Glu Glu Lys Val Pro Asp Pro Glu Gly Asn Leu Val Val
 105 110 115

ctg caa cag aat ctg ccc tat gca aat gcc aac gcc gat acc atc gtt 499
 Leu Gln Gln Asn Leu Pro Tyr Ala Asn Ala Asn Ala Asp Thr Ile Val
 120 125 130

gat cgg ttc tta aac tct cct gat cat gtc aaa cta ctg ctt gca aac 547
 Asp Arg Phe Leu Asn Ser Pro Asp His Val Lys Leu Leu Leu Ala Asn
 135 140 145

gat tat gaa gcc atc gga gtt ggt gtg gcc tac aag ggt gat cat gcg 595
 Asp Tyr Glu Ala Ile Gly Val Gly Val Ala Tyr Lys Gly Asp His Ala

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150                155                160                165
tgg ata gtg gtg gag ttc act gta gct ccc gct gat tcc gta gaa tca 643
Trp Ile Val Val Glu Phe Thr Val Ala Pro Ala Asp Ser Val Glu Ser
                170                175                180

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aca gag tgaataccaa tccgtctgaa ttc 672
Thr Glu

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<210> 1146

<211> 183

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1146

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Met Glu Thr Leu Ala Ala Gln Ala Arg Thr Leu Leu Glu Lys Trp Gly
  1                5                10                15

```

```

Val Ala Pro Thr His Ala Ser Phe Val Glu Ser Ile Ala Lys Ala Ile
      20                25                30

```

```

Pro Ile Leu Ser Ile Leu Leu Thr Leu Ile Val Thr Val Asn Gly Ile
      35                40                45

```

```

Ser Ser Gly Asn Pro Val Gln Pro Pro Ala Leu Glu Gln Val Arg Thr
      50                55                60

```

```

Asp Val Val Asn Lys Ile Asn Tyr Glu Arg Asn Leu Lys Gly Leu Val
      65                70                75                80

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```

Ser Ile Ser Pro Glu Leu Glu Leu His Thr Ala Ala Gln Thr Ile Ala
      85                90                95

```

```

Gln Arg Asn Ala Asp Ser Asp Ser Glu Glu Lys Val Pro Asp Pro Glu
      100               105               110

```

```

Gly Asn Leu Val Val Leu Gln Gln Asn Leu Pro Tyr Ala Asn Ala Asn
      115               120               125

```

```

Ala Asp Thr Ile Val Asp Arg Phe Leu Asn Ser Pro Asp His Val Lys
      130               135               140

```

```

Leu Leu Leu Ala Asn Asp Tyr Glu Ala Ile Gly Val Gly Val Ala Tyr
      145               150               155               160

```

```

Lys Gly Asp His Ala Trp Ile Val Val Glu Phe Thr Val Ala Pro Ala
      165               170               175

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Asp Ser Val Glu Ser Thr Glu
      180

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<210> 1147

<211> 672

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(649)

<223> FRXA02406

<400> 1147

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gctgggttttg gtgacaaaaa ctccggcgaa ggaccacga atg gaa acc ctt gca 115
Met Glu Thr Leu Ala
1 5

gca caa gcg cgc acc ctg cta gaa aaa tgg ggc gtc gcg ccg acg cac 163
Ala Gln Ala Arg Thr Leu Leu Glu Lys Trp Gly Val Ala Pro Thr His
10 15 20

gca tct ttc gtc gaa tcc att gca aag gcc atc ccg att ctg tcg atc 211
Ala Ser Phe Val Glu Ser Ile Ala Lys Ala Ile Pro Ile Leu Ser Ile
25 30 35

ctg ctg acg ctg att gtc acc gtg aat gga att tca agc gga aat ccg 259
Leu Leu Thr Leu Ile Val Thr Val Asn Gly Ile Ser Ser Gly Asn Pro
40 45 50

gtc cag cca cca gca ctg gaa cag gta cgg acc gat gta gtg aac aag 307
Val Gln Pro Pro Ala Leu Glu Gln Val Arg Thr Asp Val Val Asn Lys
55 60 65

atc aac tac gaa cgc aac cta aag gcc ctc gtc tcg atc agc ccg gag 355
Ile Asn Tyr Glu Arg Asn Leu Lys Gly Leu Val Ser Ile Ser Pro Glu
70 75 80 85

ctt gaa tta cac acg gca gcc caa aca att gcg cag cga aat gca gac 403
Leu Glu Leu His Thr Ala Ala Gln Thr Ile Ala Gln Arg Asn Ala Asp
90 95 100

tca gat tcc gaa gaa aaa gta ccg gat cca gag gga acc ttg gtg gtt 451
Ser Asp Ser Glu Glu Lys Val Pro Asp Pro Glu Gly Thr Leu Val Val
105 110 115

ctg caa cag aat ctg ccc tat gca aat gcc aac gcc gat acc atc gtt 499
Leu Gln Gln Asn Leu Pro Tyr Ala Asn Ala Asn Ala Asp Thr Ile Val
120 125 130

gat cgg ttc tta aac tct cct gat cat gtc aaa cta ctg ctt gca aac 547
Asp Arg Phe Leu Asn Ser Pro Asp His Val Lys Leu Leu Leu Ala Asn
135 140 145

gat tat gaa gcc atc gga gtt ggt gtg gcc tac aag ggt gat cat gcg 595
Asp Tyr Glu Ala Ile Gly Val Gly Val Ala Tyr Lys Gly Asp His Ala
150 155 160 165

tgg ata gtg gtg gag ttc act gta gct ccc gct gat tcc gta gaa tca 643
Trp Ile Val Val Glu Phe Thr Val Ala Pro Ala Asp Ser Val Glu Ser
170 175 180

aca gag tgaataccaa tccgtctgaa ttc 672
Thr Glu

<210> 1148

<211> 183

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1148

Met Glu Thr Leu Ala Ala Gln Ala Arg Thr Leu Leu Glu Lys Trp Gly
 1 5 10 15

Val Ala Pro Thr His Ala Ser Phe Val Glu Ser Ile Ala Lys Ala Ile
 20 25 30

Pro Ile Leu Ser Ile Leu Leu Thr Leu Ile Val Thr Val Asn Gly Ile
 35 40 45

Ser Ser Gly Asn Pro Val Gln Pro Pro Ala Leu Glu Gln Val Arg Thr
 50 55 60

Asp Val Val Asn Lys Ile Asn Tyr Glu Arg Asn Leu Lys Gly Leu Val
 65 70 75 80

Ser Ile Ser Pro Glu Leu Glu Leu His Thr Ala Ala Gln Thr Ile Ala
 85 90 95

Gln Arg Asn Ala Asp Ser Asp Ser Glu Glu Lys Val Pro Asp Pro Glu
 100 105 110

Gly Thr Leu Val Val Leu Gln Gln Asn Leu Pro Tyr Ala Asn Ala Asn
 115 120 125

Ala Asp Thr Ile Val Asp Arg Phe Leu Asn Ser Pro Asp His Val Lys
 130 135 140

Leu Leu Leu Ala Asn Asp Tyr Glu Ala Ile Gly Val Gly Val Ala Tyr
 145 150 155 160

Lys Gly Asp His Ala Trp Ile Val Val Glu Phe Thr Val Ala Pro Ala
 165 170 175

Asp Ser Val Glu Ser Thr Glu
 180

<210> 1149

<211> 495

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(472)

<223> RXN02407

<400> 1149

ggataaaaat ttggatgaca tatcacctaa gcttgcaatt tctactggaa tagcgcgact 60

actctgcacc aacgcatagt tgttgactag gctatttgtc atg aat agg caa aac 115
 Met Asn Arg Gln Asn
 1 5

caa ctt cac tac ccg cag gaa gtg aag gca gtg gaa agt gtg gaa tca 163
 Gln Leu His Tyr Pro Gln Glu Val Lys Ala Val Glu Ser Val Glu Ser
 10 15 20

agc ttg aac atg tgc tca cct tct gca cgc ctt gcc acg cca gat gtt 211
 Ser Leu Asn Met Ser Ser Pro Ser Ala Pro Leu Ala Thr Pro Asp Val
 25 30 35

gag ctt gat gtg cac acg ttg tgc agc gaa aac ctg cct tgg ttg tgc 259
 Glu Leu Asp Val His Thr Leu Ser Ser Glu Asn Leu Pro Trp Leu Cys
 40 45 50

atc gtg tgg gat gat cgc gtc aat ttg atg agc tat gtc acc tac gtt 307
 Ile Val Trp Asp Asp Pro Val Asn Leu Met Ser Tyr Val Thr Tyr Val
 55 60 65

ttt cag act gtg ttg ggc ttc agt aag aag agg gcc act gag ctg atg 355
 Phe Gln Thr Val Leu Gly Phe Ser Lys Lys Arg Ala Thr Glu Leu Met
 70 75 80 85

atg cag gtg cac acc gaa ggt aaa gcc gtg gtg agt tct ggc gag aag 403
 Met Gln Val His Thr Glu Gly Lys Ala Val Val Ser Ser Gly Glu Lys
 90 95 100

gac aaa gtg gag ggt gat gtg aag aaa ctc cac acc gca ggg ctg tgg 451
 Asp Lys Val Glu Gly Asp Val Lys Lys Leu His Thr Ala Gly Leu Trp
 105 110 115

gcg aca atg cag cag gca ggg taggggagaa ttttcatgca gca 495
 Ala Thr Met Gln Gln Ala Gly
 120

<210> 1150
 <211> 124
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1150
 Met Asn Arg Gln Asn Gln Leu His Tyr Pro Gln Glu Val Lys Ala Val
 1 5 10 15

Glu Ser Val Glu Ser Ser Leu Asn Met Ser Ser Pro Ser Ala Pro Leu
 20 25 30

Ala Thr Pro Asp Val Glu Leu Asp Val His Thr Leu Ser Ser Glu Asn
 35 40 45

Leu Pro Trp Leu Cys Ile Val Trp Asp Asp Pro Val Asn Leu Met Ser
 50 55 60

Tyr Val Thr Tyr Val Phe Gln Thr Val Leu Gly Phe Ser Lys Lys Arg
 65 70 75 80

Ala Thr Glu Leu Met Met Gln Val His Thr Glu Gly Lys Ala Val Val
 85 90 95

Ser Ser Gly Glu Lys Asp Lys Val Glu Gly Asp Val Lys Lys Leu His
 100 105 110

Thr Ala Gly Leu Trp Ala Thr Met Gln Gln Ala Gly
 115 120

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<220>
<221> CDS
<222> (101)..(406)
<223> FRXA02407
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<210> 1152
<211> 102
<212> PRT
<213> Corynebacterium glutamicum
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<400> 1152
Met Asn Arg Gln Asn Gln Leu His Tyr Pro Gln Glu Val Lys Ala Val
 1              5              10              15
Glu Ser Val Glu Ser Ser Leu Asn Met Ser Ser Pro Ser Ala Pro Leu
 20              25              30
Ala Thr Pro Asp Val Glu Leu Asp Val His Thr Leu Ser Ser Glu Asn
 35              40              45

```

Leu Pro Trp Leu Cys Ile Val Trp Asp Asp Pro Val Asn Leu Met Ser
 50 55 60
 Tyr Val Thr Tyr Val Phe Gln Thr Val Leu Gly Phe Ser Lys Lys Arg
 65 70 75 80
 Ala Thr Glu Leu Met Met Gln Val His Thr Glu Gly Lys Ala Val Val
 85 90 95
 Ser Ser Gly Glu Lys Asp
 100

<210> 1153
 <211> 1035
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1012)
 <223> RXN02408

<400> 1153
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 cctacaatca agagtccttg ctggaagcga tgatgaatta atg ctt atc gac gtc 115
 Met Leu Ile Asp Val
 1 5
 gcg ggc ttc ctt tta ggc cac gtc acg aag ggg gat acg ggt tgc tca 163
 Ala Gly Phe Leu Leu Gly His Val Thr Lys Gly Asp Thr Gly Cys Ser
 10 15 20
 gtg gtc att gca cct aac ggt gca ttt gcg ggc gtc gat gtc cgt ggg 211
 Val Val Ile Ala Pro Asn Gly Ala Phe Ala Gly Val Asp Val Arg Gly
 25 30 35
 gga ggc cca ggc acc agg gaa acc gac ctt cta gaa cca cac aat tct 259
 Gly Gly Pro Gly Thr Arg Glu Thr Asp Leu Leu Glu Pro His Asn Ser
 40 45 50
 gtg cag caa gca cat gcc gtg gtg ttg tgt ggc ggt tcg gcg ttc ggg 307
 Val Gln Gln Ala His Ala Val Val Leu Cys Gly Ser Ala Phe Gly
 55 60 65
 ttg gct gct gcc gat gga gtg atg aca gcc cta gaa aac cgc ggt att 355
 Leu Ala Ala Ala Asp Gly Val Met Thr Ala Leu Glu Asn Arg Gly Ile
 70 75 80 85
 ggt ttc cct gtc cgt ccc gaa ggg cct atc gtg cca atc gtt cca ggc 403
 Gly Phe Pro Val Arg Pro Glu Gly Pro Ile Val Pro Ile Val Pro Gly
 90 95 100
 gct gtg att ttt gat ttg ttg gtg ggc gat ccc aaa aac agg ccc acg 451
 Ala Val Ile Phe Asp Leu Leu Val Gly Asp Pro Lys Asn Arg Pro Thr
 105 110 115
 gca gct gat ggg gaa caa gca gtt gaa aac gct ttc gct ggt aca cac 499
 Ala Ala Asp Gly Glu Gln Ala Val Glu Asn Ala Phe Ala Gly Thr His
 120 125 130

aac ggt tcg ggc agc gtc ggt gca gga acg ggt gct aca gca ggt cgg 547
 Asn Gly Ser Gly Ser Val Gly Ala Gly Thr Gly Ala Thr Ala Gly Arg
 135 140 145
 ctg cgt ggc ggt ttt ggc caa agc tcg cgc cgg gtc gga aag tac acc 595
 Leu Arg Gly Gly Phe Gly Gln Ser Ser Arg Val Gly Lys Tyr Thr
 150 155 160 165
 atc gcg gca ggg gtc gtc gcg aat cct gtt ggg gaa gtc gtc gac cta 643
 Ile Ala Ala Gly Val Val Ala Asn Pro Val Gly Glu Val Val Asp Leu
 170 175 180
 aca act gga gct ttg ttt ggt agg ccc gaa gtg atg ggg gtc ggc gtc 691
 Thr Thr Gly Ala Leu Phe Gly Arg Pro Glu Val Met Gly Val Gly Val
 185 190 195
 gat aag cta aaa agc gcg gca gag acg ctg aac acg acc atc ggc gtc 739
 Asp Lys Leu Lys Ser Ala Ala Glu Thr Leu Asn Thr Thr Ile Gly Val
 200 205 210
 gtg gca act gac gcg ccg gtg aca aaa gcc caa gcg aag cgc ttg gcg 787
 Val Ala Thr Asp Ala Pro Val Thr Lys Ala Gln Ala Lys Arg Leu Ala
 215 220 225
 ctg gtg gcc cat gat ggt ttg gcg agg gca gtg cgg ccg tcg cat tca 835
 Leu Val Ala His Asp Gly Leu Ala Arg Ala Val Arg Pro Ser His Ser
 230 235 240 245
 ccg atg gac ggt gac aca ttt ttc gcc atg tca tcg ggt gat ggt agt 883
 Pro Met Asp Gly Asp Thr Phe Phe Ala Met Ser Ser Gly Asp Gly Ser
 250 255 260
 ggc gtt acc ccg gtt gag ctg gcg gaa ttg tcg gct cat gct gca gat 931
 Gly Val Thr Pro Val Glu Leu Ala Glu Leu Ser Ala His Ala Ala Asp
 265 270 275
 tgc gta cag gac gct atc atc gac gcc ata ctt acc gcg agt ccg gga 979
 Cys Val Gln Asp Ala Ile Ile Asp Ala Ile Leu Thr Ala Ser Pro Gly
 280 285 290
 ctc ggg ctc aaa agc ttc agg gaa ctt tta cca tgagttacaa cagcccgtat 1032
 Leu Gly Leu Lys Ser Phe Arg Glu Leu Leu Pro
 295 300
 aac 1035

<210> 1154
 <211> 304
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1154
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 1 5 10 15
 Asp Thr Gly Cys Ser Val Val Ile Ala Pro Asn Gly Ala Phe Ala Gly
 20 25 30
 Val Asp Val Arg Gly Gly Gly Pro Gly Thr Arg Glu Thr Asp Leu Leu

	35						40						45					
	Glu	Pro	His	Asn	Ser	Val	Gln	Gln	Ala	His	Ala	Val	Val	Leu	Cys	Gly		
	50						55					60						
	Gly	Ser	Ala	Phe	Gly	Leu	Ala	Ala	Ala	Asp	Gly	Val	Met	Thr	Ala	Leu		
	65					70					75					80		
	Glu	Asn	Arg	Gly	Ile	Gly	Phe	Pro	Val	Arg	Pro	Glu	Gly	Pro	Ile	Val		
					85					90					95			
	Pro	Ile	Val	Pro	Gly	Ala	Val	Ile	Phe	Asp	Leu	Leu	Val	Gly	Asp	Pro		
				100					105					110				
	Lys	Asn	Arg	Pro	Thr	Ala	Ala	Asp	Gly	Glu	Gln	Ala	Val	Glu	Asn	Ala		
				115				120					125					
	Phe	Ala	Gly	Thr	His	Asn	Gly	Ser	Gly	Ser	Val	Gly	Ala	Gly	Thr	Gly		
		130					135					140						
	Ala	Thr	Ala	Gly	Arg	Leu	Arg	Gly	Gly	Phe	Gly	Gln	Ser	Ser	Arg	Arg		
	145					150					155					160		
	Val	Gly	Lys	Tyr	Thr	Ile	Ala	Ala	Gly	Val	Val	Ala	Asn	Pro	Val	Gly		
					165					170						175		
	Glu	Val	Val	Asp	Leu	Thr	Thr	Gly	Ala	Leu	Phe	Gly	Arg	Pro	Glu	Val		
				180				185						190				
	Met	Gly	Val	Gly	Val	Asp	Lys	Leu	Lys	Ser	Ala	Ala	Glu	Thr	Leu	Asn		
			195					200					205					
	Thr	Thr	Ile	Gly	Val	Val	Ala	Thr	Asp	Ala	Pro	Val	Thr	Lys	Ala	Gln		
		210					215					220						
	Ala	Lys	Arg	Leu	Ala	Leu	Val	Ala	His	Asp	Gly	Leu	Ala	Arg	Ala	Val		
	225					230					235				240			
	Arg	Pro	Ser	His	Ser	Pro	Met	Asp	Gly	Asp	Thr	Phe	Phe	Ala	Met	Ser		
					245					250					255			
	Ser	Gly	Asp	Gly	Ser	Gly	Val	Thr	Pro	Val	Glu	Leu	Ala	Glu	Leu	Ser		
				260					265					270				
	Ala	His	Ala	Ala	Asp	Cys	Val	Gln	Asp	Ala	Ile	Ile	Asp	Ala	Ile	Leu		
		275						280					285					
	Thr	Ala	Ser	Pro	Gly	Leu	Gly	Leu	Lys	Ser	Phe	Arg	Glu	Leu	Leu	Pro		
		290					295					300						

<210> 1155

<211> 928

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<223> FRXA02408

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gcg ggc ttc ctt tta ggc cac gtc acg aag ggg gat acg ggt tgc tca 163
Ala Gly Phe Leu Leu Gly His Val Thr Lys Gly Asp Thr Gly Cys Ser
10 15 20

gga ggc cca ggc acc agg gaa acc gac ctt cta gaa cca cac aat tct 259
Gly Gly Pro Gly Thr Arg Glu Thr Asp Leu Leu Glu Pro His Asn Ser
40 45 50

ttg gct gct gcc gat gga gtg atg aca gcc cta gaa aac cgc ggt att 355
Leu Ala Ala Ala Asp Gly Val Met Thr Ala Leu Glu Asn Arg Gly Ile
70 75 80 85

gct gtg att ttt gat ttg ttg gtg ggc gat ccc aaa aac agg ccc acg 451
Ala Val Ile Phe Asp Leu Leu Val Gly Asp Pro Lys Asn Arg Pro Thr
105 110 115

aac ggt tgc ggc agc gtc ggt gca gga acg ggt gct aca gca ggt cgg 547
Asn Gly Ser Gly Ser Val Gly Ala Gly Thr Gly Ala Thr Ala Gly Arg
135 140 145

ctg cgt ggc ggt ttt ggc caa agc tgc cgc cgg gtc gga aag tac acc 595
Leu Arg Gly Gly Phe Gly Gln Ser Ser Arg Arg Val Gly Lys Tyr Thr
150 155 160 165

atc gcg gca ggg gtc gtg gcg aat cct gtt ggg gaa gtc gtg gac cta 643
Ile Ala Ala Gly Val Val Ala Asn Pro Val Gly Glu Val Val Asp Leu
170 175 180

aca act gga gct ttg ttt ggt agg ccc gaa gtg atg ggg gtg ggc gtc 691
Thr Thr Gly Ala Leu Phe Gly Arg Pro Glu Val Met Gly Val Gly Val
185 190 195

gat aag cta aaa agc gcg gca gag acg ctg aac acg acc atc ggc gtc 739
Asp Lys Leu Lys Ser Ala Ala Glu Thr Leu Asn Thr Thr Ile Gly Val
200 205 210

gtg gca act gac gcg ccg gtg aca aaa gcc caa gcg aag cgc ttg gcg 787
Val Ala Thr Asp Ala Pro Val Thr Lys Ala Gln Ala Lys Arg Leu Ala
215 220 225

ctg gtg gcc cat gat ggt ttg gcg agg gca gtg cgg ccg tcg cat tca 835
Leu Val Ala His Asp Gly Leu Ala Arg Ala Val Arg Pro Ser His Ser
230 235 240 245

ccg atg gac ggt gac aca ttt ttc gcc atg tca tcg ggt gat ggt agt 883
Pro Met Asp Gly Asp Thr Phe Phe Ala Met Ser Ser Gly Asp Gly Ser
250 255 260

ggc gtt acc ccg gtt gag ctg ggg gaa ttg tcg gct cat gct gca 928
Gly Val Thr Pro Val Glu Leu Gly Glu Leu Ser Ala His Ala Ala
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<210> 1156

<211> 276

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1156

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20 25 30

Val Asp Val Arg Gly Gly Gly Pro Gly Thr Arg Glu Thr Asp Leu Leu
35 40 45

Glu Pro His Asn Ser Val Gln Gln Ala His Ala Val Val Leu Cys Gly
50 55 60

Gly Ser Ala Phe Gly Leu Ala Ala Ala Asp Gly Val Met Thr Ala Leu
65 70 75 80

Glu Asn Arg Gly Ile Gly Phe Pro Val Arg Pro Glu Gly Pro Ile Val
85 90 95

Pro Ile Val Pro Gly Ala Val Ile Phe Asp Leu Leu Val Gly Asp Pro
100 105 110

Lys Asn Arg Pro Thr Ala Ala Asp Gly Glu Gln Ala Val Glu Asn Ala
115 120 125

Phe Ala Gly Thr His Asn Gly Ser Gly Ser Val Gly Ala Gly Thr Gly
130 135 140

Ala Thr Ala Gly Arg Leu Arg Gly Gly Phe Gly Gln Ser Ser Arg Arg
145 150 155 160

Val Gly Lys Tyr Thr Ile Ala Ala Gly Val Val Ala Asn Pro Val Gly
165 170 175

Glu Val Val Asp Leu Thr Thr Gly Ala Leu Phe Gly Arg Pro Glu Val
180 185 190

Met Gly Val Gly Val Asp Lys Leu Lys Ser Ala Ala Glu Thr Leu Asn

195 200 205

Thr Thr Ile Gly Val Val Ala Thr Asp Ala Pro Val Thr Lys Ala Gln
210 215 220

Ala Lys Arg Leu Ala Leu Val Ala His Asp Gly Leu Ala Arg Ala Val
225 230 235 240

Arg Pro Ser His Ser Pro Met Asp Gly Asp Thr Phe Phe Ala Met Ser
245 250 255

Ser Gly Asp Gly Ser Gly Val Thr Pro Val Glu Leu Gly Glu Leu Ser
260 265 270

Ala His Ala Ala
275

<210> 1157
<211> 660
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (101)..(637)
<223> RXN02409

<400> 1157
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gtgggcgaca atgcagcagg cagggtaggg gagaattttc atg cag cag tgg aag 115
Met Gln Gln Trp Lys
1 5
aag aaa aaa ggg ctg atg cgc cag gct cgt tac gcg gtg gtt ttt gag 163
Lys Lys Lys Gly Leu Met Arg Gln Ala Arg Tyr Ala Val Val Phe Glu
10 15 20
ccg atg gag cgg gaa gtg ttg ggt gat ttg tca gct gcg gtc agt gag 211
Pro Met Glu Arg Glu Val Leu Gly Asp Leu Ser Ala Ala Val Ser Glu
25 30 35
gcg ttg att cag cgt gca cag tct gtg ccg aag gat cct ctg gca gag 259
Ala Leu Ile Gln Arg Ala Gln Ser Val Pro Lys Asp Pro Leu Ala Glu
40 45 50
atg acc ggc atg aca agt gga cac aaa gaa gca cca acc gat ccg gcg 307
Met Thr Gly Met Thr Ser Gly His Lys Glu Ala Pro Thr Asp Pro Ala
55 60 65
ctt gcg cgt ttg ctc cct gat ttt cag cac gag ggc gat gag gaa tac 355
Leu Ala Arg Leu Leu Pro Asp Phe Gln His Glu Gly Asp Glu Glu Tyr
70 75 80 85
gac ggc gat aat tct ttc ctc cgt tca ctc cat gaa ggc gac atc acc 403
Asp Gly Asp Asn Ser Phe Leu Arg Ser Leu His Glu Gly Asp Ile Thr
90 95 100
cga gca aaa ctg gaa aat ctg cgc gtg att aac gat gcg ctg gga ccc 451
Arg Ala Lys Leu Glu Asn Leu Arg Val Ile Asn Asp Ala Leu Gly Pro

105	110	115	
gac gga aat gtt gcg gtc acc gcc tct gag gag gaa gcg cac gct tgg	499		
Asp Gly Asn Val Ala Val Thr Ala Ser Glu Glu Glu Ala His Ala Trp			
120	125	130	
ttg gct gcg ctc aat gac atc cgc ctg tac gtt gcc tcc ggt gat gta	547		
Leu Ala Ala Leu Asn Asp Ile Arg Leu Tyr Val Ala Ser Gly Asp Val			
135	140	145	
cgc ggc ggg gaa gcc gcc gag gaa gac cgc gaa aac ctc gtg cag tgg	595		
Arg Gly Gly Glu Ala Ala Glu Glu Asp Arg Glu Asn Leu Val Gln Trp			
150	155	160	165
ctt gcc tac aat caa gag tcc ttg ctg gaa gcg atg atg aat	637		
Leu Ala Tyr Asn Gln Glu Ser Leu Leu Glu Ala Met Met Asn			
170	175		
taatgcttat cgacgtcgcg ggc	660		

<210> 1158

<211> 179

<212> PRT

<213> Corynebacterium glutamicum

<400> 1158

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Ala Ala Val Ser Glu Ala Leu Ile Gln Arg Ala Gln Ser Val Pro Lys	
35 40 45	
Asp Pro Leu Ala Glu Met Thr Gly Met Thr Ser Gly His Lys Glu Ala	
50 55 60	
Pro Thr Asp Pro Ala Leu Ala Arg Leu Leu Pro Asp Phe Gln His Glu	
65 70 75 80	
Gly Asp Glu Glu Tyr Asp Gly Asp Asn Ser Phe Leu Arg Ser Leu His	
85 90 95	
Glu Gly Asp Ile Thr Arg Ala Lys Leu Glu Asn Leu Arg Val Ile Asn	
100 105 110	
Asp Ala Leu Gly Pro Asp Gly Asn Val Ala Val Thr Ala Ser Glu Glu	
115 120 125	
Glu Ala His Ala Trp Leu Ala Ala Leu Asn Asp Ile Arg Leu Tyr Val	
130 135 140	
Ala Ser Gly Asp Val Arg Gly Gly Glu Ala Ala Glu Glu Asp Arg Glu	
145 150 155 160	
Asn Leu Val Gln Trp Leu Ala Tyr Asn Gln Glu Ser Leu Leu Glu Ala	
165 170 175	
Met Met Asn	

<210> 1159
 <211> 437
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (1)..(414)
 <223> FRXA02409

<400> 1159
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 Arg Ala Gln Ser Val Pro Lys Asp Pro Leu Ala Glu Met Thr Gly Met
 1 5 10 15
 aca agt gga cac aaa gaa gca cca acc gat ccg gcg ctt gcg cgt ttg 96
 Thr Ser Gly His Lys Glu Ala Pro Thr Asp Pro Ala Leu Ala Arg Leu
 20 25 30
 ctc cct gat ttt cag cac gag ggc gat gag gaa tac gac ggc gat aat 144
 Leu Pro Asp Phe Gln His Glu Gly Asp Glu Glu Tyr Asp Gly Asp Asn
 35 40 45
 tct ttc ctc cgt tca ctc cat gaa ggc gac atc acc cga gca aaa ctg 192
 Ser Phe Leu Arg Ser Leu His Glu Gly Asp Ile Thr Arg Ala Lys Leu
 50 55 60
 gaa aat ctg cgc gtg att aac gat gcg ctg gga ccc gac gga aat gtt 240
 Glu Asn Leu Arg Val Ile Asn Asp Ala Leu Gly Pro Asp Gly Asn Val
 65 70 75 80
 gcg gtc acc gcc tct gag gag gaa gcg cac gct tgg ttg gct gcg ctc 288
 Ala Val Thr Ala Ser Glu Glu Glu Ala His Ala Trp Leu Ala Ala Leu
 85 90 95
 aat gac atc cgc ctg tac gtt gcc tcc ggt gat gta cgc ggc ggc gaa 336
 Asn Asp Ile Arg Leu Tyr Val Ala Ser Gly Asp Val Arg Gly Gly Glu
 100 105 110
 gcc gcc gag gaa gac cgc gaa aac ctc gtg cag tgg ctt gcc tac aat 384
 Ala Ala Glu Glu Asp Arg Glu Asn Leu Val Gln Trp Leu Ala Tyr Asn
 115 120 125
 caa gag tcc ttg ctg gaa gcg atg atg aat taatgcttat cgacgtcgcg 434
 Gln Glu Ser Leu Leu Glu Ala Met Met Asn
 130 135
 ggc 437

<210> 1160
 <211> 138
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 1160
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 1 5 10 15

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Thr Ser Gly His Lys Glu Ala Pro Thr Asp Pro Ala Leu Ala Arg Leu
      20                      25                      30

Leu Pro Asp Phe Gln His Glu Gly Asp Glu Glu Tyr Asp Gly Asp Asn
      35                      40                      45

Ser Phe Leu Arg Ser Leu His Glu Gly Asp Ile Thr Arg Ala Lys Leu
      50                      55                      60

Glu Asn Leu Arg Val Ile Asn Asp Ala Leu Gly Pro Asp Gly Asn Val
      65                      70                      75                      80

Ala Val Thr Ala Ser Glu Glu Glu Ala His Ala Trp Leu Ala Ala Leu
      85                      90                      95

Asn Asp Ile Arg Leu Tyr Val Ala Ser Gly Asp Val Arg Gly Gly Glu
      100                     105                     110

Ala Ala Glu Glu Asp Arg Glu Asn Leu Val Gln Trp Leu Ala Tyr Asn
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Gln Glu Ser Leu Leu Glu Ala Met Met Asn
      130                      135

<210> 1161
<211> 1257
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1234)
<223> RXN02428

<400> 1161
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ttcagtttagc gtgaaggtgc catcatcaca agggttgatg atg gcc gcg acg tta 115
Met Ala Ala Thr Leu
      1                      5

gat ctt cca gat aca gat ccc att gcc tat gca atg ttt gcc cac tgt 163
Asp Leu Pro Asp Thr Asp Pro Ile Ala Tyr Ala Met Phe Ala His Cys
      10                      15                      20

ttc acc gcc tca cgg ttc acg cca gcc gcc gcg cga gtc agt aaa aca 211
Phe Thr Gly Ser Arg Phe Thr Pro Ala Ala Ala Arg Val Ser Lys Thr
      25                      30                      35

ctc gca gaa tcc gcc gtc gcc tgc ctg cgt ttc gat ttc cca gga ctg 259
Leu Ala Glu Ser Gly Val Ala Cys Leu Arg Phe Asp Phe Pro Gly Leu
      40                      45                      50

agc caa tca gaa ggt gac ttc tcc aaa acc acc ttc aac tcc aat gtg 307
Ser Gln Ser Glu Gly Asp Phe Ser Lys Thr Thr Phe Asn Ser Asn Val
      55                      60                      65

gac gat atc gtg gcg gcc tcg cag tgg ttg acg gaa cac tac tcc gct 355
Asp Asp Ile Val Ala Ala Ser Gln Trp Leu Thr Glu His Tyr Ser Ala

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70	75	80	85
cca cag ttg ctc att gga cac tcc ttg ggt ggt gca gca tca ctg aaa Pro Gln Leu Leu Ile Gly His Ser Leu Gly Gly Ala Ala Ser Leu Lys 90 95 100	403		
gct gcc acc aaa atc tcc tgc ctc aaa gca gta gca acg ata ggt gca Ala Ala Thr Lys Ile Ser Cys Leu Lys Ala Val Ala Thr Ile Gly Ala 105 110 115	451		
cct ttt gat cct gcg cac gca gtc ctg cac ttt gct gat cgc ata tgt Pro Phe Asp Pro Ala His Ala Val Leu His Phe Ala Asp Arg Ile Cys 120 125 130	499		
gat gta gat gat caa ggt gct gtc act ctg cag ctc gga ggc cgg gat Asp Val Asp Asp Gln Gly Ala Val Thr Leu Gln Leu Gly Gly Arg Asp 135 140 145	547		
gtc acc att tcc cgc gaa ttc ctc gaa gac ctt gca gag gtc aac ccc Val Thr Ile Ser Arg Glu Phe Leu Glu Asp Leu Ala Glu Val Asn Pro 150 155 160 165	595		
gaa gat cac ctc cgc agg ctc cgc aaa cca ctg ctt tta ctg cat tcc Glu Asp His Leu Arg Arg Leu Arg Lys Pro Leu Leu Leu Leu His Ser 170 175 180	643		
ccc acc gac caa acc gtc ggc gtg gac aac gcg cag ctc atc ttc aga Pro Thr Asp Gln Thr Val Gly Val Asp Asn Ala Gln Leu Ile Phe Arg 185 190 195	691		
gtc act cgc tac cct aaa tcc ttg atg act ttg gac aag gca gat cac Val Thr Arg Tyr Pro Lys Ser Leu Met Thr Leu Asp Lys Ala Asp His 200 205 210	739		
ctg ctc acc aaa gat ggc acc gca cag cgt gca gcc cgg atc atc gcg Leu Leu Thr Lys Asp Gly Thr Ala Gln Arg Ala Ala Arg Ile Ile Ala 215 220 225	787		
aac tgg gtc gag ccc tac ctg gtt cca gaa aac gtc tgt gag gat ctt Asn Trp Val Glu Pro Tyr Leu Val Pro Glu Asn Val Cys Glu Asp Leu 230 235 240 245	835		
cgg gag ttt gtc gcc gaa gcc tca acc atc aaa gcc agc aaa tac ggc Pro Glu Phe Val Ala Glu Ala Ser Thr Ile Lys Ala Ser Lys Tyr Gly 250 255 260	883		
gca gcc atc cgc acc ggt ggt cac aat ttc atc acc gac cgc gac aaa Ala Ala Ile Arg Thr Gly Gly His Asn Phe Ile Thr Asp Arg Asp Lys 265 270 275	931		
tcc cag ggt ggc aaa aac ctc ggc ttc acc cct act tcc ctg ctg gtt Ser Gln Gly Gly Lys Asn Leu Gly Phe Thr Pro Thr Ser Leu Leu Val 280 285 290	979		
tcc gcg ctt gct gct gca aac tct caa acg atc aaa caa gca gcc atc Ser Ala Leu Ala Ala Ala Asn Ser Gln Thr Ile Lys Gln Ala Ala Ile 295 300 305	1027		
gac aac cgc atc aaa ggc ctt gac gat gtc aaa gtg acg atc tcc cag Asp Asn Arg Ile Lys Gly Leu Asp Asp Val Lys Val Thr Ile Ser Gln 310 315 320 325	1075		

gaa caa tca gcc gac cac ggc cag atc aaa ctc cgc cga aag atc tct 1123
 Glu Gln Ser Ala Asp His Gly Gln Ile Lys Leu Arg Arg Lys Ile Ser
 330 335 340
 ttg atc ggc aac ctc agc gat gct gac agt gct tca ett cgg gcc gca 1171
 Leu Ile Gly Asn Leu Ser Asp Ala Asp Ser Ala Ser Leu Arg Ala Ala
 345 350 355
 tct aat tcc tgc tcg att acc caa ctg ctc gcg cag gga atc gtc atc 1219
 Ser Asn Ser Cys Ser Ile Thr Gln Leu Leu Ala Gln Gly Ile Val Ile
 360 365 370
 gac gac gag gtg aac tagcgtggat tttgagttgg gta 1257
 Asp Asp Glu Val Asn
 375

<210> 1162

<211> 378

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1162

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 20 25 30
 Arg Val Ser Lys Thr Leu Ala Glu Ser Gly Val Ala Cys Leu Arg Phe
 35 40 45
 Asp Phe Pro Gly Leu Ser Gln Ser Glu Gly Asp Phe Ser Lys Thr Thr
 50 55 60
 Phe Asn Ser Asn Val Asp Asp Ile Val Ala Ala Ser Gln Trp Leu Thr
 65 70 75 80
 Glu His Tyr Ser Ala Pro Gln Leu Leu Ile Gly His Ser Leu Gly Gly
 85 90 95
 Ala Ala Ser Leu Lys Ala Ala Thr Lys Ile Ser Cys Leu Lys Ala Val
 100 105 110
 Ala Thr Ile Gly Ala Pro Phe Asp Pro Ala His Ala Val Leu His Phe
 115 120 125
 Ala Asp Arg Ile Cys Asp Val Asp Asp Gln Gly Ala Val Thr Leu Gln
 130 135 140
 Leu Gly Gly Arg Asp Val Thr Ile Ser Arg Glu Phe Leu Glu Asp Leu
 145 150 155 160
 Ala Glu Val Asn Pro Glu Asp His Leu Arg Arg Leu Arg Lys Pro Leu
 165 170 175
 Leu Leu Leu His Ser Pro Thr Asp Gln Thr Val Gly Val Asp Asn Ala
 180 185 190
 Gln Leu Ile Phe Arg Val Thr Arg Tyr Pro Lys Ser Leu Met Thr Leu

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195                200                205
Asp Lys Ala Asp His Leu Leu Thr Lys Asp Gly Thr Ala Gln Arg Ala
210                215                220
Ala Arg Ile Ile Ala Asn Trp Val Glu Pro Tyr Thr Leu Val Pro Glu Asn
225                230                235                240
Val Cys Glu Asp Leu Pro Glu Phe Val Ala Glu Ala Ser Thr Ile Lys
245                250                255
Ala Ser Lys Tyr Gly Ala Ala Ile Arg Thr Gly Gly His Asn Phe Ile
260                265                270
Thr Asp Arg Asp Lys Ser Gln Gly Gly Lys Asn Leu Gly Phe Thr Pro
275                280                285
Thr Ser Leu Leu Val Ser Ala Leu Ala Ala Ala Asn Ser Gln Thr Ile
290                295                300
Lys Gln Ala Ala Ile Asp Asn Arg Ile Lys Gly Leu Asp Asp Val Lys
305                310                315                320
Val Thr Ile Ser Gln Glu Gln Ser Ala Asp His Gly Gln Ile Lys Leu
325                330                335
Arg Arg Lys Ile Ser Leu Ile Gly Asn Leu Ser Asp Ala Asp Ser Ala
340                345                350
Ser Leu Arg Ala Ala Ser Asn Ser Cys Ser Ile Thr Gln Leu Leu Ala
355                360                365
Gln Gly Ile Val Ile Asp Asp Glu Val Asn
370                375

<210> 1163
<211> 1257
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1234)
<223> FRXA02428

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ttcagtttagc gtgaaggtgc catcatoaca agggttgatg atg gcc gcg acg tta 115
Met Ala Ala Thr Leu
1 5
gat ctt cca gat aca gat ccc att gcc tat gca atg ttt gcc cac tgt 163
Asp Leu Pro Asp Thr Asp Pro Ile Ala Tyr Ala Met Phe Ala His Cys
10 15 20
ttc acc gcc tca cgg ttc acg cca gcc gcc gcg cga gtc agt aaa aca 211
Phe Thr Gly Ser Arg Phe Thr Pro Ala Ala Ala Arg Val Ser Lys Thr
25 30 35

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ctc gca gaa tcc ggc gtc gcc tgc ctg cgt ttc gat ttc cca gga ctg	259
Leu Ala Glu Ser Gly Val Ala Cys Leu Arg Phe Asp Phe Pro Gly Leu	
40 45 50	
agc caa tca gaa ggt gac ttc tcc aaa acc acc ttc aac tcc aat gtg	307
Ser Gln Ser Glu Gly Asp Phe Ser Lys Thr Thr Phe Asn Ser Asn Val	
55 60 65	
gac gat atc gtg gcg gcc tcg cag tgg ttg acg gaa cac tac tcc gct	355
Asp Asp Ile Val Ala Ala Ser Gln Trp Leu Thr Glu His Tyr Ser Ala	
70 75 80 85	
cca cag ttg ctc att gga cac tcc ttg ggt ggt gca gca tca ctg aaa	403
Pro Gln Leu Leu Ile Gly His Ser Leu Gly Gly Ala Ala Ser Leu Lys	
90 95 100	
gct gcc acc aaa atc tcc tgc ctc aaa gca gta gca acg ata ggt gca	451
Ala Ala Thr Lys Ile Ser Cys Leu Lys Ala Val Ala Thr Ile Gly Ala	
105 110 115	
cct ttt gat cct gcg cac gca gtc ctg cac ttt gct gat cgc ata tgt	499
Pro Phe Asp Pro Ala His Ala Val Leu His Phe Ala Asp Arg Ile Cys	
120 125 130	
gat gta gat gat caa ggt gct gtc act ctg cag ctc gga ggc cgg gat	547
Asp Val Asp Asp Gln Gly Ala Val Thr Leu Gln Leu Gly Gly Arg Asp	
135 140 145	
gtc acc att tcc cgc gaa ttc ctc gaa gac ctt gca gag gtc aac ccc	595
Val Thr Ile Ser Arg Glu Phe Leu Glu Asp Leu Ala Glu Val Asn Pro	
150 155 160 165	
gaa gat cac ctc cgc agg ctc cgc aaa cca ctg ctt tta ctg cat tcc	643
Glu Asp His Leu Arg Arg Leu Arg Lys Pro Leu Leu Leu Leu His Ser	
170 175 180	
ccc acc gac caa acc gtc ggc gtg gac aac gcg cag ctc atc ttc aga	691
Pro Thr Asp Gln Thr Val Gly Val Asp Asn Ala Gln Leu Ile Phe Arg	
185 190 195	
gtc act cgc tac cct aaa tcc ttg atg act ttg gac aag gca gat cac	739
Val Thr Arg Tyr Pro Lys Ser Leu Met Thr Leu Asp Lys Ala Asp His	
200 205 210	
ctg ctc acc aaa gat ggc acc gca cag cgt gca gcc cgg atc atc gcg	787
Leu Leu Thr Lys Asp Gly Thr Ala Gln Arg Ala Ala Arg Ile Ile Ala	
215 220 225	
aac tgg gtc gag ccc tac ctg gtt cca gaa aac gtc tgt gag gat ctt	835
Asn Trp Val Glu Pro Tyr Leu Val Pro Glu Asn Val Cys Glu Asp Leu	
230 235 240 245	
ccg gag ttt gtc gcc gaa gcc tca acc atc aaa gcc agc aaa tac gcc	883
Pro Glu Phe Val Ala Glu Ala Ser Thr Ile Lys Ala Ser Lys Tyr Gly	
250 255 260	
gca gcc atc cgc acc ggt ggt cac aat ttc atc acc gac cgc gac aaa	931
Ala Ala Ile Arg Thr Gly Gly His Asn Phe Ile Thr Asp Arg Asp Lys	
265 270 275	
tcc cag ggt ggc aaa aac ctc ggc ttc acc cct act tcc ctg ctg gtt	979

Ser	Gln	Gly	Gly	Lys	Asn	Leu	Gly	Phe	Thr	Pro	Thr	Ser	Leu	Leu	Val	
	280						285					290				
tcc	gcg	ctt	gct	gct	gca	aac	tct	caa	acg	atc	aaa	caa	gca	gcc	atc	1027
Ser	Ala	Leu	Ala	Ala	Ala	Asn	Ser	Gln	Thr	Ile	Lys	Gln	Ala	Ala	Ile	
	295					300					305					
gac	aac	cgc	atc	aaa	ggc	ctt	gac	gat	gtc	aaa	gtg	acg	atc	tcc	cag	1075
Asp	Asn	Arg	Ile	Lys	Gly	Leu	Asp	Asp	Val	Lys	Val	Thr	Ile	Ser	Gln	
	310				315					320					325	
gaa	caa	tca	gcc	gac	cac	ggc	cag	atc	aaa	ctc	cgc	cga	aag	atc	tct	1123
Glu	Gln	Ser	Ala	Asp	His	Gly	Gln	Ile	Lys	Leu	Arg	Arg	Lys	Ile	Ser	
				330					335					340		
ttg	atc	ggc	aac	ctc	agc	gat	gct	gac	agt	gct	tca	ctt	cgg	gcc	gca	1171
Leu	Ile	Gly	Asn	Leu	Ser	Asp	Ala	Asp	Ser	Ala	Ser	Leu	Arg	Ala	Ala	
				345				350					355			
tct	aat	tcc	tgc	tcg	att	acc	caa	ctg	ctc	gcg	cag	gga	atc	gtc	atc	1219
Ser	Asn	Ser	Cys	Ser	Ile	Thr	Gln	Leu	Leu	Ala	Gln	Gly	Ile	Val	Ile	
	360						365				370					
gac	gac	gag	gtg	aac	tagcgtggat	tttgagttgg	gta									1257
Asp	Asp	Glu	Val	Asn												
	375															

<210> 1164
 <211> 378
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 1164

Met	Ala	Ala	Thr	Leu	Asp	Leu	Pro	Asp	Thr	Asp	Pro	Ile	Ala	Tyr	Ala	
	1			5					10					15		
Met	Phe	Ala	His	Cys	Phe	Thr	Gly	Ser	Arg	Phe	Thr	Pro	Ala	Ala	Ala	
		20						25					30			
Arg	Val	Ser	Lys	Thr	Leu	Ala	Glu	Ser	Gly	Val	Ala	Cys	Leu	Arg	Phe	
	35						40					45				
Asp	Phe	Pro	Gly	Leu	Ser	Gln	Ser	Glu	Gly	Asp	Phe	Ser	Lys	Thr	Thr	
	50					55					60					
Phe	Asn	Ser	Asn	Val	Asp	Asp	Ile	Val	Ala	Ala	Ser	Gln	Trp	Leu	Thr	
	65				70				75					80		
Glu	His	Tyr	Ser	Ala	Pro	Gln	Leu	Leu	Ile	Gly	His	Ser	Leu	Gly	Gly	
				85					90					95		
Ala	Ala	Ser	Leu	Lys	Ala	Ala	Thr	Lys	Ile	Ser	Cys	Leu	Lys	Ala	Val	
			100					105					110			
Ala	Thr	Ile	Gly	Ala	Pro	Phe	Asp	Pro	Ala	His	Ala	Val	Leu	His	Phe	
	115						120					125				
Ala	Asp	Arg	Ile	Cys	Asp	Val	Asp	Asp	Gln	Gly	Ala	Val	Thr	Leu	Gln	
	130					135					140					

Leu Gly Gly Arg Asp Val Thr Ile Ser Arg Glu Phe Leu Glu Asp Leu
 145 150 155 160
 Ala Glu Val Asn Pro Glu Asp His Leu Arg Arg Leu Arg Lys Pro Leu
 165 170 175
 Leu Leu Leu His Ser Pro Thr Asp Gln Thr Val Gly Val Asp Asn Ala
 180 185 190
 Gln Leu Ile Phe Arg Val Thr Arg Tyr Pro Lys Ser Leu Met Thr Leu
 195 200 205
 Asp Lys Ala Asp His Leu Leu Thr Lys Asp Gly Thr Ala Gln Arg Ala
 210 215 220
 Ala Arg Ile Ile Ala Asn Trp Val Glu Pro Tyr Leu Val Pro Glu Asn
 225 230 235 240
 Val Cys Glu Asp Leu Pro Glu Phe Val Ala Glu Ala Ser Thr Ile Lys
 245 250 255
 Ala Ser Lys Tyr Gly Ala Ala Ile Arg Thr Gly Gly His Asn Phe Ile
 260 265 270
 Thr Asp Arg Asp Lys Ser Gln Gly Gly Lys Asn Leu Gly Phe Thr Pro
 275 280 285
 Thr Ser Leu Leu Val Ser Ala Leu Ala Ala Ala Asn Ser Gln Thr Ile
 290 295 300
 Lys Gln Ala Ala Ile Asp Asn Arg Ile Lys Gly Leu Asp Asp Val Lys
 305 310 315 320
 Val Thr Ile Ser Gln Glu Gln Ser Ala Asp His Gly Gln Ile Lys Leu
 325 330 335
 Arg Arg Lys Ile Ser Leu Ile Gly Asn Leu Ser Asp Ala Asp Ser Ala
 340 345 350
 Ser Leu Arg Ala Ala Ser Asn Ser Cys Ser Ile Thr Gln Leu Leu Ala
 355 360 365
 Gln Gly Ile Val Ile Asp Asp Glu Val Asn
 370 375

<210> 1165

<211> 1365

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1342)

<223> RXN02454

<400> 1165

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 gttctagcca taatcagcag aaaaggtgga gtgattcgcc atg aaa gag tcc atg 115
 Met Lys Glu Ser Met

1

5

agc atc acc tcg tcg acg tac gcg tcg gca ctg ctg aca ctg ccc tgg	163
Ser Ile Thr Ser Ser Thr Tyr Ala Ser Ala Leu Leu Thr Leu Pro Trp	
10 15 20	
ggt aca ccc ctg gaa cag tgg ccc gat aat ctc atc gcc gcg ctg ccc	211
Gly Thr Pro Leu Glu Gln Trp Pro Asp Asn Leu Ile Ala Ala Leu Pro	
25 30 35	
agg ggt att tcc cgg cac atc gtg cgt ttc gtg ggg atc aac cgt ggc	259
Arg Gly Ile Ser Arg His Ile Val Arg Phe Val Gly Ile Asn Arg Gly	
40 45 50	
atc gtc gcg gtc aaa att ggt gcg cgt acc gcc cac cac gag tac	307
Ile Val Ala Val Lys Glu Ile Gly Ala Arg Thr Ala His His Glu Tyr	
55 60 65	
aag atg ctg cgt gaa ctg cag cgc ctt ggt gcc ccc agt gtg cgc ccc	355
Lys Met Leu Arg Glu Leu Gln Arg Leu Gly Ala Pro Ser Val Arg Pro	
70 75 80 85	
gta gcc gtg atc acc gga cgc cat ccg gca gag gaa gac tac ggg gag	403
Val Ala Val Ile Thr Gly Arg His Pro Ala Glu Glu Asp Tyr Gly Glu	
90 95 100	
ctc acc gca gct ttg gtg acc gag cac ttg gag ttt tcc ctg ccc tat	451
Leu Thr Ala Ala Leu Val Thr Glu His Leu Glu Phe Ser Leu Pro Tyr	
105 110 115	
cgc gag atc ttt tct cgg cac ctc acg gtc gtg gaa tcg gag aag ctc	499
Arg Glu Ile Phe Ser Arg His Leu Thr Val Val Glu Ser Glu Lys Leu	
120 125 130	
atc cgc gcc ctg tcc gtg ctg ttg gtg cgg atg cat ctg ctc aac ttc	547
Ile Arg Ala Leu Ser Val Leu Leu Val Arg Met His Leu Leu Asn Phe	
135 140 145	
tac tgg gga gat gtg tca ctg tct aat act ctc ttt cgt cgc gat gct	595
Tyr Trp Gly Asp Val Ser Leu Ser Asn Thr Leu Phe Arg Arg Asp Ala	
150 155 160 165	
gaa acc tat tcc gcc tat ctc gtc gat gcc gaa acc ggg gag ttc cag	643
Glu Thr Tyr Ser Ala Tyr Leu Val Asp Ala Glu Thr Gly Glu Phe Gln	
170 175 180	
ccc aac ctc tct gaa tca cgc agg ctt tac gac gtc gac atc gcc cgc	691
Pro Asn Leu Ser Glu Ser Arg Arg Leu Tyr Asp Val Asp Ile Ala Arg	
185 190 195	
gtc aac atc att ggc gaa ctc atg gac cta cag gcg ggt gaa tgc cta	739
Val Asn Ile Ile Gly Glu Leu Met Asp Leu Gln Ala Gly Glu Cys Leu	
200 205 210	
gat aag tcc atc gat gtc atc gcc cta gga ggc ctt gtc gaa agc tct	787
Asp Lys Ser Ile Asp Val Ile Ala Leu Gly Gly Leu Val Glu Ser Ser	
215 220 225	
tat ctt gaa ttg tgg acg gag ctc acc gcg gag gaa tcc gtc gat gcc	835
Tyr Leu Glu Leu Trp Thr Glu Leu Thr Ala Glu Glu Ser Val Asp Ala	
230 235 240 245	

agt gaa tat tgg cgc ctc tct gag aga att gac cgg ctc aat caa ctg 883
 Ser Glu Tyr Trp Arg Leu Ser Glu Arg Ile Asp Arg Leu Asn Gln Leu
 250 255 260

ggc ttt gac gta ggg gag ctc aag gtc acg aag gac gat tgc cgg cag 931
 Gly Phe Asp Val Gly Glu Leu Lys Val Thr Lys Asp Ser Arg Gln
 265 270 275

gtt gtg cgc att cgc cct gta gtg gtg gat ccg ggc cac tat cgt gca 979
 Val Val Arg Ile Arg Pro Val Val Val Asp Pro Gly His Tyr Arg Ala
 280 285 290

gag cta ttg agc tta acc ggg ctg agc gtc gag gaa cac cag gcc caa 1027
 Glu Leu Leu Ser Leu Thr Gly Leu Ser Val Glu Glu His Gln Ala Gln
 295 300 305

cgc cta ttg ggc tgc atc cag gcc tat cag gcc gtc gaa tgc gga ccg 1075
 Arg Leu Leu Gly Ser Ile Gln Ala Tyr Gln Ala Val Glu Cys Gly Pro
 310 315 320 325

cat gta ggt ctt acc caa gcc gcg cat ctc tgg atg acg aat gaa tac 1123
 His Val Gly Leu Thr Gln Ala Ala His Leu Trp Met Thr Asn Glu Tyr
 330 335 340

gaa ccg act atc gcc gcc gtc ccc gtg gag atg tta gac aag ctg gag 1171
 Glu Pro Thr Ile Ala Ala Val Pro Val Glu Met Leu Asp Lys Leu Glu
 345 350 355

cca gca caa atc ttc cac gaa atc gtc gac cac cgc tgg ttc ctc gcc 1219
 Pro Ala Gln Ile Phe His Glu Ile Val Asp His Arg Trp Phe Leu Ala
 360 365 370

caa gaa agg gga ggg gct gtc acc ctc cca gag gcc acg gca tcc tat 1267
 Gln Glu Arg Gly Gly Ala Val Thr Leu Pro Glu Ala Thr Ala Ser Tyr
 375 380 385

ctt gaa tcc gtg ctt ccg gcc cgc cgc gac gag gct cgc ctc ctc agc 1315
 Leu Glu Ser Val Leu Pro Ala Arg Arg Asp Glu Ala Arg Leu Leu Ser
 390 395 400 405

aca aac cct tca gac gaa gac ttg tca taacctctcg cgtgccccaa 1362
 Thr Asn Pro Ser Asp Glu Asp Leu Ser
 410

cgg 1365

<210> 1166

<211> 414

<212> PRT

<213> Corynebacterium glutamicum

<400> 1166

Met Lys Glu Ser Met Ser Ile Thr Ser Ser Thr Tyr Ala Ser Ala Leu
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Leu Thr Leu Pro Trp Gly Thr Pro Leu Glu Gln Trp Pro Asp Asn Leu
 20 25 30

Ile Ala Ala Leu Pro Arg Gly Ile Ser Arg His Ile Val Arg Phe Val

35					40					45					
Gly	Ile	Asn	Arg	Gly	Ile	Val	Ala	Val	Lys	Glu	Ile	Gly	Ala	Arg	Thr
50					55					60					
Ala	His	His	Glu	Tyr	Lys	Met	Leu	Arg	Glu	Leu	Gln	Arg	Leu	Gly	Ala
65				70					75						80
Pro	Ser	Val	Arg	Pro	Val	Ala	Val	Ile	Thr	Gly	Arg	His	Pro	Ala	Glu
			85						90					95	
Glu	Asp	Tyr	Gly	Glu	Leu	Thr	Ala	Ala	Leu	Val	Thr	Glu	His	Leu	Glu
			100				105						110		
Phe	Ser	Leu	Pro	Tyr	Arg	Glu	Ile	Phe	Ser	Arg	His	Leu	Thr	Val	Val
		115				120					125				
Glu	Ser	Glu	Lys	Leu	Ile	Arg	Ala	Leu	Ser	Val	Leu	Leu	Val	Arg	Met
		130				135					140				
His	Leu	Leu	Asn	Phe	Tyr	Trp	Gly	Asp	Val	Ser	Leu	Ser	Asn	Thr	Leu
145					150				155						160
Phe	Arg	Arg	Asp	Ala	Glu	Thr	Tyr	Ser	Ala	Tyr	Leu	Val	Asp	Ala	Glu
			165						170					175	
Thr	Gly	Glu	Phe	Gln	Pro	Asn	Leu	Ser	Glu	Ser	Arg	Arg	Leu	Tyr	Asp
			180					185					190		
Val	Asp	Ile	Ala	Arg	Val	Asn	Ile	Ile	Gly	Glu	Leu	Met	Asp	Leu	Gln
		195					200					205			
Ala	Gly	Glu	Cys	Leu	Asp	Lys	Ser	Ile	Asp	Val	Ile	Ala	Leu	Gly	Gly
		210				215					220				
Leu	Val	Glu	Ser	Ser	Tyr	Leu	Glu	Leu	Trp	Thr	Glu	Leu	Thr	Ala	Glu
225					230					235				240	
Glu	Ser	Val	Asp	Ala	Ser	Glu	Tyr	Trp	Arg	Leu	Ser	Glu	Arg	Ile	Asp
			245					250						255	
Arg	Leu	Asn	Gln	Leu	Gly	Phe	Asp	Val	Gly	Glu	Leu	Lys	Val	Thr	Lys
		260					265						270		
Asp	Asp	Ser	Arg	Gln	Val	Val	Arg	Ile	Arg	Pro	Val	Val	Val	Asp	Pro
		275					280					285			
Gly	His	Tyr	Arg	Ala	Glu	Leu	Leu	Ser	Leu	Thr	Gly	Leu	Ser	Val	Glu
		290				295					300				
Glu	His	Gln	Ala	Gln	Arg	Leu	Leu	Gly	Ser	Ile	Gln	Ala	Tyr	Gln	Ala
305					310					315					320
Val	Glu	Cys	Gly	Pro	His	Val	Gly	Leu	Thr	Gln	Ala	Ala	His	Leu	Trp
			325					330						335	
Met	Thr	Asn	Glu	Tyr	Glu	Pro	Thr	Ile	Ala	Ala	Val	Pro	Val	Glu	Met
		340					345						350		
Leu	Asp	Lys	Leu	Glu	Pro	Ala	Gln	Ile	Phe	His	Glu	Ile	Val	Asp	His
		355					360					365			

Arg Trp Phe Leu Ala Gln Glu Arg Gly Gly Ala Val Thr Leu Pro Glu
370 375 380

Ala Thr Ala Ser Tyr Leu Glu Ser Val Leu Pro Ala Arg Arg Asp Glu
385 390 395 400

Ala Arg Leu Leu Ser Thr Asn Pro Ser Asp Glu Asp Leu Ser
405 410

<210> 1167

<211> 836

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(813)

<223> FRXA02454

<400> 1167

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1 5 10 15

ctc ttt cgt cgc gat gct gaa acc tat tcc gcc tat ctc gtc gat gcc 96
Leu Phe Arg Arg Asp Ala Glu Thr Tyr Ser Ala Tyr Leu Val Asp Ala
20 25 30

gaa acc ggg gag ttc cag ccc aac ctc tct gaa tca cgc agg ctt tac 144
Glu Thr Gly Glu Phe Gln Pro Asn Leu Ser Glu Ser Arg Arg Leu Tyr
35 40 45

gac gtc gac atc gcc cgc gtc aac atc att gcc gaa ctc atg gac cta 192
Asp Val Asp Ile Ala Arg Val Asn Ile Ile Gly Glu Leu Met Asp Leu
50 55 60

cag gcg ggt gaa tgc cta gat aag tcc atc gat gtc atc gcc cta gga 240
Gln Ala Gly Glu Cys Leu Asp Lys Ser Ile Asp Val Ile Ala Leu Gly
65 70 75 80

ggc ctt gtc gaa agc tct tat ctt gaa ttg tgg acg gag ctc acc gcg 288
Gly Leu Val Glu Ser Ser Tyr Leu Glu Leu Trp Thr Glu Leu Thr Ala
85 90 95

gag gaa tcc gtc gat gcc agt gaa tat tgg cgc ctc tct gag aga att 336
Glu Glu Ser Val Asp Ala Ser Glu Tyr Trp Arg Leu Ser Glu Arg Ile
100 105 110

gac cgg ctc aat caa ctg gcc ttt gac gta ggg gag ctc aag gtc acg 384
Asp Arg Leu Asn Gln Leu Gly Phe Asp Val Gly Glu Leu Lys Val Thr
115 120 125

aag gac gat tcg cgg cag gtt gtg cgc att cgc cct gta gtg gtg gat 432
Lys Asp Asp Ser Arg Gln Val Val Arg Ile Arg Pro Val Val Val Asp
130 135 140

ccg gcc cac tat cgt gca gag cta ttg agc tta acc ggg ctg agc gtc 480
Pro Gly His Tyr Arg Ala Glu Leu Leu Ser Leu Thr Gly Leu Ser Val
145 150 155 160

gag gaa cac cag gcc caa cgc cta ttg ggc tcg atc cag gcc tat cag 528
 Glu Glu His Gln Ala Gln Arg Leu Leu Gly Ser Ile Gln Ala Tyr Gln
 165 170 175

gcc gtc gaa tgc gga cgc cat gta ggt ctt acc caa gcc gcg cat ctc 576
 Ala Val Glu Cys Gly Pro His Val Gly Leu Thr Gln Ala Ala His Leu
 180 185 190

tgg atg acg aat gaa tac gaa ccg act atc gcc gcc gtc ccc gtg gag 624
 Trp Met Thr Asn Glu Tyr Glu Pro Thr Ile Ala Ala Val Pro Val Glu
 195 200 205

atg tta gac aag ctg gag cca gca caa atc ttc cac gaa atc gtc gac 672
 Met Leu Asp Lys Leu Glu Pro Ala Gln Ile Phe His Glu Ile Val Asp
 210 215 220

cac cgc tgg ttc ctc gcc caa gaa agg gga ggg gct gtc acc ctc cca 720
 His Arg Trp Phe Leu Ala Gln Glu Arg Gly Gly Ala Val Thr Leu Pro
 225 230 235 240

gag gcc acg gca tcc tat ctt gaa tcc gtg ctt ccg gcc cgc cgc gac 768
 Glu Ala Thr Ala Ser Tyr Leu Glu Ser Val Leu Pro Ala Arg Arg Asp
 245 250 255

gag gct cgc ctc ctc agc aca aac cct tca gac gaa gac ttg tca 813
 Glu Ala Arg Leu Leu Ser Thr Asn Pro Ser Asp Glu Asp Leu Ser
 260 265 270

taacctctcg cgtgcccaaa cgg 836

<210> 1168
 <211> 271
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1168
 Met His Leu Leu Asn Phe Tyr Trp Gly Asp Val Ser Leu Ser Asn Thr
 1 5 10 15
 Leu Phe Arg Arg Asp Ala Glu Thr Tyr Ser Ala Tyr Leu Val Asp Ala
 20 25 30
 Glu Thr Gly Glu Phe Gln Pro Asn Leu Ser Glu Ser Arg Arg Leu Tyr
 35 40 45
 Asp Val Asp Ile Ala Arg Val Asn Ile Ile Gly Glu Leu Met Asp Leu
 50 55 60
 Gln Ala Gly Glu Cys Leu Asp Lys Ser Ile Asp Val Ile Ala Leu Gly
 65 70 75 80
 Gly Leu Val Glu Ser Ser Tyr Leu Glu Leu Trp Thr Glu Leu Thr Ala
 85 90 95
 Glu Glu Ser Val Asp Ala Ser Glu Tyr Trp Arg Leu Ser Glu Arg Ile
 100 105 110
 Asp Arg Leu Asn Gln Leu Gly Phe Asp Val Gly Glu Leu Lys Val Thr
 115 120 125

Lys Asp Asp Ser Arg Gln Val Val Arg Ile Arg Pro Val Val Val Asp
130 135 140

Pro Gly His Tyr Arg Ala Glu Leu Leu Ser Leu Thr Gly Leu Ser Val
145 150 155 160

Glu Glu His Gln Ala Gln Arg Leu Leu Gly Ser Ile Gln Ala Tyr Gln
165 170 175

Ala Val Glu Cys Gly Pro His Val Gly Leu Thr Gln Ala Ala His Leu
180 185 190

Trp Met Thr Asn Glu Tyr Glu Pro Thr Ile Ala Ala Val Pro Val Glu
195 200 205

Met Leu Asp Lys Leu Glu Pro Ala Gln Ile Phe His Glu Ile Val Asp
210 215 220

His Arg Trp Phe Leu Ala Gln Glu Arg Gly Gly Ala Val Thr Leu Pro
225 230 235 240

Glu Ala Thr Ala Ser Tyr Leu Glu Ser Val Leu Pro Ala Arg Arg Asp
245 250 255

Glu Ala Arg Leu Leu Ser Thr Asn Pro Ser Asp Glu Asp Leu Ser
260 265 270

<210> 1169

<211> 1233

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1210)

<223> RXN02457

<400> 1169

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agtagaaca tatgtaccac ttcaaatcta gggggaaca atg ttc tac ttc acc 115
Met Phe Tyr Phe Thr
1 5

gtc aat aat ccg cag gat cct tta agc acc gaa att gtt gag act aat 163
Val Asn Asn Pro Gln Asp Pro Leu Ser Thr Glu Ile Val Glu Thr Asn
10 15 20

cgc cgt gac ctc gca ttt tgg cat cga tta cgc ccc aaa gat gac gat 211
Arg Arg Asp Leu Ala Phe Trp His Arg Leu Arg Pro Lys Asp Asp Asp
25 30 35

gat tta gcc aca gcc atc aac aaa ata tgc gtg cgc aca ggc tta tcc 259
Asp Leu Ala Thr Ala Ile Asn Lys Ile Cys Val Arg Thr Gly Leu Ser
40 45 50

cgc aaa ctg atc gcc gct tgt tta ttt agc atc tgc ttc ctg ccg tac 307
Arg Lys Leu Ile Ala Ala Cys Leu Phe Ser Ile Cys Phe Leu Pro Tyr
55 60 65

tta ccc aac ttc cac aaa ctc gtc gaa aag ctt ggt cat ctc gac atg	355
Leu Pro Asn Phe His Lys Leu Val Glu Lys Leu Gly His Leu Asp Met	
70 75 80 85	
gcg cgc atc aac gcg atc act aaa gct ggc gaa aaa gtg cca agc gag	403
Ala Arg Ile Asn Ala Ile Thr Lys Ala Gly Glu Lys Val Pro Ser Glu	
90 95 100	
aag aga gag ctt ttc gac gcc tac ctc gtc gat tac ctg acg cct cga	451
Lys Arg Glu Leu Phe Asp Ala Tyr Leu Val Asp Tyr Leu Thr Pro Arg	
105 110 115	
gcg gag gct cag tgc ttg ccc cag gca agc tca att tcc gca atg atg	499
Ala Glu Ala Ala Gln Cys Leu Pro Gln Ala Ser Ser Ile Ser Ala Met Met	
120 125 130	
cgg aaa ttt atc gca caa cac tgc ccc gac gac aag gcc tcc tca gcc	547
Arg Lys Phe Ile Ala Gln His Cys Pro Asp Asp Lys Ala Ser Ser Ala	
135 140 145	
acc aat gat ggc tcc atc cgc tac cgc aga aac aac aaa ggc ggg atc	595
Thr Asn Asp Gly Ser Ile Arg Tyr Arg Arg Asn Asn Lys Gly Gly Ile	
150 155 160 165	
agt atc acc gtc gat gcc acc gcc agc gaa gta aca gaa atc aaa gct	643
Ser Ile Thr Val Asp Ala Thr Ala Ser Glu Val Thr Glu Ile Lys Ala	
170 175 180	
gcc ctg gaa caa atg tcc aaa gat aag gac tgc aca cca ggc act tcc	691
Ala Leu Glu Gln Met Ser Lys Asp Lys Asp Cys Thr Pro Glu Thr Ser	
185 190 195	
cta ctc cac atc att cgt ggc ctg ccg aca aaa gtc gta ctc aac acc	739
Leu Leu His Ile Ile Arg Gly Leu Pro Thr Lys Val Val Leu Asn Thr	
200 205 210	
tac ggc acc aaa gac agc cct gaa tac tta gaa gga gga acc tgg ctg	787
Tyr Gly Thr Lys Asp Ser Pro Glu Tyr Leu Glu Gly Gly Thr Trp Leu	
215 220 225	
tca aag gaa cag tct gag ttc tgg aaa acc cga acc acg tcc agt cgg	835
Ser Lys Glu Gln Ser Glu Phe Trp Lys Thr Arg Thr Thr Ser Ser Arg	
230 235 240 245	
gat atg gac gcc gcc cac ttc tct tac acc acc gcc tac gct cca acc	883
Asp Met Asp Ala Ala His Phe Ser Tyr Thr Thr Ala Tyr Ala Pro Thr	
250 255 260	
cga gaa atg cgc gtc tac atc aaa ggt cta cgc acc acc tgt agc gtc	931
Arg Glu Met Arg Val Tyr Ile Lys Gly Leu Arg Thr Thr Cys Ser Val	
265 270 275	
cct ggc tgc agt gta gcg gtc gaa aac tgc caa ctg gac cac atc atc	979
Pro Gly Cys Ser Val Ala Val Glu Asn Cys Gln Leu Asp His Ile Ile	
280 285 290	
ccc tgg ggt gaa gga ggg ccg aca aca ccg tgg aat att cat ccc ctg	1027
Pro Trp Gly Glu Gly Gly Pro Thr Thr Pro Trp Asn Ile His Pro Leu	
295 300 305	

tgt gtc ttc cac cac atc cag aag act gaa ggg agg ctc cag tgc tat 1075
 Cys Val Phe His His Ile Gln Lys Thr Glu Gly Arg Leu Gln Cys Tyr
 310 315 320 325

cca cta ccg gac ggc acc gtc cta ttc cta gtg gat gga ata ccg gtg 1123
 Pro Leu Pro Asp Gly Thr Val Leu Phe Leu Val Asp Gly Ile Pro Val
 330 335 340

ttc tcc atc ccc gac ggg cct tta tct aaa tgg aat aaa acc tgg ggg 1171
 Phe Ser Ile Pro Asp Gly Pro Leu Ser Lys Ser Asn Lys Thr Trp Gly
 345 350 355

aca aag ttc ggc aaa tac atg gag cgt cga atc gcc gcc taatccagca 1220
 Thr Lys Phe Gly Lys Tyr Met Glu Arg Arg Ile Ala Ala
 360 365 370

agccagcgtg atc 1233

<210> 1170

<211> 370

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1170

Met Phe Tyr Phe Thr Val Asn Asn Pro Gln Asp Pro Leu Ser Thr Glu
 1 5 10 15

Ile Val Glu Thr Asn Arg Arg Asp Leu Ala Phe Trp His Arg Leu Arg
 20 25 30

Pro Lys Asp Asp Asp Asp Leu Ala Thr Ala Ile Asn Lys Ile Cys Val
 35 40 45

Arg Thr Gly Leu Ser Arg Lys Leu Ile Ala Ala Cys Leu Phe Ser Ile
 50 55 60

Cys Phe Leu Pro Tyr Leu Pro Asn Phe His Lys Leu Val Glu Lys Leu
 65 70 75 80

Gly His Leu Asp Met Ala Arg Ile Asn Ala Ile Thr Lys Ala Gly Glu
 85 90 95

Lys Val Pro Ser Glu Lys Arg Glu Leu Phe Asp Ala Tyr Leu Val Asp
 100 105 110

Tyr Leu Thr Pro Arg Ala Glu Ala Gln Cys Leu Pro Gln Ala Ser Ser
 115 120 125

Ile Ser Ala Met Met Arg Lys Phe Ile Ala Gln His Cys Pro Asp Asp
 130 135 140

Lys Ala Ser Ser Ala Thr Asn Asp Gly Ser Ile Arg Tyr Arg Arg Asn
 145 150 155 160

Asn Lys Gly Gly Ile Ser Ile Thr Val Asp Ala Thr Ala Ser Glu Val
 165 170 175

Thr Glu Ile Lys Ala Ala Leu Glu Gln Met Ser Lys Asp Lys Asp Cys
 180 185 190

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Thr Pro Gly Thr Ser Leu Leu His Ile Ile Arg Gly Leu Pro Thr Lys
195 200 205
Val Val Leu Asn Thr Tyr Gly Thr Lys Asp Ser Pro Glu Tyr Leu Glu
210 215 220
Gly Gly Thr Trp Leu Ser Lys Glu Gln Ser Glu Phe Trp Lys Thr Arg
225 230 235 240
Thr Thr Ser Ser Arg Asp Met Asp Ala Ala His Phe Ser Tyr Thr Thr
245 250 255
Ala Tyr Ala Pro Thr Arg Glu Met Arg Val Tyr Ile Lys Gly Leu Arg
260 265 270
Thr Thr Cys Ser Val Pro Gly Cys Ser Val Ala Val Glu Asn Cys Gln
275 280 285
Leu Asp His Ile Ile Pro Trp Gly Glu Gly Gly Pro Thr Thr Pro Trp
290 295 300
Asn Ile His Pro Leu Cys Val Phe His His Ile Gln Lys Thr Glu Gly
305 310 315 320
Arg Leu Gln Cys Tyr Pro Leu Pro Asp Gly Thr Val Leu Phe Leu Val
325 330 335
Asp Gly Ile Pro Val Phe Ser Ile Pro Asp Gly Pro Leu Ser Lys Ser
340 345 350
Asn Lys Thr Trp Gly Thr Lys Phe Gly Lys Tyr Met Glu Arg Arg Ile
355 360 365
Ala Ala
370

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<210> 1171
<211> 1233
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(1210)
<223> FRXA02457

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agttagaaca tatgtaccac ttcaaatcta gggggaaaca atg ttc tac ttc acc 115
Met Phe Tyr Phe Thr
1 5
gtc aat aat ccg cag gat cct tta agc acc gaa att gtt gag act aat 163
Val Asn Asn Pro Gln Asp Pro Leu Ser Thr Glu Ile Val Glu Thr Asn
10 15 20
cgc cgt gac ctc gca ttt tgg cat cga tta cgc ccc aaa gat gac gat 211
Arg Arg Asp Leu Ala Phe Trp His Arg Leu Arg Pro Lys Asp Asp Asp
25 30 35

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gat tta gcc aca gcc atc aac aaa ata tgc gtg cgc aca ggc tta tcc 259
 Asp Leu Ala Thr Ala Ile Asn Lys Ile Cys Val Arg Thr Gly Leu Ser
 40 45 50

cgc aaa ctg atc gcc gct tgt tta ttt agc atc tgc ttc ctg ccg tac 307
 Arg Lys Leu Ile Ala Ala Cys Leu Phe Ser Ile Cys Phe Leu Pro Tyr
 55 60 65

tta ccc aac ttc cac aaa ctc gtc gaa aag ctt ggt cat ctc gac atg 355
 Leu Pro Asn Phe His Lys Leu Val Glu Lys Leu Gly His Leu Asp Met 85
 70 75 80

gcg cgc atc aac gcg atc act aaa gct ggc gaa aaa gtg cca agc gag 403
 Ala Arg Ile Asn Ala Ile Thr Lys Ala Gly Glu Lys Val Pro Ser Glu
 90 95 100

aag aga gag ctt ttc gac gcc tac ctc gtc gat tac ctg acg cct cga 451
 Lys Arg Glu Leu Phe Asp Ala Tyr Leu Val Asp Tyr Leu Thr Pro Arg
 105 110 115

gcg gag gct cag tgc ttg ccc cag gca agc tca att tcc gca atg atg 499
 Ala Glu Ala Gln Cys Leu Pro Gln Ala Ser Ser Ile Ser Ala Met Met
 120 125 130

cgg aaa ttt atc gca caa cac tgc ccc gac gac aag gcc tcc tca gcc 547
 Arg Lys Phe Ile Ala Gln His Cys Pro Asp Asp Lys Ala Ser Ser Ala
 135 140 145

acc aat gat ggc tcc atc cgc tac cgc aga aac aac aaa ggc ggg atc 595
 Thr Asn Asp Gly Ser Ile Arg Tyr Arg Arg Asn Lys Gly Gly Ile
 150 155 160 165

agt atc acc gtc gat gcc acc gcc agc gaa gta aca gaa atc aaa gct 643
 Ser Ile Thr Val Asp Ala Thr Ala Ser Glu Val Thr Glu Ile Lys Ala
 170 175 180

gcc ctg gaa caa atg tcc aaa gat aag gac tgc aca cca ggc act tcc 691
 Ala Leu Glu Gln Met Ser Lys Asp Lys Asp Cys Thr Pro Gly Thr Ser
 185 190 195

cta ctc cac atc att cgt ggc ctg ccg aca aaa gtc gta ctc aac acc 739
 Leu Leu His Ile Ile Arg Gly Leu Pro Thr Lys Val Val Leu Asn Thr
 200 205 210

tac ggc acc aaa gac agc cct gaa tac tta gaa gga gga acc tgg ctg 787
 Tyr Gly Thr Lys Asp Ser Pro Glu Tyr Leu Glu Gly Gly Thr Trp Leu
 215 220 225

tca aag gaa cag tct gag ttc tgg aaa acc cga acc acg tcc agt cgg 835
 Ser Lys Glu Gln Ser Glu Phe Trp Lys Thr Arg Thr Thr Ser Ser Arg
 230 235 240 245

gat atg gac gcc gcc cac ttc tct tac acc acc gcc tac gct cca acc 883
 Asp Met Asp Ala Ala His Phe Ser Tyr Thr Thr Ala Tyr Ala Pro Thr
 250 255 260

cga gaa atg cgc gtc tac atc aaa ggt cta cgc acc acc tgt agc gtc 931
 Arg Glu Met Arg Val Tyr Ile Lys Gly Leu Arg Thr Thr Cys Ser Val
 265 270 275

cct ggc tgc agt gta gcg gtc gaa aac tgc caa ctg gac cac atc atc 979
 Pro Gly Cys Ser Val Ala Val Glu Asn Cys Gln Leu Asp His Ile Ile
 280 285 290

ccc tgg ggt gaa gga ggg ccg aca aca ccg tgg aat att cat ccc ctg 1027
 Pro Trp Gly Glu Gly Gly Pro Thr Thr Pro Trp Asn Ile His Pro Leu
 295 300 305

tgt gtc ttc cac cac atc cag aag act gaa ggg agg ctc cag tgc tat 1075
 Cys Val Phe His His Ile Gln Lys Thr Glu Gly Arg Leu Gln Cys Tyr
 310 315 320 325

cca cta ccg gac ggc acc gtc cta ttc cta gtg gat gga ata ccg gtg 1123
 Pro Leu Pro Asp Gly Thr Val Leu Phe Leu Val Asp Gly Ile Pro Val
 330 335 340

ttc tcc atc ccc gac ggg cct tta tct aaa tcg aat aaa acc tgg ggg 1171
 Phe Ser Ile Pro Asp Gly Pro Leu Ser Lys Ser Asn Lys Thr Trp Gly
 345 350 355

aca aag ttc ggc aaa tac atg gag cgt cga atc gcc gcc taatccagca 1220
 Thr Lys Phe Gly Lys Tyr Met Glu Arg Arg Ile Ala Ala
 360 365 370

agccagcgtg atc 1233

<210> 1172
 <211> 370
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1172
 Met Phe Tyr Phe Thr Val Asn Asn Pro Gln Asp Pro Leu Ser Thr Glu
 1 5 10 15

Ile Val Glu Thr Asn Arg Arg Asp Leu Ala Phe Trp His Arg Leu Arg
 20 25 30

Pro Lys Asp Asp Asp Asp Leu Ala Thr Ala Ile Asn Lys Ile Cys Val
 35 40 45

Arg Thr Gly Leu Ser Arg Lys Leu Ile Ala Ala Cys Leu Phe Ser Ile
 50 55 60

Cys Phe Leu Pro Tyr Leu Pro Asn Phe His Lys Leu Val Glu Lys Leu
 65 70 75 80

Gly His Leu Asp Met Ala Arg Ile Asn Ala Ile Thr Lys Ala Gly Glu
 85 90 95

Lys Val Pro Ser Glu Lys Arg Glu Leu Phe Asp Ala Tyr Leu Val Asp
 100 105 110

Tyr Leu Thr Pro Arg Ala Glu Ala Gln Cys Leu Pro Gln Ala Ser Ser
 115 120 125

Ile Ser Ala Met Met Arg Lys Phe Ile Ala Gln His Cys Pro Asp Asp
 130 135 140

Lys Ala Ser Ser Ala Thr Asn Asp Gly Ser Ile Arg Tyr Arg Arg Asn

145 150 155 160
 Asn Lys Gly Gly Ile Ser Ile Thr Val Asp Ala Thr Ala Ser Glu Val
 165 170 175
 Thr Glu Ile Lys Ala Ala Leu Glu Gln Met Ser Lys Asp Lys Asp Cys
 180 185 190
 Thr Pro Gly Thr Ser Leu Leu His Ile Ile Arg Gly Leu Pro Thr Lys
 195 200 205
 Val Val Leu Asn Thr Tyr Gly Thr Lys Asp Ser Pro Glu Tyr Leu Glu
 210 215 220
 Gly Gly Thr Trp Leu Ser Lys Glu Gln Ser Glu Phe Trp Lys Thr Arg
 225 230 235 240
 Thr Thr Ser Ser Arg Asp Met Asp Ala Ala His Phe Ser Tyr Thr Thr
 245 250 255
 Ala Tyr Ala Pro Thr Arg Glu Met Arg Val Tyr Ile Lys Gly Leu Arg
 260 265 270
 Thr Thr Cys Ser Val Pro Gly Cys Ser Val Ala Val Glu Asn Cys Gln
 275 280 285
 Leu Asp His Ile Ile Pro Trp Gly Glu Gly Gly Pro Thr Thr Pro Trp
 290 295 300
 Asn Ile His Pro Leu Cys Val Phe His His Ile Gln Lys Thr Glu Gly
 305 310 315 320
 Arg Leu Gln Cys Tyr Pro Leu Pro Asp Gly Thr Val Leu Phe Leu Val
 325 330 335
 Asp Gly Ile Pro Val Phe Ser Ile Pro Asp Gly Pro Leu Ser Lys Ser
 340 345 350
 Asn Lys Thr Trp Gly Thr Lys Phe Gly Lys Tyr Met Glu Arg Arg Ile
 355 360 365
 Ala Ala
 370

<210> 1173

<211> 627

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(604)

<223> RXN02460

<400> 1173

gcgccgtcga agccggactc gtaggcgtct actaccagca atttgaccgt gcagtcgtcg 60

aaatcgtcgg actgttcggg ctagaaggag aattctaatac ttg cgc gtc tac atc 115

 Leu Arg Val Tyr Ile
 1 5

cca gca acg ttt tcc aca ctc cgc gga ctc aat gaa tcc cgc gtc atc 163
 Pro Ala Thr Phe Ser Thr Leu Arg Gly Leu Asn Glu Ser Arg Val Ile
 10 15 20

aca gca cgc tcc gga tac ggt ttc gca gtc acc cca gca ctc ctt gac 211
 Thr Ala Arg Ser Gly Tyr Gly Phe Ala Val Thr Pro Ala Leu Leu Asp
 25 30 35

ttc tac acc gac ggt gac gaa gaa gaa atc gca cat gca gcc ttc caa 259
 Phe Tyr Thr Asp Gly Asp Glu Glu Glu Ile Ala His Ala Ala Phe Gln
 40 45 50

gac gcc gca gaa gcc tcc atc cga ctc ctc gca atc gcc gac gaa gaa 307
 Asp Ala Ala Glu Ala Ser Ile Arg Leu Leu Ala Ile Gly Asp Glu Glu
 55 60 65

aca ttt ccc tac cgc aga gtc gtc gtc tca gta gat gtt gac gac tcc 355
 Thr Phe Pro Tyr Arg Arg Val Val Val Ser Val Asp Val Asp Asp Ser
 70 75 80 85

gtg gtg acc tac cag cct gaa aac ggc gaa tcc gta gtc aaa ctc agc 403
 Val Val Thr Tyr Gln Pro Glu Asn Gly Glu Ser Val Val Lys Leu Ser
 90 95 100

cca gcg cac atc aac ctc gac gac gtg gca gca atc cac atc gac gtt 451
 Pro Ala His Ile Asn Leu Asp Asp Val Ala Ala Ile His Ile Asp Val
 105 110 115

gaa gcc tcc gaa gca gac acc aaa aaa gct atc gaa gtc atc gac gaa 499
 Glu Ala Ser Glu Ala Asp Thr Lys Lys Ala Ile Glu Val Ile Asp Glu
 120 125 130

tcc gac ctc gcc gaa gaa gac gcc gaa ctc acc gtc gga gac gcc caa 547
 Ser Asp Leu Gly Glu Glu Asp Ala Glu Leu Thr Val Gly Asp Ala Gln
 135 140 145

gac aac ttc atg gcc tgg tac gac cca gaa gag ctc ccc ttc cta gtc 595
 Asp Asn Phe Met Ala Trp Tyr Asp Pro Glu Glu Leu Pro Phe Leu Val
 150 155 160 165

gag ctc ctc tagatcacat atcccacgag tcg 627
 Glu Leu Leu

<210> 1174

<211> 168

<212> PRT

<213> Corynebacterium glutamicum

<400> 1174

Leu Arg Val Tyr Ile Pro Ala Thr Phe Ser Thr Leu Arg Gly Leu Asn
 1 5 10 15

Glu Ser Arg Val Ile Thr Ala Arg Ser Gly Tyr Gly Phe Ala Val Thr
 20 25 30

Pro Ala Leu Leu Asp Phe Tyr Thr Asp Gly Asp Glu Glu Ile Ala
 35 40 45

His Ala Ala Phe Gln Asp Ala Ala Glu Ala Ser Ile Arg Leu Leu Ala
 50 55 60
 Ile Gly Asp Glu Glu Thr Phe Pro Tyr Arg Arg Val Val Val Ser Val
 65 70 75 80
 Asp Val Asp Asp Ser Val Val Thr Tyr Gln Pro Glu Asn Gly Glu Ser
 85 90 95
 Val Val Lys Leu Ser Pro Ala His Ile Asn Leu Asp Asp Val Ala Ala
 100 105 110
 Ile His Ile Asp Val Glu Ala Ser Glu Ala Asp Thr Lys Lys Ala Ile
 115 120 125
 Glu Val Ile Asp Glu Ser Asp Leu Gly Glu Glu Asp Ala Glu Leu Thr
 130 135 140
 Val Gly Asp Ala Gln Asp Asn Phe Met Ala Trp Tyr Asp Pro Glu Glu
 145 150 155 160
 Leu Pro Phe Leu Val Glu Leu Leu
 165

<210> 1175

<211> 627

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(604)

<223> FRXA02460

<400> 1175

gagccgtcga agccggactc gtaggcgtct actaccagca atttgacctg gcagtcgtcg 60

aaatcgtcgg actgttcggg ctagaaggag aattctaattc ttg cgc gtc tac atc 115
 Leu Arg Val Tyr Ile
 1 5

cca gca acg ttt tcc aca ctc cgc gga ctc aat gaa tcc cgc gtc atc 163
 Pro Ala Thr Phe Ser Thr Leu Arg Gly Leu Asn Glu Ser Arg Val Ile
 10 15 20

aca gca cgc tcc gga tac ggt ttc gca gtc acc cca gca ctc ctt gac 211
 Thr Ala Arg Ser Gly Tyr Gly Phe Ala Val Thr Pro Ala Leu Leu Asp
 25 30 35

ttc tac acc gac ggt gac gaa gaa gaa atc gca cat gca gcc ttc caa 259
 Phe Tyr Thr Asp Gly Asp Glu Glu Glu Ile Ala His Ala Ala Phe Gln
 40 45 50

gac gcc gca gaa gcc tcc atc cga ctc ctc gca atc ggc gac gaa gaa 307
 Asp Ala Ala Glu Ala Ser Ile Arg Leu Leu Ala Ile Gly Asp Glu Glu
 55 60 65

aca ttt ccc tac cgc aga gtc gtc gtc tca gta gat gtt gac gac tcc 355
 Thr Phe Pro Tyr Arg Arg Val Val Val Ser Val Asp Val Asp Asp Ser
 70 75 80 85

gtg gtg acc tac cag cct gaa aac ggc gaa tcc gta gtc aaa ctc agc 403
Val Val Thr Tyr Gln Pro Glu Asn Gly Glu Ser Val Val Lys Leu Ser
90 95 100

cca gcg cac atc aac ctc gac gac gtc gca gca atc cac atc gac gtt 451
Pro Ala His Ile Asn Leu Asp Asp Val Ala Ala Ile His Ile Asp Val
105 110 115

gaa gcc tcc gaa gca gac acc aaa aaa gct atc gaa gtc atc gac gaa 499
Glu Ala Ser Glu Ala Asp Thr Lys Lys Ala Ile Glu Val Ile Asp Glu
120 125 130

tcc gac ctc ggc gaa gaa gac gcc gaa ctc acc gtc gga gac gcc caa 547
Ser Asp Leu Gly Glu Glu Asp Ala Glu Leu Thr Val Gly Asp Ala Gln
135 140 145

gac aac ttc atg gcc tgg tac gac cca gaa gag ctc ccc ttc cta gtc 595
Asp Asn Phe Met Ala Trp Tyr Asp Pro Glu Glu Leu Pro Phe Leu Val
150 155 160 165

gag ctc ctc tagatcacat atcccacgcg tcg 627
Glu Leu Leu

<210> 1176

<211> 168

<212> PRT

<213> Corynebacterium glutamicum

<400> 1176

Leu Arg Val Tyr Ile Pro Ala Thr Phe Ser Thr Leu Arg Gly Leu Asn
1 5 10 15

Glu Ser Arg Val Ile Thr Ala Arg Ser Gly Tyr Gly Phe Ala Val Thr
20 25 30

Pro Ala Leu Asp Phe Tyr Thr Asp Gly Asp Glu Glu Ile Ala
35 40 45

His Ala Ala Phe Gln Asp Ala Ala Glu Ala Ser Ile Arg Leu Leu Ala
50 55 60

Ile Gly Asp Glu Glu Thr Phe Pro Tyr Arg Arg Val Val Val Ser Val
65 70 75 80

Asp Val Asp Asp Ser Val Val Thr Tyr Gln Pro Glu Asn Gly Glu Ser
85 90 95

Val Val Lys Leu Ser Pro Ala His Ile Asn Leu Asp Asp Val Ala Ala
100 105 110

Ile His Ile Asp Val Glu Ala Ser Glu Ala Asp Thr Lys Lys Ala Ile
115 120 125

Glu Val Ile Asp Glu Ser Asp Leu Gly Glu Glu Asp Ala Glu Leu Thr
130 135 140

Val Gly Asp Ala Gln Asp Asn Phe Met Ala Trp Tyr Asp Pro Glu Glu
145 150 155 160

Leu Pro Phe Leu Val Glu Leu Leu
165

<210> 1177

<211> 1323

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1300)

<223> RXN02464

<400> 1177

actcgacatc ccagaaggtg tcaccgaacg agtcggacca ccaaccaaag ttctaggcgg 60

aacagcccca cgaccaccac gccgcacccg gaaataactt atg gca gca aag ctt 115
Met Ala Ala Lys Leu
1 5

caa cca ctc aaa cgc acc aaa aaa gac ctc atc gca acc ggt gtc atc 163
Gln Pro Leu Lys Arg Thr Lys Lys Asp Leu Ile Ala Thr Gly Val Ile
10 15 20

aca gca cta gca gtc att ggc gtc ggc acg gtc tgg gca acc gca cca 211
Thr Ala Leu Ala Val Ile Gly Val Gly Thr Val Trp Ala Thr Ala Pro
25 30 35

ata cga gga tct gaa ctc acc ccc gcc gac gaa cca ttc att ggc tca 259
Ile Arg Gly Ser Glu Leu Thr Pro Ala Asp Glu Pro Phe Ile Gly Ser
40 45 50

acc aca ctg gac gcc atc ccc gaa aca ctc agc gaa cat tgg cga gcc 307
Thr Thr Leu Asp Ala Ile Pro Glu Thr Leu Ser Glu His Trp Arg Ala
55 60 65

acc gac acc tta aca aac cac aaa ccc ctc atc acc ggc gga gtc atc 355
Thr Asp Thr Leu Thr Asn His Lys Pro Leu Ile Thr Gly Gly Val Ile
70 75 80 85

ttc acc gcc gac ggc aac acc att aag acc tac acc ccc gac ggc gcc 403
Phe Thr Ala Asp Gly Asn Thr Ile Lys Thr Tyr Thr Pro Asp Gly Ala
90 95 100

ctc ctg tgg agc tac gaa cgc gac aaa gaa ctc tgc agc ctc tcc gta 451
Leu Leu Trp Ser Tyr Glu Arg Asp Lys Glu Leu Cys Ser Leu Ser Val
105 110 115

gga ttc gac gcc gcc gtc gcc acc tac aaa acc gga atc gga tgt ggc 499
Gly Phe Asp Ala Ala Val Ala Thr Tyr Lys Thr Gly Ile Gly Cys Gly
120 125 130

gac gtc acc gcc atc aac gcc aac gac ggc caa tac caa gca aca cgc 547
Asp Val Thr Ala Ile Asn Ala Asn Asp Gly Gln Tyr Gln Ala Thr Arg
135 140 145

agc gca atc tcc agc gac cac gta gca ccg atc tcc tcg aac gat cgg 595
Ser Ala Ile Ser Ser Asp His Val Ala Pro Ile Ser Ser Asn Asp Arg
150 155 160 165

atc ggt gtt ctc ggg aca gaa cgc ttg gag ctt tgg cga tcc gat ctg 643
 Ile Gly Val Leu Gly Thr Glu Arg Leu Glu Leu Trp Arg Ser Asp Leu
 170 175 180

gtg cga acc atc gaa tac ggc gat gtg gaa gct cct caa gaa tct ggg 691
 Val Arg Thr Ile Glu Tyr Gly Asp Val Glu Ala Pro Gln Glu Ser Gly
 185 190 195

caa caa cca cat ccg gaa tgc tgc att acg tcc gcc atg aca cgc aaa 739
 Gln Gln Pro His Pro Glu Cys Ser Ile Thr Ser Ala Met Thr Arg Lys
 200 205 210

gat cta ttg gct atc acc gag gat tgc cct gac gga tct tct tac ttg 787
 Asp Leu Leu Ala Ile Thr Glu Asp Cys Pro Asp Gly Ser Ser Tyr Leu
 215 220 225

agg ttc atg ggc aca aca cca gac gat tcc cga act cct gaa atc acc 835
 Arg Phe Met Gly Thr Thr Pro Asp Asp Ser Arg Thr Pro Glu Ile Thr
 230 235 240 245

caa gac ata gaa ata acc gat ggc agg atc gtt gcc atc ggt caa tca 883
 Gln Asp Ile Glu Ile Thr Asp Gly Arg Ile Val Ala Ile Gly Gln Ser
 250 255 260

gtg gct gcg gtg tat aca aac gat cct tgc cct cga atc gtc tcc tac 931
 Val Ala Ala Val Tyr Thr Asn Asp Pro Ser Pro Arg Ile Val Ser Tyr
 265 270 275

aac gat gat ggt gaa cta gtt gga gaa caa gca gtc gat gag gtt gag 979
 Asn Asp Asp Gly Glu Leu Val Gly Glu Gln Ala Val Asp Glu Val Glu
 280 285 290

ttc ccg gat ccg ccg ttt caa agc gcg acc gct gat ctt cca cac cat 1027
 Phe Pro Asp Pro Pro Phe Gln Ser Ala Thr Ala Asp Leu Pro His His
 295 300 305

atg agt tgg ttc aac gga gac agc ctc gta ctg ttc tct ccc act cag 1075
 Met Ser Trp Phe Asn Gly Asp Ser Leu Val Leu Phe Ser Pro Thr Gln
 310 315 320 325

ctc aat gta cga caa agc ttc aat gat gct tta gga acc ggc att gcg 1123
 Leu Asn Val Arg Gln Ser Phe Asn Asp Ala Leu Gly Thr Gly Ile Ala
 330 335 340

ttg aac gga agt ctc ctc tac ccc acc gct gag ggc atc acg gta gct 1171
 Leu Asn Gly Ser Leu Leu Tyr Pro Thr Ala Glu Gly Ile Thr Val Ala
 345 350 355

aat tgg gac acc gga gag gtg cag cgc acc att ccg gtg gac cgt gcg 1219
 Asn Trp Asp Thr Gly Glu Val Gln Arg Thr Ile Pro Val Asp Arg Ala
 360 365 370

ggc tac gac ggt gaa gtt gcg ctc ggc gtt gta ggg cag gtg atc gtc 1267
 Gly Tyr Asp Gly Glu Val Ala Leu Gly Val Val Gly Gln Val Ile Val
 375 380 385

gaa aag cgt ggc tct gag atc gtt gct cta ggc tagatctcgt tgttagccca 1320
 Glu Lys Arg Gly Ser Glu Ile Val Ala Leu Gly
 390 395 400

aag

1323

<210> 1178

<211> 400

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1178

Met Ala Ala Lys Leu Gln Pro Leu Lys Arg Thr Lys Lys Asp Leu Ile
 1 5 10 15

Ala Thr Gly Val Ile Thr Ala Leu Ala Val Ile Gly Val Gly Thr Val
 20 25 30

Trp Ala Thr Ala Pro Ile Arg Gly Ser Glu Leu Thr Pro Ala Asp Glu
 35 40 45

Pro Phe Ile Gly Ser Thr Thr Leu Asp Ala Ile Pro Glu Thr Leu Ser
 50 55 60

Glu His Trp Arg Ala Thr Asp Thr Leu Thr Asn His Lys Pro Leu Ile
 65 70 75 80

Thr Gly Gly Val Ile Phe Thr Ala Asp Gly Asn Thr Ile Lys Thr Tyr
 85 90 95

Thr Pro Asp Gly Ala Leu Leu Trp Ser Tyr Glu Arg Asp Lys Glu Leu
 100 105 110

Cys Ser Leu Ser Val Gly Phe Asp Ala Ala Val Ala Thr Tyr Lys Thr
 115 120 125

Gly Ile Gly Cys Gly Asp Val Thr Ala Ile Asn Ala Asn Asp Gly Gln
 130 135 140

Tyr Gln Ala Thr Arg Ser Ala Ile Ser Ser Asp His Val Ala Pro Ile
 145 150 155 160

Ser Ser Asn Asp Arg Ile Gly Val Leu Gly Thr Glu Arg Leu Glu Leu
 165 170 175

Trp Arg Ser Asp Leu Val Arg Thr Ile Glu Tyr Gly Asp Val Glu Ala
 180 185 190

Pro Gln Glu Ser Gly Gln Gln Pro His Pro Glu Cys Ser Ile Thr Ser
 195 200 205

Ala Met Thr Arg Lys Asp Leu Leu Ala Ile Thr Glu Asp Cys Pro Asp
 210 215 220

Gly Ser Ser Tyr Leu Arg Phe Met Gly Thr Thr Pro Asp Asp Ser Arg
 225 230 235 240

Thr Pro Glu Ile Thr Gln Asp Ile Glu Ile Thr Asp Gly Arg Ile Val
 245 250 255

Ala Ile Gly Gln Ser Val Ala Ala Val Tyr Thr Asn Asp Pro Ser Pro
 260 265 270

Arg Ile Val Ser Tyr Asn Asp Asp Gly Glu Leu Val Gly Glu Gln Ala

275

280

285

Val Asp Glu Val Glu Phe Pro Asp Pro Pro Phe Gln Ser Ala Thr Ala
290 295 300

Asp Leu Pro His His Met Ser Trp Phe Asn Gly Asp Ser Leu Val Leu
305 310 315 320

Phe Ser Pro Thr Gln Leu Asn Val Arg Gln Ser Phe Asn Asp Ala Leu
325 330 335

Gly Thr Gly Ile Ala Leu Asn Gly Ser Leu Leu Tyr Pro Thr Ala Glu
340 345 350

Gly Ile Thr Val Ala Asn Trp Asp Thr Gly Glu Val Gln Arg Thr Ile
355 360 365

Pro Val Asp Arg Ala Gly Tyr Asp Gly Glu Val Ala Leu Gly Val Val
370 375 380

Gly Gln Val Ile Val Glu Lys Arg Gly Ser Glu Ile Val Ala Leu Gly
385 390 395 400

<210> 1179

<211> 630

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(607)

<223> FRXA02464

<400> 1179

acaaccacat ccggaatgct cgattacgtc cgccatgaca cgcaaagatc tattggctat 60

caccgaggat tgccctgacg gatctttotta cttgagggttc atg ggc aca aca cca 115
Met Gly Thr Thr Pro 5

gac gat tcc cga act cct gaa atc acc caa gac ata gaa ata acc gat 163
Asp Asp Ser Arg Thr Pro Glu Ile Thr Gln Asp Ile Glu Ile Thr Asp 10 15 20

ggc agg atc gtt gcc atc ggt caa tca gtg gct gcg gtg tat aca aac 211
Gly Arg Ile Val Ala Ile Gly Gln Ser Val Ala Ala Val Tyr Thr Asn 25 30 35

gat cct tcg cct cga atc gtc tcc tac aac gat gat ggt gaa cta gtt 259
Asp Pro Ser Pro Arg Ile Val Ser Tyr Asn Asp Asp Gly Glu Leu Val 40 45 50

gga gaa caa gca gtc gat gag gtt gag ttc ccg gat ccg ccg ttt caa 307
Gly Glu Gln Ala Val Asp Glu Val Glu Phe Pro Asp Pro Pro Phe Gln 55 60 65

agc gcg acc gct gat ctt cca cac cat atg agt tgg ttc aac gga gac 355

Ser Ala Thr Ala Asp Leu Pro His His Met Ser Trp Phe Asn Gly Asp
 70 75 80 85
 agc ctc gta ctg ttc tct ccc act cag ctc aat gta cga caa agc ttc 403
 Ser Leu Val Leu Phe Ser Pro Thr Gln Leu Asn Val Arg Gln Ser Phe
 90 95 100
 aat gat gct tta gga acc ggc att gcg ttg aac gga agt ctc ctc tac 451
 Asn Asp Ala Leu Gly Thr Gly Ile Ala Leu Asn Gly Ser Leu Leu Tyr
 105 110 115
 ccc acc gct gag ggc atc acg gta gct aat tgg gac acc gga gag gtg 499
 Pro Thr Ala Glu Gly Ile Thr Val Ala Asn Trp Asp Thr Gly Glu Val
 120 125 130
 cag cgc acc att ccg gtg gac cgt gcg ggc tac gac ggt gaa gtt gcg 547
 Gln Arg Thr Ile Pro Val Asp Arg Ala Gly Tyr Asp Gly Glu Val Ala
 135 140 145
 ctc ggc gtt gta ggg cag gtg atc gtc gaa aag cgt ggc tct gag atc 595
 Leu Gly Val Val Gly Gln Val Ile Val Glu Lys Arg Gly Ser Glu Ile
 150 155 160 165
 gtt gct cta ggc tagatctcgt tgtagccca aag 630
 Val Ala Leu Gly

 <210> 1180
 <211> 169
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 1180
 Met Gly Thr Thr Pro Asp Asp Ser Arg Thr Pro Glu Ile Thr Gln Asp
 1 5 10 15
 Ile Glu Ile Thr Asp Gly Arg Ile Val Ala Ile Gly Gln Ser Val Ala
 20 25 30
 Ala Val Tyr Thr Asn Asp Pro Ser Pro Arg Ile Val Ser Tyr Asn Asp
 35 40 45
 Asp Gly Glu Leu Val Gly Glu Gln Ala Val Asp Glu Val Glu Phe Pro
 50 55 60
 Asp Pro Pro Phe Gln Ser Ala Thr Ala Asp Leu Pro His His Met Ser
 65 70 75 80
 Trp Phe Asn Gly Asp Ser Leu Val Leu Phe Ser Pro Thr Gln Leu Asn
 85 90 95
 Val Arg Gln Ser Phe Asn Asp Ala Leu Gly Thr Gly Ile Ala Leu Asn
 100 105 110
 Gly Ser Leu Leu Tyr Pro Thr Ala Glu Gly Ile Thr Val Ala Asn Trp
 115 120 125
 Asp Thr Gly Glu Val Gln Arg Thr Ile Pro Val Asp Arg Ala Gly Tyr
 130 135 140

Asp Gly Glu Val Ala Leu Gly Val Val Gly Gln Val Ile Val Glu Lys
 145 150 155 160

Arg Gly Ser Glu Ile Val Ala Leu Gly
 165

<210> 1181

<211> 522

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(499)

<223> RXN02465

<400> 1181

ctgggtgcaat ataaaagtta accaaaccagt catccaatat gtcgcctaag tagtcttccc 60

aaagttaaca gctagaatca tggccgtgac ttctccgaac atg cct gca tca att 115
 Met Pro Ala Ser Ile
 1 5

cgc tgg ggc ggc atc gtc gcc ctc att caa tcc acc atc gga ttc ggt 163
 Arg Trp Gly Gly Ile Val Ala Leu Ile Gln Ser Thr Ile Gly Phe Gly
 10 15 20

tac gcc ttt ttc ctt att tac agg gaa gct acg ggc gag acg gat cca 211
 Tyr Ala Phe Phe Leu Ile Tyr Arg Glu Ala Thr Gly Glu Thr Asp Pro
 25 30 35

agc atc gtc tac gaa acc gat aac gcc aac acg tgg gtt ggc tac ggt 259
 Ser Ile Val Tyr Glu Thr Asp Asn Ala Asn Thr Trp Val Gly Tyr Gly
 40 45 50

acc gct gca ttc ttc atc att gtg ttc gga acg gtt gtt gca ggc gca 307
 Thr Ala Ala Phe Phe Ile Ile Val Phe Gly Thr Val Val Ala Gly Ala
 55 60 65

atc aac atg atg aag ggg cat cgc tgg gga cgc gga gct gtc gtc atg 355
 Ile Asn Met Met Lys Gly His Arg Trp Gly Arg Gly Ala Val Val Met
 70 75 80 85

ctg aat att att ttg ttg ccg gct gcg tat tac atg ttt atc gaa ggc 403
 Leu Asn Ile Ile Leu Leu Pro Ala Ala Tyr Tyr Met Phe Ile Glu Gly
 90 95 100

cga ttc tcc tgg gcg atc gtc aca gga atc tca gct ctc ttc gtt ttg 451
 Arg Phe Ser Trp Ala Ile Val Thr Gly Ile Ser Ala Leu Phe Val Leu
 105 110 115

ggc gca ctg ttt aat aag cgc gcc gtc ctt tgg gct aac aac gag atc 499
 Gly Ala Leu Phe Asn Lys Arg Ala Val Leu Trp Ala Asn Asn Glu Ile
 120 125 130

tagcctagag caacgatctc aga 522

<210> 1182

<211> 133

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1182

Met Pro Ala Ser Ile Arg Trp Gly Gly Ile Val Ala Leu Ile Gln Ser
 1 5 10 15

Thr Ile Gly Phe Gly Tyr Ala Phe Phe Leu Ile Tyr Arg Glu Ala Thr
 20 25 30

Gly Glu Thr Asp Pro Ser Ile Val Tyr Glu Thr Asp Asn Ala Asn Thr
 35 40 45

Trp Val Gly Tyr Gly Thr Ala Ala Phe Phe Ile Ile Val Phe Gly Thr
 50 55 60

Val Val Ala Gly Ala Ile Asn Met Met Lys Gly His Arg Trp Gly Arg
 65 70 75 80

Gly Ala Val Val Met Leu Asn Ile Ile Leu Leu Pro Ala Ala Tyr Tyr
 85 90 95

Met Phe Ile Glu Gly Arg Phe Ser Trp Ala Ile Val Thr Gly Ile Ser
 100 105 110

Ala Leu Phe Val Leu Gly Ala Leu Phe Asn Lys Arg Ala Val Leu Trp
 115 120 125

Ala Asn Asn Glu Ile
 130

<210> 1183

<211> 522

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(499)

<223> FRXA02465

<400> 1183

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aaagttaaca gctagaatca tggccgtgac ttctccgaac atg cct gca tca att 115
 Met Pro Ala Ser Ile
 1 5

cgc tgg ggc ggc atc gtc gcc ctc att caa tcc acc atc gga ttc ggt 163
 Arg Trp Gly Gly Ile Val Ala Leu Ile Gln Ser Thr Ile Gly Phe Gly
 10 15 20

tac gcc ttt ttc ctt att tac agg gaa gct acg ggc gag acg gat cca 211
 Tyr Ala Phe Phe Leu Ile Tyr Arg Glu Ala Thr Gly Glu Thr Asp Pro
 25 30 35

agc atc gtc tac gaa acc gat aac gcc aac acg tgg gtt ggc tac ggt 259
 Ser Ile Val Tyr Glu Thr Asp Asn Ala Asn Thr Trp Val Gly Tyr Gly
 40 45 50

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acc gct gca ttc ttc atc att gtg ttc gga acg gtt gtt gca ggc gca 307
Thr Ala Ala Phe Phe Ile Ile Val Phe Gly Thr Val Val Ala Gly Ala
    55                      60                      65

atc aac atg atg aag ggg cat cgc tgg gga cgc gga gct gtc gtc atg 355
Ile Asn Met Met Lys Gly His Arg Trp Gly Arg Gly Ala Val Val Met
    70                      75                      80                      85

ctg aat att att ttg ttg ccg gct gcg tat tac atg ttt atc gaa ggc 403
Leu Asn Ile Ile Leu Leu Pro Ala Ala Tyr Tyr Met Phe Ile Glu Gly
    90                      95                      100

cga ttc tcc tgg gcg atc gtc aca gga atc tca gct ctc ttc gtt ttg 451
Arg Phe Ser Trp Ala Ile Val Thr Gly Ile Ser Ala Leu Phe Val Leu
    105                      110                      115

ggc gca ctg ttt aat aag cgc gcc gtc ctt tgg gct aac aac gag atc 499
Gly Ala Leu Phe Asn Lys Arg Ala Val Leu Trp Ala Asn Asn Glu Ile
    120                      125                      130

tagcctagag caacgatctc aga 522

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<210> 1184
<211> 133
<212> PRT
<213> Corynebacterium glutamicum

<400> 1184
Met Pro Ala Ser Ile Arg Trp Gly Gly Ile Val Ala Leu Ile Gln Ser
  1           5           10           15

Thr Ile Gly Phe Gly Tyr Ala Phe Phe Leu Ile Tyr Arg Glu Ala Thr
          20           25           30

Gly Glu Thr Asp Pro Ser Ile Val Tyr Glu Thr Asp Asn Ala Asn Thr
          35           40           45

Trp Val Gly Tyr Gly Thr Ala Ala Phe Phe Ile Ile Val Phe Gly Thr
  50           55           60

Val Val Ala Gly Ala Ile Asn Met Met Lys Gly His Arg Trp Gly Arg
  65           70           75           80

Gly Ala Val Val Met Leu Asn Ile Ile Leu Leu Pro Ala Ala Tyr Tyr
          85           90           95

Met Phe Ile Glu Gly Arg Phe Ser Trp Ala Ile Val Thr Gly Ile Ser
    100           105           110

Ala Leu Phe Val Leu Gly Ala Leu Phe Asn Lys Arg Ala Val Leu Trp
    115           120           125

Ala Asn Asn Glu Ile
    130

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<210> 1185
<211> 187
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> {101}..(187)
<223> RXN02466

<400> 1185
cgaaccgcaa agcgttcgc tgacggaact gcgcctggc ggcagctaca ccgaaaccgg 60

tgctggcact ttccgccagg tcggcgctgc ttttcctcgc gtg ggc gag ggg cag 115
                                         Val Gly Glu Gly Gln
                                         1           5

gaa caa act ttt acg tac gtc att gag att gag gat ggc gtc aac acg 163
Glu Gln Thr Phe Thr Tyr Val Ile Glu Ile Glu Asp Gly Val Asn Thr
                10                15                20

gcc gct tat ggt ggc gac gat gcg 187
Ala Ala Tyr Gly Gly Asp Asp Ala
                25

```

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<210> 1186
<211> 29
<212> PRT
<213> Corynebacterium glutamicum

<400> 1186
Val Gly Glu Gly Gln Glu Gln Thr Phe Thr Tyr Val Ile Glu Ile Glu
  1           5           10           15

Asp Gly Val Asn Thr Ala Ala Tyr Gly Gly Asp Asp Ala
                20                25

<210> 1187
<211> 187
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> {101}..(187)
<223> FRXA02466

<400> 1187
cgaaccgcaa agcgttcgc tgacggaact gcgcctggc ggcagctaca ccgaaaccgg 60

tgctggcact ttccgccagg tcggcgctgc ttttcctcgc gtg ggc gag ggg cag 115
                                         Val Gly Glu Gly Gln
                                         1           5

gaa caa act ttt acg tac gtc att gag att gag gat ggc gtc aac acg 163
Glu Gln Thr Phe Thr Tyr Val Ile Glu Ile Glu Asp Gly Val Asn Thr
                10                15                20

gcc gct tat ggt ggc gac gat gcg 187
Ala Ala Tyr Gly Gly Asp Asp Ala
                25

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<210> 1188
 <211> 29
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1188
 Val Gly Glu Gly Gln Glu Gln Thr Phe Thr Tyr Val Ile Glu Ile Glu
 1 5 10 15

Asp Gly Val Asn Thr Ala Ala Tyr Gly Gly Asp Asp Ala
 20 25

<210> 1189
 <211> 294
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(271)
 <223> RXN02505

<400> 1189
 tcggaaagca atccggaaca ttcaggttgt agacaatgtc atcagttcag ttgacogtcc 60

cattaagcgc actggtcggt tgcgtattcc gggggtcttt gtg gct ggc act cat 115
 Val Ala Gly Thr His
 1 5

gcg tat gtc aat gaa act ctt tcg gaa aat gag ttc agc atg tgc cga 163
 Ala Tyr Val Asn Glu Thr Leu Ser Glu Asn Glu Phe Ser Met Cys Arg
 10 15 20

aag aat gaa cct ggt ttg gtc att gag ctg gag aac atc agc atc gat 211
 Lys Asn Glu Pro Gly Leu Val Ile Glu Leu Glu Asn Ile Ser Ile Asp
 25 30 35

cgc att gtc att tcc aca cca gat gcc cac cgc tat gcg gat gag ctc 259
 Arg Ile Val Ile Ser Thr Pro Asp Ala His Arg Tyr Ala Asp Glu Leu
 40 45 50

atg gcg gct gtt tagaactcag tttccgtcaa taa 294
 Met Ala Ala Val
 55

<210> 1190
 <211> 57
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1190
 Val Ala Gly Thr His Ala Tyr Val Asn Glu Thr Leu Ser Glu Asn Glu
 1 5 10 15

Phe Ser Met Cys Arg Lys Asn Glu Pro Gly Leu Val Ile Glu Leu Glu
 20 25 30

Asn Ile Ser Ile Asp Arg Ile Val Ile Ser Thr Pro Asp Ala His Arg
 35 40 45

Tyr Ala Asp Glu Leu Met Ala Ala Val
50 55

<210> 1191
<211> 294
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(271)
<223> FRXA02505

<400> 1191
tcggaaagca atccggaaca ttcaggttgt agacaatgtc atcagttcag ttgaccgtcc 60
cattaagcgc actggtcggt tgcgtattcc ggggggtcttt gtg gct ggc act cat 115
Val Ala Gly Thr His
1 5

gcg tat gtc aat gaa act ctt tcg gaa aat gag ttc agc atg tgc cga 163
Ala Tyr Val Asn Glu Thr Leu Ser Glu Asn Glu Phe Ser Met Cys Arg
10 15 20

aag aat gaa cct ggt ttg gtc att gag ctg gag aac atc agc atc gat 211
Lys Asn Glu Pro Gly Leu Val Ile Glu Leu Glu Asn Ile Ser Ile Asp
25 30 35

cgc att gtc att tcc aca cca gat gcc cac cgc tat gcg gat gag ctc 259
Arg Ile Val Ile Ser Thr Pro Asp Ala His Arg Tyr Ala Asp Glu Leu
40 45 50

atg gcg gct gtt tagaactcag ttccggtcaa taa 294
Met Ala Ala Val
55

<210> 1192
<211> 57
<212> PRT
<213> Corynebacterium glutamicum

<400> 1192
Val Ala Gly Thr His Ala Tyr Val Asn Glu Thr Leu Ser Glu Asn Glu
1 5 10 15

Phe Ser Met Cys Arg Lys Asn Glu Pro Gly Leu Val Ile Glu Leu Glu
20 25 30

Asn Ile Ser Ile Asp Arg Ile Val Ile Ser Thr Pro Asp Ala His Arg
35 40 45

Tyr Ala Asp Glu Leu Met Ala Ala Val
50 55

<210> 1193
<211> 759
<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(736)

<223> RXN02510

<400> 1193

cccgtcgatg aggcgaatgc tgtgatttct tcttgattg gtgacgcgat caatgatcag 60

ccgagcgagg actccattgc agctgcgagg tagccctgag atg gac tca tct gac 115
 Met Asp Ser Ser Asp
 1 5

agc cac gtt ggt cag gat gta tat gtt gat caa ggt cta ggg gag ccc 163
 Ser His Val Gly Gln Asp Val Tyr Val Asp Gln Gly Leu Gly Glu Pro
 10 15 20

gac aga ctg gaa cgt ctg tgg gcg ccc tac cgg atg agc tac atc aac 211
 Asp Arg Leu Glu Arg Leu Trp Ala Pro Tyr Arg Met Ser Tyr Ile Asn
 25 30 35

act cga tct ggc ggt aag caa tca act acc gcc aag cgg gac ccc ttc 259
 Thr Arg Ser Gly Gly Lys Gln Ser Thr Thr Ala Lys Arg Asp Pro Phe
 40 45 50

att gag gtt ccc aaa atg agt gat gag gac ggc ctg atc gtt gcg cgg 307
 Ile Glu Val Pro Lys Met Ser Asp Glu Asp Gly Leu Ile Val Ala Arg
 55 60 65

ggc gag ctg gtg tat tgc gta ctc aac ttg tat ccc tac aac gct gga 355
 Gly Glu Leu Val Tyr Cys Val Leu Asn Leu Tyr Pro Tyr Asn Ala Gly
 70 75 80 85

cac atg atg gtg atc cca ttc cgt aag gaa aag aat cta gag gat ttg 403
 His Met Met Val Ile Pro Phe Arg Lys Glu Lys Asn Leu Glu Asp Leu
 90 95 100

agc ttg gca gaa tct gcg gag ttg atg ctc ttt acc caa acg gcc atc 451
 Ser Leu Ala Glu Ser Ala Glu Leu Met Leu Phe Thr Gln Thr Ala Ile
 105 110 115

aag gcg ctg aag cag gtg tca aac cct gat gct gtc aat gtt ggt tta 499
 Lys Ala Leu Lys Gln Val Ser Asn Pro Asp Ala Val Asn Val Gly Leu
 120 125 130

aac ctt ggc aaa gca tgc ggt ggc tca gtg gga gat cac ctt cat gtc 547
 Asn Leu Gly Lys Ala Ser Gly Gly Ser Val Gly Asp His Leu His Val
 135 140 145

cat gtg gtg cct agg tgg tgc ggt gat gct aat ttc atg act gtg att 595
 His Val Val Pro Arg Trp Ser Gly Asp Ala Asn Phe Met Thr Val Ile
 150 155 160 165

gac ggt gtc aaa gtg cta ccg cag acc ctg cgt caa acc agg gcc atg 643
 Asp Gly Val Lys Val Leu Pro Gln Thr Leu Arg Gln Thr Arg Ala Met
 170 175 180

ctt gcg caa gca tgg ggc acc att gat ggg gca cca ggc act gtc gac 691
 Leu Ala Gln Ala Trp Gly Thr Ile Asp Gly Ala Pro Gly Thr Val Asp
 185 190 195

cca acg ctg act tca gcg atc cgt acc gca gca ccg aag gag cac 736
 Pro Thr Leu Thr Ser Ala Ile Arg Thr Ala Ala Pro Lys Glu His
 200 205 210

tgatgctggg acttcacgga cgt 759

<210> 1194

<211> 212

<212> PRT

<213> Corynebacterium glutamicum

<400> 1194

Met Asp Ser Ser Asp Ser His Val Gly Gln Asp Val Tyr Val Asp Gln
 1 5 10 15

Gly Leu Gly Glu Pro Asp Arg Leu Glu Arg Leu Trp Ala Pro Tyr Arg
 20 25 30

Met Ser Tyr Ile Asn Thr Arg Ser Gly Gly Lys Gln Ser Thr Thr Ala
 35 40 45

Lys Arg Asp Pro Phe Ile Glu Val Pro Lys Met Ser Asp Glu Asp Gly
 50 55 60

Leu Ile Val Ala Arg Gly Glu Leu Val Tyr Cys Val Leu Asn Leu Tyr
 65 70 75 80

Pro Tyr Asn Ala Gly His Met Met Val Ile Pro Phe Arg Lys Glu Lys
 85 90 95

Asn Leu Glu Asp Leu Ser Leu Ala Glu Ser Ala Glu Leu Met Leu Phe
 100 105 110

Thr Gln Thr Ala Ile Lys Ala Leu Lys Gln Val Ser Asn Pro Asp Ala
 115 120 125

Val Asn Val Gly Leu Asn Leu Gly Lys Ala Ser Gly Gly Ser Val Gly
 130 135 140

Asp His Leu His Val His Val Val Pro Arg Trp Ser Gly Asp Ala Asn
 145 150 155 160

Phe Met Thr Val Ile Asp Gly Val Lys Val Leu Pro Gln Thr Leu Arg
 165 170 175

Gln Thr Arg Ala Met Leu Ala Gln Ala Trp Gly Thr Ile Asp Gly Ala
 180 185 190

Pro Gly Thr Val Asp Pro Thr Leu Thr Ser Ala Ile Arg Thr Ala Ala
 195 200 205

Pro Lys Glu His
 210

<210> 1195

<211> 759

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(736)

<223> FRXA02510

<400> 1195

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ccgagcgagg actccattgc agctcgagg tagccctgag atg gac tca tct gac 115
 Met Asp Ser Ser Asp
 1 5

agc cac gtt ggt cag gat gta tat gtt gat caa ggt cta ggg gag ccc 163
 Ser His Val Gly Gln Asp Val Tyr Val Asp Gln Gly Leu Gly Glu Pro
 10 15 20

gac aga ctg gaa cgt ctg tgg gcg ccc tac cgg atg agc tac atc aac 211
 Asp Arg Leu Glu Arg Leu Trp Ala Pro Tyr Arg Met Ser Tyr Ile Asn
 25 30 35

act cga tct ggc ggt aag caa tca act acc gcc aag cgg gac ccc ttc 259
 Thr Arg Ser Gly Gly Lys Gln Ser Thr Thr Ala Lys Arg Asp Pro Phe
 40 45 50

att gag gtt ccc aaa atg agt gat gag gac ggc ctg atc gtt gcg cgg 307
 Ile Glu Val Pro Lys Met Ser Asp Glu Asp Gly Leu Ile Val Ala Arg
 55 60 65

ggt gag ctg gtg tat tgc gta ctc aac ttg tat ccc tac aac gct gga 355
 Gly Glu Leu Val Tyr Cys Val Leu Asn Leu Tyr Pro Tyr Asn Ala Gly
 70 75 80 85

cac atg atg gtg atc cca ttc cgt aag gaa aag aat cta gag gat ttg 403
 His Met Met Val Ile Pro Phe Arg Lys Glu Lys Asn Leu Glu Asp Leu
 90 95 100

agc ttg gca gaa tct gcg gag ttg atg ctc ttt acc caa acg gcc atc 451
 Ser Leu Ala Glu Ser Ala Glu Leu Met Leu Phe Thr Gln Thr Ala Ile
 105 110 115

aag gcg ctg aag cag gtg tca aac cct gat gct gtc aat gtt ggt tta 499
 Lys Ala Leu Lys Gln Val Ser Asn Pro Asp Ala Val Asn Val Gly Leu
 120 125 130

aac ctt ggc aaa gca tcg ggt ggc tca gtg gga gat cac ctt cat gtc 547
 Asn Leu Gly Lys Ala Ser Gly Gly Ser Val Gly Asp His Leu His Val
 135 140 145

cat gtg gtg cct agg tgg tcg ggt gat gct aat ttc atg act gtg att 595
 His Val Val Pro Arg Trp Ser Gly Asp Ala Asn Phe Met Thr Val Ile
 150 155 160 165

gac ggt gtc aaa gtg cta cgg cag acc ctg cgt caa acc agg gcc atg 643
 Asp Gly Val Lys Val Leu Pro Gln Thr Leu Arg Gln Thr Arg Ala Met
 170 175 180

ctt gcg caa gca tgg ggc acc att gat ggg gca cca ggc act gtc gac 691
 Leu Ala Gln Ala Trp Gly Thr Ile Asp Gly Ala Pro Gly Thr Val Asp
 185 190 195

cca acg ctg act tca gcg atc cgt acc gca gca ccg aag gag cac 736
 Pro Thr Leu Thr Ser Ala Ile Arg Thr Ala Ala Pro Lys Glu His
 200 205 210

tgatgctggg acttcacatga cgt 759

<210> 1196

<211> 212

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1196

Met Asp Ser Ser Asp Ser His Val Gly Gln Asp Val Tyr Val Asp Gln
 1 5 10 15

Gly Leu Gly Glu Pro Asp Arg Leu Glu Arg Leu Trp Ala Pro Tyr Arg
 20 25 30

Met Ser Tyr Ile Asn Thr Arg Ser Gly Gly Lys Gln Ser Thr Thr Ala
 35 40 45

Lys Arg Asp Pro Phe Ile Glu Val Pro Lys Met Ser Asp Glu Asp Gly
 50 55 60

Leu Ile Val Ala Arg Gly Glu Leu Val Tyr Cys Val Leu Asn Leu Tyr
 65 70 75 80

Pro Tyr Asn Ala Gly His Met Met Val Ile Pro Phe Arg Lys Glu Lys
 85 90 95

Asn Leu Glu Asp Leu Ser Leu Ala Glu Ser Ala Glu Leu Met Leu Phe
 100 105 110

Thr Gln Thr Ala Ile Lys Ala Leu Lys Gln Val Ser Asn Pro Asp Ala
 115 120 125

Val Asn Val Gly Leu Asn Leu Gly Lys Ala Ser Gly Gly Ser Val Gly
 130 135 140

Asp His Leu His Val His Val Val Pro Arg Trp Ser Gly Asp Ala Asn
 145 150 155 160

Phe Met Thr Val Ile Asp Gly Val Lys Val Leu Pro Gln Thr Leu Arg
 165 170 175

Gln Thr Arg Ala Met Leu Ala Gln Ala Trp Gly Thr Ile Asp Gly Ala
 180 185 190

Pro Gly Thr Val Asp Pro Thr Leu Thr Ser Ala Ile Arg Thr Ala Ala
 195 200 205

Pro Lys Glu His
 210

<210> 1197

<211> 1752

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> {101}..(1729)

<223> RXN02519

<400> 1197

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gcgcacgcgc accgctgggt ccagatcagc gacctocac gtg gaa gac gag cag 115
 Val Glu Asp Glu Gln
 1 5

agc cct tta ggg gca acg ctt ttc gac gtc gcg acc ggc gcg agc tcc 163
 Ser Pro Leu Gly Ala Thr Leu Phe Asp Val Ala Thr Gly Ala Ser Ser
 10 15 20

atc aac gac cgc gat acc gac gcc tca ggg ctt gag cct gaa aag att 211
 Ile Asn Asp Arg Asp Thr Asp Ala Ser Gly Leu Glu Pro Glu Lys Ile
 25 30 35

cgc cga ttt gca tgg ctg cgc ctg atc ggc acc atg ggt gcg tta atg 259
 Arg Arg Phe Ala Trp Leu Arg Ile Gly Thr Met Gly Ala Leu Met
 40 45 50

atc gcg ttt ggt gcg ctg ggc gcg ggt gca ctt ccg gtg gtg aat aat 307
 Ile Ala Phe Gly Ala Leu Gly Ala Gly Ala Leu Pro Val Val Asn Asn
 55 60 65

ccg tat gtg gat ttc cct ggc gga aac ttc atg agc cga atg ctg cag 355
 Pro Tyr Val Asp Phe Pro Gly Gly Asn Phe Met Ser Arg Met Leu Gln
 70 75 80 85

acc tct tcc atg atc gtg ctc atc ggc gtg gga ttt ttg gtg ctg gcg 403
 Thr Ser Ser Met Ile Val Leu Ile Gly Val Gly Phe Leu Val Leu Ala
 90 95 100

tgg gtg tta atg gca ccg ctg gtg ggt att cct ttt aaa cgc agc gga 451
 Trp Val Leu Met Ala Pro Leu Val Gly Ile Pro Phe Lys Arg Ser Gly
 105 110 115

aac aga aca gcc agc gtg agt ttg tcc atg ctg cgc cgc aca ttt ggc 499
 Asn Arg Thr Ala Ser Val Ser Leu Ser Met Leu Arg Arg Thr Phe Gly
 120 125 130

gcc tgg gta gcg ccc atc atg ctc acc gcc cca ctg ttt act caa gac 547
 Ala Trp Val Ala Pro Ile Met Leu Thr Ala Pro Leu Phe Thr Gln Asp
 135 140 145

att tat tct tat ctg gca caa ggc tct gtg acc gcg cag gga atg gat 595
 Ile Tyr Ser Tyr Leu Ala Gln Gly Ser Val Thr Ala Gln Gly Met Asp
 150 155 160 165

gcc tac gcc ggt gga ccg ctt gaa cta ttg ggg ccc gat aat cat ctg 643
 Ala Tyr Ala Gly Gly Pro Leu Glu Leu Leu Gly Pro Asp Asn His Leu
 170 175 180

gca cgg tcc gtg ccc ttt att tgg gcc cag tgg ccc tgg ccc tac gcc 691
 Ala Arg Ser Val Pro Phe Ile Trp Ala Gln Ser Pro Ser Pro Tyr Gly
 185 190 195

cct gtt gcg ctg agc atc gcg gcg tgg ata agc gtt att act aat gac 739

Pro Val Ala Leu Ser Ile Ala Ala Ser Ile Ser Val Ile Thr Asn Asp
200 205 210

agc atc gtt gga ggc gtg ctg gcg cac cgt att gcg tcg ctg ctg ggc 787
Ser Ile Val Gly Gly Val Leu Ala His Arg Ile Ala Ser Leu Leu Gly
215 220 225

gtt gtg gct gca ggc tgg gcg atc acc atg ctg gcc agg cgc tgt cgg 835
Val Val Ala Ala Gly Trp Ala Ile Thr Met Leu Ala Arg Arg Cys Arg
230 235 240 245

gta tct gaa gaa gcg tcc ttt tac ctg ggc gta ctt aat ccg ctg ctg 883
Val Ser Glu Glu Ala Ser Phe Tyr Leu Gly Val Leu Asn Pro Leu Leu
250 255 260

att ctg cac ctg atc ggc ggt att cac aac gaa tcc atc ctg ctg gga 931
Ile Leu His Leu Ile Gly Gly Ile His Asn Glu Ser Ile Leu Leu Gly
265 270 275

ttt tta ctt gtt ggc ctg gaa ctc gga ctg cgt ggc acc gac cgg att 979
Phe Leu Leu Val Gly Leu Glu Leu Gly Leu Arg Gly Thr Asp Arg Ile
280 285 290

caa aca ggg ctg tgg ggg cct gcg tgg aca tat att gca ctg agt ggc 1027
Gln Thr Gly Leu Trp Gly Pro Ala Trp Thr Tyr Ile Ala Leu Ser Gly
295 300 305

gta ttg att tct tgc gca ggc ctg gtc aag gtg acc ggc ttt att ggg 1075
Val Leu Ile Ser Cys Ala Gly Leu Val Lys Val Thr Gly Phe Ile Gly
310 315 320 325

ctc ggt ttt gtg ggc atg gcc ttg gcc agg gcg ttt cat gca cgt gga 1123
Leu Gly Phe Val Gly Met Ala Leu Ala Arg Ala Phe His Ala Arg Gly
330 335 340

cat cga cac gtc gtt gcg atc ggc gtt gca ggc ctc gtt caa gta gca 1171
His Arg His Val Val Ala Ile Gly Val Ala Gly Leu Val Gln Val Ala
345 350 355

gcc ctg gtg atc acc gtg gtt gtt ctc agt gtg att acc gga atc agt 1219
Ala Leu Val Ile Thr Val Val Val Leu Ser Val Ile Thr Gly Ile Ser
360 365 370

ttg ggg tgg atc aca ggt caa ggt ggc gct gcg acg atc cga agc tgg 1267
Leu Gly Trp Ile Thr Gly Gln Gly Gly Ala Ala Thr Ile Arg Ser Trp
375 380 385

atg tct atg acc acc aac att ggc gtt att tct gga ttc atc gga atg 1315
Met Ser Met Thr Thr Asn Ile Gly Val Ile Ser Gly Phe Ile Gly Met
390 395 400 405

aat ttg ggg cta ggc gac cac acc gca gcc atg ctc gtt gtg acc cgt 1363
Asn Leu Gly Leu Gly Asp His Thr Ala Ala Met Leu Val Val Thr Arg
410 415 420

gca gcc gga atc gcg gta gct gcc gcc ttc atg gtt cgt atg ttg ttt 1411
Ala Ala Gly Ile Ala Val Ala Ala Ala Phe Met Val Arg Met Leu Phe
425 430 435

gcc aca tat aga ggt cac att cac gct gtg ggc gga ctg gcc gtg gcg 1459
Ala Thr Tyr Arg Gly His Ile His Ala Val Gly Gly Leu Gly Val Ala

440	445	450	
act ttc gtc ctc gtt atc ctc	ttc ccc gtg gtg cat ccg	tgg tac atg	1507
Thr Phe Val Leu Val Ile	Leu Phe Pro Val Val His	Pro Trp Tyr Met	
455	460	465	
ctg tgg gct atc gtg ccg cta	gct tcc tgg gca aat aga	ctg ttc ttc	1555
Leu Trp Ala Ile Val	Pro Leu Ala Ser Trp	Ala Asn Arg Leu Phe Phe	
470	475	480	485
cag ctc gga gtg att gcc tac	tcc act gcc ttc agt ttc	ttt gtg ctg	1603
Gln Leu Gly Val	Ile Ala Tyr Ser Thr	Ala Phe Ser Phe Phe Val Leu	
490	495	500	
cct cgc ggg ctt gca ctt cca	gtc gga act gtc ttt tcc	atc tac ttc	1651
Pro Arg Gly	Leu Ala Leu Pro Val	Gly Thr Val Phe Ser Ile Tyr Phe	
505	510	515	
ggc gca gcg ctc gga ttc agc	att ctc cta tta gtt gga	tgg tgg agt	1699
Gly Ala Ala Leu Gly Phe	Ser Ile Leu Leu Leu Val	Gly Trp Trp Ser	
520	525	530	
ttg agg cgg aat cca acc ttt	ggt tta cac tgatcaactg	tgactactga	1749
Leu Arg Arg Asn Pro Thr	Phe Gly Leu His		
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Glu Pro Glu Lys Ile Arg Arg	Phe Ala Trp Leu Arg Leu	Ile Gly Thr	
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Met Gly Ala Leu Met Ile Ala	Phe Gly Ala Leu Gly Ala	Gly Ala Leu	
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Ser Arg Met Leu Gln Thr Ser	Ser Met Ile Val Leu Ile	Gly Val Gly	
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Phe Leu Val Leu Ala Trp Val	Leu Met Ala Pro Leu Val	Gly Ile Pro	
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Phe Lys Arg Ser Gly Asn Arg	Thr Ala Ser Val Ser Leu	Ser Met Leu	
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Arg Arg Thr Phe Gly Ala Trp	Val Ala Pro Ile Met Leu	Thr Ala Pro	
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 Ala Gln Gly Met Asp Ala Tyr Ala Gly Gly Pro Leu Glu Leu Leu Gly
 165 170 175
 Pro Asp Asn His Leu Ala Arg Ser Val Pro Phe Ile Trp Ala Gln Ser
 180 185 190
 Pro Ser Pro Tyr Gly Pro Val Ala Leu Ser Ile Ala Ala Ser Ile Ser
 195 200 205
 Val Ile Thr Asn Asp Ser Ile Val Gly Gly Val Leu Ala His Arg Ile
 210 215 220
 Ala Ser Leu Leu Gly Val Val Ala Ala Gly Trp Ala Ile Thr Met Leu
 225 230 235 240
 Ala Arg Arg Cys Arg Val Ser Glu Glu Ala Ser Phe Tyr Leu Gly Val
 245 250 255
 Leu Asn Pro Leu Leu Ile Leu His Leu Ile Gly Gly Ile His Asn Glu
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 Ser Ile Leu Leu Gly Phe Leu Leu Val Gly Leu Glu Leu Gly Leu Arg
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 Gly Thr Asp Arg Ile Gln Thr Gly Leu Trp Gly Pro Ala Trp Thr Tyr
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 Ile Ala Leu Ser Gly Val Leu Ile Ser Cys Ala Gly Leu Val Lys Val
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 Thr Gly Phe Ile Gly Leu Gly Phe Val Gly Met Ala Leu Ala Arg Ala
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 Phe His Ala Arg Gly His Arg His Val Val Ala Ile Gly Val Ala Gly
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 Thr Ile Arg Ser Trp Met Ser Met Thr Thr Asn Ile Gly Val Ile Ser
 385 390 395 400
 Gly Phe Ile Gly Met Asn Leu Gly Leu Gly Asp His Thr Ala Ala Met
 405 410 415
 Leu Val Val Thr Arg Ala Ala Gly Ile Ala Val Ala Ala Ala Phe Met
 420 425 430
 Val Arg Met Leu Phe Ala Thr Tyr Arg Gly His Ile His Ala Val Gly
 435 440 445
 Gly Leu Gly Val Ala Thr Phe Val Leu Val Ile Leu Phe Pro Val Val
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His Pro Trp Tyr Met Leu Trp Ala Ile Val Pro Leu Ala Ser Trp Ala
465 470 475 480

Asn Arg Leu Phe Phe Gln Leu Gly Val Ile Ala Tyr Ser Thr Ala Phe
485 490 495

Ser Phe Phe Val Leu Pro Arg Gly Leu Ala Leu Pro Val Gly Thr Val
500 505 510

Phe Ser Ile Tyr Phe Gly Ala Ala Leu Gly Phe Ser Ile Leu Leu Leu
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<211> 1929

<212> DNA

<213> *Corynebacterium glutamicum*

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<222> (101)..(1906)

<223> FRXA02519

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Met Phe Ser Ala Pro
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tgc aac gcc cct gaa aac aga aaa tgg ttt cct cgg gca cct cgt ccc 211
Ser Asn Ala Pro Glu Asn Arg Lys Trp Phe Pro Arg Ala Pro Arg Pro
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cta cgc caa ttt ctc gac act ttg ccg cgc atc gcc acc gct ggt tcc 259
Leu Arg Gln Phe Leu Asp Thr Leu Pro Arg Ile Gly Thr Ala Gly Ser
40 45 50

aga tca gcg acc ctc cac gtg gaa gac gag cag agc cct tta ggg gca 307
Arg Ser Ala Thr Leu His Val Glu Asp Glu Gln Ser Pro Leu Gly Ala
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Thr Leu Phe Asp Val Ala Thr Gly Ala Ser Ser Ile Asn Asp Arg Asp
70 75 80 85

acc gac gcc tca ggg ctt gag cct gaa aag att cgc cga ttt gca tgg 403
Thr Asp Ala Ser Gly Leu Glu Pro Glu Lys Ile Arg Arg Phe Ala Trp
90 95 100

ctg cgc ctg atc gcc acc atg ggt gcg tta atg atc gcg ttt ggt gcg 451
Leu Arg Leu Ile Gly Thr Met Gly Ala Leu Met Ile Ala Phe Gly Ala
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Leu Gly Ala Gly Ala Leu Pro Val Val Asn Asn Pro Tyr Val Asp Phe	
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Pro Gly Gly Asn Phe Met Ser Arg Met Leu Gln Thr Ser Ser Met Ile	
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Pro Leu Val Gly Ile Pro Phe Lys Arg Ser Gly Asn Arg Thr Ala Ser	
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Ile Met Leu Thr Ala Pro Leu Phe Thr Gln Asp Ile Tyr Ser Tyr Leu	
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gca caa ggc tct gtg acc ggc cag gga atg gat gcc tac gcc ggt gga	787
Ala Gln Gly Ser Val Thr Ala Gln Gly Met Asp Ala Tyr Ala Gly Gly	
215 220 225	
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Pro Leu Glu Leu Leu Gly Pro Asp Asn His Leu Ala Arg Ser Val Pro	
230 235 240 245	
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Phe Ile Trp Ala Gln Ser Pro Ser Pro Tyr Gly Pro Val Ala Leu Ser	
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Ile Ala Ala Ser Ile Ser Val Ile Thr Asn Asp Ser Ile Val Gly Gly	
265 270 275	
gtg ctg gcg cac cgt att gcg tcg ctg ctg ggc gtt gtg gct gca ggc	979
Val Leu Ala His Arg Ile Ala Ser Leu Leu Gly Val Val Ala Ala Gly	
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Trp Ala Ile Thr Met Leu Ala Arg Arg Cys Arg Val Ser Glu Glu Ala	
295 300 305	
tcc ttt tac ctg ggc gta ctt aat ccg ctg ctg att ctg cac ctg atc	1075
Ser Phe Tyr Leu Gly Val Leu Asn Pro Leu Leu Ile Leu His Leu Ile	
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Gly Gly Ile His Asn Glu Ser Ile Leu Leu Gly Phe Leu Leu Val Gly	
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Leu Glu Leu Gly Leu Arg Gly Thr Asp Arg Ile Gln Thr Gly Leu Trp	
345 350 355	
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Gly	Pro	Ala	Trp	Thr	Tyr	Ile	Ala	Leu	Ser	Gly	Val	Leu	Ile	Ser	Cys	
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Ala	Gly	Leu	Val	Lys	Val	Thr	Gly	Phe	Ile	Gly	Leu	Gly	Phe	Val	Gly	
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Met	Ala	Leu	Ala	Arg	Ala	Phe	His	Ala	Arg	Gly	His	Arg	His	Val	Val	
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Ala	Ile	Gly	Val	Ala	Gly	Leu	Val	Gln	Val	Ala	Ala	Leu	Val	Ile	Thr	
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Gly	Gln	Gly	Gly	Ala	Ala	Thr	Ile	Arg	Ser	Trp	Met	Ser	Met	Thr	Thr	
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Asn	Ile	Gly	Val	Ile	Ser	Gly	Phe	Ile	Gly	Met	Asn	Leu	Gly	Leu	Gly	
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Asp	His	Thr	Ala	Ala	Met	Leu	Val	Val	Thr	Arg	Ala	Ala	Gly	Ile	Ala	
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gta	gct	gcc	gcc	ttc	atg	gtt	cgt	atg	ttg	ttt	gcc	aca	tat	aga	ggt	1603
Val	Ala	Ala	Ala	Phe	Met	Val	Arg	Met	Leu	Phe	Ala	Thr	Tyr	Arg	Gly	
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cac	att	cac	gct	gtg	ggc	gga	ctg	ggc	gtg	gcg	act	ttc	gtc	ctc	gtt	1651
His	Ile	His	Ala	Val	Gly	Gly	Leu	Gly	Val	Ala	Thr	Phe	Val	Leu	Val	
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Ile	Leu	Phe	Pro	Val	Val	His	Pro	Trp	Tyr	Met	Leu	Trp	Ala	Ile	Val	
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Pro	Leu	Ala	Ser	Trp	Ala	Asn	Arg	Leu	Phe	Phe	Gln	Leu	Gly	Val	Ile	
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Ala	Tyr	Ser	Thr	Ala	Phe	Ser	Phe	Phe	Val	Leu	Pro	Arg	Gly	Leu	Ala	
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Leu	Pro	Val	Gly	Thr	Val	Phe	Ser	Ile	Tyr	Phe	Gly	Ala	Ala	Leu	Gly	
570																
ttc	agc	att	ctc	cta	tta	gtt	gga	tgg	tgg	agt	ttg	agg	cgg	aat	cca	1891
Phe	Ser	Ile	Leu	Leu	Leu	Val	Gly	Trp	Trp	Ser	Leu	Arg	Arg	Asn	Pro	
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<212> PRT

<213> Corynebacterium glutamicum

<400> 1200

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 35 40 45

Gly Thr Ala Gly Ser Arg Ser Ala Thr Leu His Val Glu Asp Glu Gln
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Ser Pro Leu Gly Ala Thr Leu Phe Asp Val Ala Thr Gly Ala Ser Ser
 65 70 75 80

Ile Asn Asp Arg Asp Thr Asp Ala Ser Gly Leu Glu Pro Glu Lys Ile
 85 90 95

Arg Arg Phe Ala Trp Leu Arg Leu Ile Gly Thr Met Gly Ala Leu Met
 100 105 110

Ile Ala Phe Gly Ala Leu Gly Ala Gly Ala Leu Pro Val Val Asn Asn
 115 120 125

Pro Tyr Val Asp Phe Pro Gly Gly Asn Phe Met Ser Arg Met Leu Gln
 130 135 140

Thr Ser Ser Met Ile Val Leu Ile Gly Val Gly Phe Leu Val Leu Ala
 145 150 155 160

Trp Val Leu Met Ala Pro Leu Val Gly Ile Pro Phe Lys Arg Ser Gly
 165 170 175

Asn Arg Thr Ala Ser Val Ser Leu Ser Met Leu Arg Arg Thr Phe Gly
 180 185 190

Ala Trp Val Ala Pro Ile Met Leu Thr Ala Pro Leu Phe Thr Gln Asp
 195 200 205

Ile Tyr Ser Tyr Leu Ala Gln Gly Ser Val Thr Ala Gln Gly Met Asp
 210 215 220

Ala Tyr Ala Gly Gly Pro Leu Glu Leu Leu Gly Pro Asp Asn His Leu
 225 230 235 240

Ala Arg Ser Val Pro Phe Ile Trp Ala Gln Ser Pro Ser Pro Tyr Gly
 245 250 255

Pro Val Ala Leu Ser Ile Ala Ala Ser Ile Ser Val Ile Thr Asn Asp
 260 265 270

Ser Ile Val Gly Gly Val Leu Ala His Arg Ile Ala Ser Leu Leu Gly

275					280					285					
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Val	Ser	Glu	Glu	Ala	Ser	Phe	Tyr	Leu	Gly	Val	Leu	Asn	Pro	Leu	Leu
305					310					315					
Ile	Leu	His	Leu	Ile	Gly	Gly	Ile	His	Asn	Glu	Ser	Ile	Leu	Leu	Gly
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Phe	Leu	Leu	Val	Gly	Leu	Glu	Leu	Gly	Leu	Arg	Gly	Thr	Asp	Arg	Ile
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Gln	Thr	Gly	Leu	Trp	Gly	Pro	Ala	Trp	Thr	Tyr	Ile	Ala	Leu	Ser	Gly
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Val	Leu	Ile	Ser	Cys	Ala	Gly	Leu	Val	Lys	Val	Thr	Gly	Phe	Ile	Gly
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Leu	Gly	Phe	Val	Gly	Met	Ala	Leu	Ala	Arg	Ala	Phe	His	Ala	Arg	Gly
385					390					395					
His	Arg	His	Val	Val	Ala	Ile	Gly	Val	Ala	Gly	Leu	Val	Gln	Val	Ala
405					410					415					
Ala	Leu	Val	Ile	Thr	Val	Val	Val	Leu	Ser	Val	Ile	Thr	Gly	Ile	Ser
420					425					430					
Leu	Gly	Trp	Ile	Thr	Gly	Gln	Gly	Gly	Ala	Ala	Thr	Ile	Arg	Ser	Trp
435					440					445					
Met	Ser	Met	Thr	Thr	Asn	Ile	Gly	Val	Ile	Ser	Gly	Phe	Ile	Gly	Met
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Asn	Leu	Gly	Leu	Gly	Asp	His	Thr	Ala	Ala	Met	Leu	Val	Val	Thr	Arg
465					470					475					
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Ala	Thr	Tyr	Arg	Gly	His	Ile	His	Ala	Val	Gly	Gly	Leu	Gly	Val	Ala
500					505					510					
Thr	Phe	Val	Leu	Val	Ile	Leu	Phe	Pro	Val	Val	His	Pro	Trp	Tyr	Met
515					520					525					
Leu	Trp	Ala	Ile	Val	Pro	Leu	Ala	Ser	Trp	Ala	Asn	Arg	Leu	Phe	Phe
530					535					540					
Gln	Leu	Gly	Val	Ile	Ala	Tyr	Ser	Thr	Ala	Phe	Ser	Phe	Phe	Val	Leu
545					550					555					
Pro	Arg	Gly	Leu	Ala	Leu	Pro	Val	Gly	Thr	Val	Phe	Ser	Ile	Tyr	Phe
565					570					575					
Gly	Ala	Ala	Leu	Gly	Phe	Ser	Ile	Leu	Leu	Val	Gly	Trp	Trp	Ser	
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<222> (101)..(784)
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aaa ggc aac gac gcg cac acc gga gac ggt gat acg cgc cga aaa att	10 15 20	163
Lys Gly Asn Asp Ala His Thr Gly Asp Gly Asp Thr Arg Arg Lys Ile		
ctt ctc atc ctg ttg gaa cgt gca cgg gtg atc gct tca gat att gct	25 30 35	211
Leu Leu Ile Leu Leu Glu Arg Ala Pro Val Ile Ala Ser Asp Ile Ala		
gaa cag ctt cag ctt tca act gtg gga gtg cgc agg cac cta gac aac	40 45 50	259
Glu Gln Leu Leu Leu Ser Thr Val Gly Val Arg Arg His Leu Asp Asn		
ttg gtt gaa gaa aat ctg gcg gag cgc gca aat cgg cgc cag aac cca	55 60 65	307
Leu Val Glu Glu Glu Asn Leu Ala Glu Ala Ala Asn Pro Arg Gln Asn Pro		
tat gag ccc aaa atg cgc ggt agg cca gca aaa act tat cgg ctt act	70 75 80 85	355
Tyr Glu Pro Lys Met Arg Gly Arg Pro Ala Lys Thr Tyr Arg Leu Thr		
gat aaa ggt cgc tca atc ttc ggc cac gaa tat gat tcc ctt gct gcg	90 95 100	403
Asp Lys Gly Arg Ser Ile Phe Gly His Glu Tyr Asp Ser Leu Ala Ala		
gca gct cta gcc act ctt cga gag gtc ggc gga gat gat gca gta agg	105 110 115	451
Ala Ala Leu Ala Thr Leu Arg Glu Val Gly Gly Asp Ala Val Arg		
caa ttt gct aga aag cgg atc gaa aca att gtt gag ggt att acc cca	120 125 130	499
Gln Phe Ala Ala Arg Lys Arg Ile Glu Thr Thr Ile Val Glu Gly Ile Thr Pro		
gca gat gtc aca gat caa tca atc gaa gat aca gcc aaa tct tta gtt	135 140 145	547
Ala Asp Val Thr Asp Gln Ser Ile Glu Asp Thr Ala Lys Ser Leu Val		
gaa gct ttt agt cgg cat ggt tat gca gca act gat gac gcc act cga	150 155 160 165	595
Glu Ala Phe Ser Arg His Gly Tyr Ala Ala Thr Val Asp Ala Thr Arg		
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Arg	His	Leu	Asp	Asn	Leu	Val	Glu	Glu	Asn	Leu	Ala	Glu	Ala	Ala	Asn		
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Thr	Tyr	Arg	Leu	Thr	Asp	Lys	Gly	Arg	Ser	Ile	Phe	Gly	His	Glu	Tyr		
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Asp	Ser	Leu	Ala	Ala	Ala	Leu	Ala	Thr	Leu	Arg	Glu	Val	Gly	Gly			
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Glu	Gly	Ile	Thr	Pro	Ala	Asp	Val	Thr	Asp	Gln	Ser	Ile	Glu	Asp	Thr		
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Ala	Lys	Ser	Leu	Val	Glu	Ala	Phe	Ser	Arg	His	Gly	Tyr	Ala	Ala	Thr		
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Gln	Ala	Val	Ser	Glu	Leu	Leu	Gly	Gln	His	Thr	Gln	Pro	Leu	Ala	Thr		
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Ile Lys His Ser
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<211> 807

<212> DNA

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<222> (101)..(784)

<223> FRXA02520

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 Val Gly Asp Val Val
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 Lys Gly Asn Asp Ala His Thr Gly Asp Gly Asp Thr Arg Arg Lys Ile
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 Glu Gln Leu Gln Leu Ser Thr Val Gly Val Arg Arg His Leu Asp Asn
 40 45 50

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tat gag ccc aaa atg cgc ggt agg cca gca aaa act tat cgg ctt act 355
 Tyr Glu Pro Lys Met Arg Gly Arg Pro Ala Lys Thr Tyr Arg Leu Thr
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gat aaa ggt cgc tca atc ttc ggc cac gaa tat gat tcc ctt gct gcg 403
 Asp Lys Gly Arg Ser Ile Phe Gly His Glu Tyr Asp Ser Leu Ala Ala
 90 95 100

gca gct cta gcc act ctt cga gag gtc ggc gga gat gat gca gta agg 451
 Ala Ala Leu Ala Thr Leu Arg Glu Val Gly Gly Asp Asp Ala Val Arg
 105 110 115

caa ttt gct aga aag cgg atc gaa aca att gtt gag ggt att acc cca 499
 Gln Phe Ala Arg Lys Arg Ile Glu Thr Ile Val Glu Gly Ile Thr Pro
 120 125 130

gca gat gtc aca gat caa tca atc gaa gat aca gcc aaa tct tta gtt 547
 Ala Asp Val Thr Asp Gln Ser Ile Glu Asp Thr Ala Lys Ser Leu Val
 135 140 145

gaa gct ttt agt cgg cat ggt tat gca gca act gtc gat gcc act cga 595
 Glu Ala Phe Ser Arg His Gly Tyr Ala Ala Thr Val Asp Ala Thr Arg
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 aac ggg ttg caa ctc tgc cag cat cac tgt cca ata tct aca gtc gcc 643
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 170 175 180

 acg gaa ttt ccg gaa ctg tgt gag gca gag cat caa gca gtc tca gaa 691
 Thr Glu Phe Pro Glu Leu Cys Glu Ala Glu His Gln Ala Val Ser Glu
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 200 205 210

 ggc atc tgc aca aca aat att gca ttg aca ccc atc aaa cac tcc 784
 Gly Ile Cys Thr Thr Asn Ile Ala Leu Thr Pro Ile Lys His Ser
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 tgatgaaagg agcggatcat gac 807

<210> 1204

<211> 228

<212> PRT

<213> Corynebacterium glutamicum

<400> 1204

Val Gly Asp Val Val Lys Gly Asn Asp Ala His Thr Gly Asp Gly Asp
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 20 25 30

Ala Ser Asp Ile Ala Glu Gln Leu Gln Leu Ser Thr Val Gly Val Arg
 35 40 45

Arg His Leu Asp Asn Leu Val Glu Glu Asn Leu Ala Glu Ala Ala Asn
 50 55 60

Pro Arg Gln Asn Pro Tyr Glu Pro Lys Met Arg Gly Arg Pro Ala Lys
 65 70 75 80

Thr Tyr Arg Leu Thr Asp Lys Gly Arg Ser Ile Phe Gly His Glu Tyr
 85 90 95

Asp Ser Leu Ala Ala Ala Leu Ala Thr Leu Arg Glu Val Gly Gly
 100 105 110

Asp Asp Ala Val Arg Gln Phe Ala Arg Lys Arg Ile Glu Thr Ile Val
 115 120 125

Glu Gly Ile Thr Pro Ala Asp Val Thr Asp Gln Ser Ile Glu Asp Thr
 130 135 140

Ala Lys Ser Leu Val Glu Ala Phe Ser Arg His Gly Tyr Ala Ala Thr
 145 150 155 160

Val Asp Ala Thr Arg Asn Gly Leu Gln Leu Cys Gln His His Cys Pro
 165 170 175

Ile Ser Thr Val Ala Thr Glu Phe Pro Glu Leu Cys Glu Ala Glu His
180 185 190

Gln Ala Val Ser Glu Leu Leu Gly Gln His Thr Gln Pro Leu Ala Thr
195 200 205

Ile Ala Asp Gly His Gly Ile Cys Thr Thr Asn Ile Ala Leu Thr Pro
210 215 220

Ile Lys His Ser
225

<210> 1205

<211> 927

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(904)

<223> RXN02534

<400> 1205

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tacattataa aaactcagat tcaggaatac acagaccatg atg aat tca ccg aac 115
Met Asn Ser Pro Asn
1 5

gcg gac att att tta gta gtt aac aag ctg tcc aag ttt att gat atc 163
Ala Asp Ile Ile Leu Val Val Asn Lys Leu Ser Lys Phe Ile Asp Ile
10 15 20

gaa aat att atg ctc gtt gga gca cga tgt aga gac att cac cag caa 211
Glu Asn Ile Met Leu Val Gly Ala Arg Cys Arg Asp Ile His Gln Gln
25 30 35

aaa tat cgc gat caa aca gcg ggt aga aga act aag gat gtt gac ttc 259
Lys Tyr Arg Asp Gln Thr Ala Gly Arg Arg Thr Lys Asp Val Asp Phe
40 45 50

gct tta gct tta gaa agc tgg gac gac ttc aat cta tta aag caa caa 307
Ala Leu Ala Leu Glu Ser Trp Asp Asp Phe Asn Leu Leu Lys Gln Gln
55 60 65

ttc tca ccg act ggt aac gca tgg caa gga atc acc att gga aat att 355
Phe Ser Pro Thr Gly Asn Ala Trp Gln Gly Ile Thr Ile Gly Asn Ile
70 75 80 85

cca gta gat ctc gtg cca ttc gga aat att gaa aac cca ccc ggt gaa 403
Pro Val Asp Leu Val Pro Phe Gly Asn Ile Glu Asn Pro Pro Gly Glu
90 95 100

gtc ttg tcc aga aaa ggt cat cta ctt aat gtc gct ggg ttc aag gaa 451
Val Leu Ser Arg Lys Gly His Leu Leu Asn Val Ala Gly Phe Lys Glu
105 110 115

gta ttc gag caa gct gag cta tat ccc cta aat gat gcg ata gac att 499
Val Phe Glu Gln Ala Glu Leu Tyr Pro Leu Asn Asp Ala Ile Asp Ile

120	125	130	
aag ttg tct aca gtt ccc gga ctt act gcg cta aag cta cat gca tgg			547
Lys Leu Ser Thr Val Pro Gly Leu Thr Ala Leu Lys Leu His Ala Trp			
135	140	145	
ctc gac cgt aaa gaa aat aac atc aaa gat gca agc gat cta gca tta			595
Leu Asp Arg Lys Glu Asn Asn Ile Lys Asp Ala Ser Asp Leu Ala Leu			
150	155	160	165
atc ttg tgg tgg tac gaa gag gat gta gaa act tta tgg aat cgc tat			643
Ile Leu Ser Trp Tyr Glu Glu Asp Val Glu Thr Leu Trp Asn Arg Tyr			
170	175	180	
ttt gcc ctg gaa aat caa gga tac ata ggt gaa cca gag gca atg gca			691
Phe Ala Leu Glu Asn Gln Gly Tyr Ile Gly Glu Pro Glu Ala Met Ala			
185	190	195	
gct gaa tta cta gga ctt gac act gga aga ata ctc ggc cac aag gaa			739
Ala Glu Leu Leu Gly Leu Asp Thr Gly Arg Ile Leu Gly His Lys Glu			
200	205	210	
act caa gcc ctc ctt gat cga ttt aat gaa cag tct cct cct gag cta			787
Thr Gln Ala Leu Leu Asp Arg Phe Asn Glu Gln Ser Pro Pro Glu Leu			
215	220	225	
aac caa ttt gct gaa tca ctt gaa gcc cct cct gaa cac agt cac cca			835
Asn Gln Phe Ala Glu Ser Leu Glu Ala Pro Pro Glu His Ser His Pro			
230	235	240	245
tta gaa cgg cgt cgt atc cag gtc gag gca ctg tta ggt gga ctt aga			883
Leu Glu Arg Arg Arg Ile Gln Val Glu Ala Leu Leu Gly Gly Leu Arg			
250	255	260	
gat tcc ctc ggt tac gat gaa tagcttccaa tccgcattg ttc			927
Asp Ser Leu Gly Tyr Asp Glu			
265			

<210> 1206

<211> 268

<212> PRT

<213> Corynebacterium glutamicum

<400> 1206

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1

5

10

15

Lys Phe Ile Asp Ile Glu Asn Ile Met Leu Val Gly Ala Arg Cys Arg

20

25

30

Asp Ile His Gln Gln Lys Tyr Arg Asp Gln Thr Ala Gly Arg Arg Thr

35

40

45

Lys Asp Val Asp Phe Ala Leu Ala Leu Glu Ser Trp Asp Asp Phe Asn

50

55

60

Leu Leu Lys Gln Gln Phe Ser Pro Thr Gly Asn Ala Trp Gln Gly Ile

65

70

75

80

Thr Ile Gly Asn Ile Pro Val Asp Leu Val Pro Phe Gly Asn Ile Glu

85										90										95																																			
Asn	Pro	Pro	Gly	Glu	Val	Leu	Ser	Arg	Lys	Gly	His	Leu	Leu	Asn	Val																																								
			100					105						110																																									
Ala	Gly	Phe	Lys	Glu	Val	Phe	Glu	Gln	Ala	Glu	Leu	Tyr	Pro	Leu	Asn																																								
		115						120					125																																										
Asp	Ala	Ile	Asp	Ile	Lys	Leu	Ser	Thr	Val	Pro	Gly	Leu	Thr	Ala	Leu																																								
		130					135					140																																											
Lys	Leu	His	Ala	Trp	Leu	Asp	Arg	Lys	Glu	Asn	Asn	Ile	Lys	Asp	Ala																																								
	145				150					155				160																																									
Ser	Asp	Leu	Ala	Leu	Ile	Leu	Ser	Trp	Tyr	Glu	Glu	Asp	Val	Glu	Thr																																								
				165					170					175																																									
Leu	Trp	Asn	Arg	Tyr	Phe	Ala	Leu	Glu	Asn	Gln	Gly	Tyr	Ile	Gly	Glu																																								
				180					185				190																																										
Pro	Glu	Ala	Met	Ala	Ala	Glu	Leu	Leu	Gly	Leu	Asp	Thr	Gly	Arg	Ile																																								
		195					200				205																																												
Leu	Gly	His	Lys	Glu	Thr	Gln	Ala	Leu	Leu	Asp	Arg	Phe	Asn	Glu	Gln																																								
		210				215					220																																												
Ser	Pro	Pro	Glu	Leu	Asn	Gln	Phe	Ala	Glu	Ser	Leu	Glu	Ala	Pro	Pro																																								
		225				230				235				240																																									
Glu	His	Ser	His	Pro	Leu	Glu	Arg	Arg	Arg	Ile	Gln	Val	Glu	Ala	Leu																																								
				245					250					255																																									
Leu	Gly	Gly	Leu	Arg	Asp	Ser	Leu	Gly	Tyr	Asp	Glu																																												
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gcg gac att att tta gta gtt aac aag ctg tcc aag ttt att gat atc																				163																																			
Ala Asp Ile Ile Leu Val Val Asn Lys																				Leu Ser Lys Phe Ile Asp Ile 20																																			
																				10 15																																			
gaa aat att atg ctc gtt gga gca cga tgt aga gac att cac cag caa																				211																																			
Glu Asn Ile Met Leu Val Gly Ala Arg																				Cys Arg Asp Ile His Gln Gln 35																																			
																				25 30																																			

aaa tat cgc gat caa aca gcg ggt aga aga act aag gat gtt gac ttc 259
 Lys Tyr Arg Asp Gln Thr Ala Gly Arg Arg Thr Lys Asp Val Asp Phe
 40 45 50

gct tta gct tta gaa agc tgg gac gac ttc aat cta tta aag caa caa 307
 Ala Leu Ala Leu Glu Ser Trp Asp Asp Phe Asn Leu Leu Lys Gln Gln
 55 60 65

ttc tca ccg act ggt aac gca tgg caa gga atc acc att gga aat att 355
 Phe Ser Pro Thr Gly Asn Ala Trp Gln Gly Ile Thr Ile Gly Asn Ile
 70 75 80 85

cca gta gat ctc tgg cca ttc gga aat att gaa aac cca ccc ggt gaa 403
 Pro Val Asp Leu Val Pro Phe Gly Asn Ile Glu Asn Pro Pro Gly Glu
 90 95 100

gtc ttg tcc aga aaa ggt cat cta ctt aat gtc gct ggg ttc aag gaa 451
 Val Leu Ser Arg Lys Gly His Leu Leu Asn Val Ala Gly Phe Lys Glu
 105 110 115

gta ttc gag caa gct gag cta tat ccc cta aat gat gcg ata gac att 499
 Val Phe Glu Gln Ala Glu Leu Tyr Pro Leu Asn Asp Ala Ile Asp Ile
 120 125 130

aag ttg tct aca gtt ccc gga ctt act gcg cta aag cta cat gca tgg 547
 Lys Leu Ser Thr Val Pro Gly Leu Thr Ala Leu Lys Leu His Ala Trp
 135 140 145

ctc gac cgt aaa gaa aat aac atc aaa gat gca agc gat cta gca tta 595
 Leu Asp Arg Lys Glu Asn Asn Ile Lys Asp Ala Ser Asp Leu Ala Leu
 150 155 160 165

atc ttg tgg tgg tac gaa gag gat gta gaa act tta tgg aat cgc tat 643
 Ile Leu Ser Trp Tyr Glu Glu Asp Val Glu Thr Leu Trp Asn Arg Tyr
 170 175 180

ttt gcc ctg gaa aat caa gga tac ata ggt gaa cca gag gca atg gca 691
 Phe Ala Leu Glu Asn Gln Gly Tyr Ile Gly Glu Pro Glu Ala Met Ala
 185 190 195

gct gaa tta cta gga ctt gac act gga aga ata ctc ggc cac aag gaa 739
 Ala Glu Leu Leu Gly Leu Asp Thr Gly Arg Ile Leu Gly His Lys Glu
 200 205 210

act caa gcc ctc ctt gat cga ttt aat gaa cag tct cct cct gag cta 787
 Thr Gln Ala Leu Leu Asp Arg Phe Asn Glu Gln Ser Pro Pro Glu Leu
 215 220 225

aac caa ttt gct gaa tca ctt gaa gcc cct cct gaa cac agt cac cca 835
 Asn Gln Phe Ala Glu Ser Leu Glu Ala Pro Pro Glu His Ser His Pro
 230 235 240 245

tta gaa cgg cgt cgt atc cag gtc gag gca ctg tta ggt gga ctt aga 883
 Leu Glu Arg Arg Arg Ile Gln Val Glu Ala Leu Leu Gly Gly Leu Arg
 250 255 260

gat tcc ctc ggt tac gat gaa tagcttccaa tccgcattg ttc 927
 Asp Ser Leu Gly Tyr Asp Glu
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<210> 1208

<211> 268

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1208

Met Asn Ser Pro Asn Ala Asp Ile Ile Leu Val Val Asn Lys Leu Ser
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Lys Phe Ile Asp Ile Glu Asn Ile Met Leu Val Gly Ala Arg Cys Arg
 20 25 30

Asp Ile His Gln Gln Lys Tyr Arg Asp Gln Thr Ala Gly Arg Arg Thr
 35 40 45

Lys Asp Val Asp Phe Ala Leu Ala Leu Glu Ser Trp Asp Asp Phe Asn
 50 55 60

Leu Leu Lys Gln Gln Phe Ser Pro Thr Gly Asn Ala Trp Gln Gly Ile
 65 70 75 80

Thr Ile Gly Asn Ile Pro Val Asp Leu Val Pro Phe Gly Asn Ile Glu
 85 90 95

Asn Pro Pro Gly Glu Val Leu Ser Arg Lys Gly His Leu Leu Asn Val
 100 105 110

Ala Gly Phe Lys Glu Val Phe Glu Gln Ala Glu Leu Tyr Pro Leu Asn
 115 120 125

Asp Ala Ile Asp Ile Lys Leu Ser Thr Val Pro Gly Leu Thr Ala Leu
 130 135 140

Lys Leu His Ala Trp Leu Asp Arg Lys Glu Asn Asn Ile Lys Asp Ala
 145 150 155 160

Ser Asp Leu Ala Leu Ile Leu Ser Trp Tyr Glu Glu Asp Val Glu Thr
 165 170 175

Leu Trp Asn Arg Tyr Phe Ala Leu Glu Asn Gln Gly Tyr Ile Gly Glu
 180 185 190

Pro Glu Ala Met Ala Ala Glu Leu Leu Gly Leu Asp Thr Gly Arg Ile
 195 200 205

Leu Gly His Lys Glu Thr Gln Ala Leu Leu Asp Arg Phe Asn Glu Gln
 210 215 220

Ser Pro Pro Glu Leu Asn Gln Phe Ala Glu Ser Leu Glu Ala Pro Pro
 225 230 235 240

Glu His Ser His Pro Leu Glu Arg Arg Arg Ile Gln Val Glu Ala Leu
 245 250 255

Leu Gly Gly Leu Arg Asp Ser Leu Gly Tyr Asp Glu
 260 265

<210> 1209

<211> 585

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(562)

<223> RXN02537

<400> 1209

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				Met	Leu	Ala	Leu	Lys	
				1				5	

agt tca gaa tta gaa ggc ata gcc aca tca ctc acc gcc gtg gcg ggt	163
Ser Ser Glu Leu Glu Gly Ile Ala Thr Ser Leu Thr Ala Val Ala Gly	
	10 15 20

gcg ctc cac gaa tca aac act gac cgg ttg cag tcc tgg cag cag ctc	211
Ala Leu His Ser Asn Thr Asp Arg Leu Gln Ser Trp Gln Gln Leu	
	25 30 35

gaa acg atg acc tct gcc agc tcc ctt atc cag ggc ttt atc aag ctt	259
Glu Thr Met Thr Ser Ala Ser Ser Leu Ile Gln Gly Phe Ile Lys Leu	
	40 45 50

gtc gat tac aac cga ccc aca gtg aat atc gtg gaa caa atg cac aaa	307
Val Asp Tyr Asn Arg Pro Thr Val Asn Ile Val Glu Gln Met His Lys	
	55 60 65

acc gca tcc acg ctt ttc aac acc gct gat ttc cta cgc act ttg gaa	355
Thr Ala Ser Thr Leu Phe Asn Thr Ala Asp Phe Leu Arg Thr Leu Glu	
	70 75 80 85

ggc tat gtt gat gta ctg gaa aaa caa gcc gat aaa tct ata acg ctc	403
Gly Tyr Val Asp Val Leu Glu Lys Gln Ala Asp Lys Ser Ile Thr Leu	
	90 95 100

acc gtc atg ctt cga tat att gcc agc ttg agt agc ctt tta gac ctc	451
Thr Val Met Leu Arg Tyr Ile Ala Ser Leu Ser Ser Leu Leu Asp Leu	
	105 110 115

atg tgt gca cgc gag atc aac gcg ttg tgc aca gcg att act cca gaa	499
Met Cys Ala Arg Glu Ile Asn Ala Leu Cys Thr Ala Ile Thr Pro Glu	
	120 125 130

cca ttg aag cat ctg ggc gat ttt ggc act cta cgg cct cag caa tcc	547
Pro Leu Lys His Leu Gly Asp Phe Gly Thr Leu Pro Pro Gln Gln Ser	
	135 140 145

acg agt ttc att tgg tgaatgcccc accagaaatc cgt	585
Thr Ser Phe Ile Trp	
	150

<210> 1210

<211> 154

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1210

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Met Leu Ala Leu Lys Ser Ser Glu Leu Glu Gly Ile Ala Thr Ser Leu
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Thr Ala Val Ala Gly Ala Leu His Glu Ser Asn Thr Asp Arg Leu Gln
             20             25             30

Ser Trp Gln Gln Leu Glu Thr Met Thr Ser Ala Ser Ser Leu Ile Gln
             35             40             45

Gly Phe Ile Lys Leu Val Asp Tyr Asn Arg Pro Thr Val Asn Ile Val
 50             55             60

Glu Gln Met His Lys Thr Ala Ser Thr Leu Phe Asn Thr Ala Asp Phe
 65             70             75             80

Leu Arg Thr Leu Glu Gly Tyr Val Asp Val Leu Glu Lys Gln Ala Asp
             85             90             95

Lys Ser Ile Thr Leu Thr Val Met Leu Arg Tyr Ile Ala Ser Leu Ser
             100            105            110

Ser Leu Leu Asp Leu Met Cys Ala Arg Glu Ile Asn Ala Leu Cys Thr
             115            120            125

Ala Ile Thr Pro Glu Pro Leu Lys His Leu Gly Asp Phe Gly Thr Leu
             130            135            140

Pro Pro Gln Gln Ser Thr Ser Phe Ile Trp
145             150

<210> 1211
<211> 585
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(562)
<223> FRXA02537

<400> 1211
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Met Leu Ala Leu Lys
1             5

agt tca gaa tta gaa ggc ata gcc aca tca ctc acc gcc gtg gcg ggt 163
Ser Ser Glu Leu Glu Gly Ile Ala Thr Ser Leu Thr Ala Val Ala Gly
             10             15             20

gcg ctc cac gaa tca aac act gac cgg ttg cag tcc tgg cag cag ctc 211
Ala Leu His Glu Ser Asn Thr Asp Arg Leu Gln Ser Trp Gln Gln Leu
             25             30             35

gaa acg atg acc tct gcc agc tcc ctt atc cag gcc ttt atc aag ctt 259
Glu Thr Met Thr Ser Ala Ser Ser Leu Ile Gln Gly Phe Ile Lys Leu
             40             45             50

gtc gat tac aac cga ccc aca gtg aat atc gtg gaa caa atg cac aaa 307

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Val Asp Tyr Asn Arg Pro Thr Val Asn Ile Val Glu Gln Met His Lys
  55                      60                      65
acc gca tcc acg ctt ttc aac acc gct gat ttc cta cgc act ttg gaa 355
Thr Ala Ser Thr Leu Phe Asn Thr Ala Asp Phe Leu Arg Thr Leu Glu
  70                      75                      80                      85

ggc tat gtt gat gta ctg gaa aaa caa gcc gat aaa tct ata acg ctc 403
Gly Tyr Val Asp Val Leu Glu Lys Gln Ala Asp Lys Ser Ile Thr Leu
                      90                      95                      100

acc gtc atg ctt cga tat att gcc agc ttg agt agc ctt tta gac ctc 451
Thr Val Met Leu Arg Tyr Ile Ala Ser Leu Ser Ser Leu Leu Asp Leu
                      105                      110                      115

atg tgt gca cgc gag atc aac gcg ttg tgc aca gcg att act cca gaa 499
Met Cys Ala Arg Glu Ile Asn Ala Leu Cys Thr Ala Ile Thr Pro Glu
                      120                      125                      130

cca ttg aag cat ctg ggc gat ttt ggc act cta ccg cct cag caa tcc 547
Pro Leu Lys His Leu Gly Asp Phe Gly Thr Leu Pro Pro Gln Gln Ser
                      135                      140                      145

acg agt ttc att tgg tgaatgcccc accagaaatc cgt 585
Thr Ser Phe Ile Trp
150

<210> 1212
<211> 154
<212> PRT
<213> Corynebacterium glutamicum

<400> 1212
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Thr Ala Val Ala Gly Ala Leu His Glu Ser Asn Thr Asp Arg Leu Gln
                      20                      25                      30

Ser Trp Gln Gln Leu Glu Thr Met Thr Ser Ala Ser Ser Leu Ile Gln
                      35                      40                      45

Gly Phe Ile Lys Leu Val Asp Tyr Asn Arg Pro Thr Val Asn Ile Val
  50                      55                      60

Glu Gln Met His Lys Thr Ala Ser Thr Leu Phe Asn Thr Ala Asp Phe
  65                      70                      75                      80

Leu Arg Thr Leu Glu Gly Tyr Val Asp Val Leu Glu Lys Gln Ala Asp
                      85                      90                      95

Lys Ser Ile Thr Leu Thr Val Met Leu Arg Tyr Ile Ala Ser Leu Ser
                      100                      105                      110

Ser Leu Leu Asp Leu Met Cys Ala Arg Glu Ile Asn Ala Leu Cys Thr
                      115                      120                      125

Ala Ile Thr Pro Glu Pro Leu Lys His Leu Gly Asp Phe Gly Thr Leu
                      130                      135                      140

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Pro Pro Gln Gln Ser Thr Ser Phe Ile Trp
145 150

<210> 1213

<211> 795

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(772)

<223> RXN02538

<400> 1213

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Val Asn Ala Pro Pro
1 5

gaa atc cgt gcc tta gcc gaa gcc cat ccc gat atg cag atc cta gaa 163
Glu Ile Arg Ala Leu Ala Glu Ala His Pro Asp Met Gln Ile Leu Glu
10 15 20

gcc ggc gat ggt tca ttg gta gca tcg ttt ggg gat att gat agg gct 211
Ala Gly Asp Gly Ser Leu Val Ala Ser Phe Gly Asp Ile Asp Arg Ala
25 30 35

acg acc gtg acc acc atc gtg gca ggt gtg ggt tcc tcc aac cca gaa 259
Thr Thr Val Thr Thr Ile Val Ala Gly Val Gly Ser Ser Asn Pro Glu
40 45 50

ggg tgg aat aca tat gtt gac cgt gcc cgc aca gta tct gct tcc acc 307
Gly Trp Asn Thr Tyr Val Asp Arg Ala Arg Thr Val Ser Ala Ser Thr
55 60 65

ggg tcc gca acg gtg ttg tgg ctg gga tat caa gca ccc gct tcg att 355
Gly Ser Ala Thr Val Leu Trp Leu Gly Tyr Gln Ala Pro Ala Ser Ile
70 75 80 85

cct gct gcg gta tcc ggc gcg gca gcg aat cgc gct gcc gcg gat ctc 403
Pro Ala Ala Val Ser Gly Ala Ala Ala Asn Arg Ala Ala Ala Asp Leu
90 95 100

cag agg ttt caa gcg gca cta cag tcc cgc aat ccc cac caa aga aaa 451
Gln Arg Phe Gln Ala Ala Leu Gln Ser Arg Asn Pro His Gln Arg Lys
105 110 115

gta gtg atg ggc tac agc tac ggt tcc aca gtg gtg gga aaa gct gcg 499
Val Val Met Gly Tyr Ser Tyr Gly Ser Thr Val Val Gly Lys Ala Ala
120 125 130

tct tcc gcc gag ctc agt gcc gat gcg ttg gta ttg gtt gcc agt ccc 547
Ser Ser Gly Glu Leu Ser Ala Asp Ala Leu Val Leu Val Gly Ser Pro
135 140 145

ggc gcg ggt gtc tcg cac tct tcc cag ctt ggc gca cct gtg tat gcg 595
Gly Ala Gly Val Ser His Ser Ser Gln Leu Gly Ala Pro Val Tyr Ala
150 155 160 165

gta aca ggg tct gct gat ccc atc ggt ttt gcc ggc acc caa tat gac 643
 Val Thr Gly Ser Ala Asp Pro Ile Gly Phe Ala Gly Thr Gln Tyr Asp
 170 175 180

ggc atc cac ggc act gat ccc acc gct gcc cta ttc ggt gca aca gtg 691
 Gly Ile His Gly Thr Asp Pro Thr Ala Ala Leu Phe Gly Ala Thr Val
 185 190 195

tgg gat tcg ccc tca acg cat tcc ggt tat tgg aat gac cag gag ttc 739
 Trp Asp Ser Pro Ser Thr His Ser Gly Tyr Trp Asn Asp Gln Glu Phe
 200 205 210

ctg ggc aat gtg gcg gag gtg gtt cgc ggc aaa tagaaaagcc gccgcacact 792
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 215 220

gga 795

<210> 1214

<211> 224

<212> PRT

<213> Corynebacterium glutamicum

<400> 1214

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 20 25 30

Asp Ile Asp Arg Ala Thr Thr Val Thr Thr Ile Val Ala Gly Val Gly
 35 40 45

Ser Ser Asn Pro Glu Gly Trp Asn Thr Tyr Val Asp Arg Ala Arg Thr
 50 55 60

Val Ser Ala Ser Thr Gly Ser Ala Thr Val Leu Trp Leu Gly Tyr Gln
 65 70 75 80

Ala Pro Ala Ser Ile Pro Ala Ala Val Ser Gly Ala Ala Ala Asn Arg
 85 90 95

Ala Ala Ala Asp Leu Gln Arg Phe Gln Ala Ala Leu Gln Ser Arg Asn
 100 105 110

Pro His Gln Arg Lys Val Val Met Gly Tyr Ser Tyr Gly Ser Thr Val
 115 120 125

Val Gly Lys Ala Ala Ser Ser Gly Glu Leu Ser Ala Asp Ala Leu Val
 130 135 140

Leu Val Gly Ser Pro Gly Ala Gly Val Ser His Ser Ser Gln Leu Gly
 145 150 155 160

Ala Pro Val Tyr Ala Val Thr Gly Ser Ala Asp Pro Ile Gly Phe Ala
 165 170 175

Gly Thr Gln Tyr Asp Gly Ile His Gly Thr Asp Pro Thr Ala Ala Leu
 180 185 190

Phe Gly Ala Thr Val Trp Asp Ser Pro Ser Thr His Ser Gly Tyr Trp
 195 200
 Asn Asp Gln Glu Phe Leu Gly Asn Val Ala Glu Val Val Arg Gly Lys
 210 215 220

<210> 1215
 <211> 795
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(772)
 <223> FRXA02538

<400> 1215
 gcgagatcaa cgcgttggtgc acagcgatta ctccagaacc attgaagcat ctggggcgatt 60
 ttggcactct accgcctcag caatccacga gtttcatttg gtg aat gcc cca cca 115
 Val Asn Ala Pro Pro
 1 5
 gaa atc cgt gcc tta gcc gaa gcc cat ccc gat atg cag atc cta gaa 163
 Glu Ile Arg Ala Leu Ala Glu Ala His Pro Asp Met Gln Ile Leu Glu
 10 15 20
 gcc ggc gat ggt tca ttg gta gca tgc ttt ggg gat att gat agg gct 211
 Ala Gly Asp Gly Ser Leu Val Ala Ser Phe Gly Asp Ile Asp Arg Ala
 25 30 35
 acg acc gtg acc acc atc gtg gca ggt gtg ggt tcc tcc aac cca gaa 259
 Thr Thr Val Thr Thr Ile Val Ala Gly Val Gly Ser Ser Asn Pro Glu
 40 45 50
 ggg tgg aat aca tat gtt gac cgt gcc cgc aca gta tct gct tcc acc 307
 Gly Trp Asn Thr Tyr Val Asp Arg Ala Arg Thr Val Ser Ala Ser Thr
 55 60 65
 ggt tcc gca acg gtg ttg tgg ctg gga tat caa gca ccc gct tgc att 355
 Gly Ser Ala Thr Val Leu Trp Leu Gly Tyr Gln Ala Pro Ala Ser Ile
 70 75 80 85
 cct gct gcg gta tcc ggc gcg gca gcg aat cgc gct gcc gcg gat ctc 403
 Pro Ala Ala Val Ser Gly Ala Ala Ala Asn Arg Ala Ala Ala Asp Leu
 90 95 100
 cag agg ttt caa gcg gca cta cag tcc cgc aat ccc cac caa aga aaa 451
 Gln Arg Phe Gln Ala Ala Leu Gln Ser Arg Asn Pro His Gln Arg Lys
 105 110 115
 gta gtg atg ggc tac agc tac ggt tcc aca gtg gtg gga aaa gct gcg 499
 Val Val Met Gly Tyr Ser Tyr Gly Ser Thr Val Val Gly Lys Ala Ala
 120 125 130
 tct tcc gcc gag ctc agt gcc gat gcg ttg gta ttg gtt gcc agt ccc 547
 Ser Ser Gly Glu Leu Ser Ala Asp Ala Leu Val Leu Val Gly Ser Pro

135	140	145	
ggc gcg ggt gtc tgc cac tct tcc cag ctt ggc gca cct gtg tat gcg			595
Gly Ala Gly Val Ser His Ser Ser Gln Leu Gly Ala Pro Val Tyr Ala			
150	155	160	165
gta aca ggg tct gct gat ccc atc ggt ttt gcc ggc acc caa tat gac			643
Val Thr Gly Ser Ala Asp Pro Ile Gly Phe Ala Gly Thr Gln Tyr Asp			
	170	175	180
ggc atc cac ggc act gat ccc acc gct gcc cta ttc ggt gca aca gtg			691
Gly Ile His Gly Thr Asp Pro Thr Ala Ala Leu Phe Gly Ala Thr Val			
	185	190	195
tgg gat tgc ccc tca acg cat tcc ggt tat tgg aat gac cag gag ttc			739
Trp Asp Ser Pro Ser Thr His Ser Gly Tyr Trp Asn Asp Gln Glu Phe			
	200	205	210
ctg ggc aat gtg gcg gag gtg gtt cgc ggc aaa tagaaaaacc gccgcacact			792
Leu Gly Asn Val Ala Glu Val Val Arg Gly Lys			
	215	220	
gga			795
<210> 1216			
<211> 224			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 1216			
Val Asn Ala Pro Pro Glu Ile Arg Ala Leu Ala Glu Ala His Pro Asp			
1	5	10	15
Met Gln Ile Leu Glu Ala Gly Asp Gly Ser Leu Val Ala Ser Phe Gly			
	20	25	30
Asp Ile Asp Arg Ala Thr Thr Val Thr Thr Ile Val Ala Gly Val Gly			
	35	40	45
Ser Ser Asn Pro Glu Gly Trp Asn Thr Tyr Val Asp Arg Ala Arg Thr			
	50	55	60
Val Ser Ala Ser Thr Gly Ser Ala Thr Val Leu Trp Leu Gly Tyr Gln			
	65	70	80
Ala Pro Ala Ser Ile Pro Ala Ala Val Ser Gly Ala Ala Ala Asn Arg			
	85	90	95
Ala Ala Ala Asp Leu Gln Arg Phe Gln Ala Ala Leu Gln Ser Arg Asn			
	100	105	110
Pro His Gln Arg Lys Val Val Met Gly Tyr Ser Tyr Gly Ser Thr Val			
	115	120	125
Val Gly Lys Ala Ala Ser Ser Gly Glu Leu Ser Ala Asp Ala Leu Val			
	130	135	140
Leu Val Gly Ser Pro Gly Ala Gly Val Ser His Ser Ser Gln Leu Gly			
	145	150	155
			160

Ala Pro Val Tyr Ala Val Thr Gly Ser Ala Asp Pro Ile Gly Phe Ala
 165 170 175

Gly Thr Gln Tyr Asp Gly Ile His Gly Thr Asp Pro Thr Ala Ala Leu
 180 185 190

Phe Gly Ala Thr Val Trp Asp Ser Pro Ser Thr His Ser Gly Tyr Trp
 195 200 205

Asn Asp Gln Glu Phe Leu Gly Asn Val Ala Glu Val Val Arg Gly Lys
 210 215 220

<210> 1217

<211> 726

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(703)

<223> RXN02555

<400> 1217

gttttatcgc tatttaatac aggcctaccc ccaactcccc cattcagttc agggaaatccc 60

cggatttaaa acaattaataa accctctaga atgagacatt atg ggc gaa caa ttt 115
 Met Gly Glu Gln Phe
 1 5

cca ggc gat aaa aac atc cga gtc agc gac acc gaa aga tca gca gca 163
 Pro Gly Asp Lys Asn Ile Arg Val Ser Asp Thr Glu Arg Ser Ala Ala
 10 15 20

cta gca gca ctc ggc cag ttc tac gca gaa ggt cgc ctc tcc cta gaa 211
 Leu Ala Ala Leu Gly Gln Phe Tyr Ala Glu Gly Arg Leu Ser Leu Glu
 25 30 35

gaa acc gac gac cgc tgc gaa gcc gtc gcc gac gcc aaa acc cgc gcc 259
 Glu Thr Asp Asp Arg Cys Glu Ala Val Ala Asp Ala Lys Thr Arg Gly
 40 45 50

gac ctc aac gcc atc ttc tac gat ctg ccc aac caa caa atc gca gtc 307
 Asp Leu Asn Ala Ile Phe Tyr Asp Leu Pro Asn Gln Ile Ala Val
 55 60 65

gtc gac cgc tcc gaa caa acc tac aca gcc acc gaa gtt gcc gaa ctc 355
 Val Asp Arg Ser Glu Gln Thr Tyr Thr Ala Thr Glu Val Ala Glu Leu
 70 75 80 85

cac cgc aaa ggc gca cgc cca cgc gcc gga atc ctc gga ctc acc aca 403
 His Arg Lys Gly Ala Arg Pro Arg Ala Gly Ile Leu Gly Leu Thr Thr
 90 95 100

gtt tta gcc atc acc ggt acc gct gct ttc gcc agc acc aca gct ttt 451
 Val Leu Ala Ile Thr Gly Thr Ala Ala Phe Ala Ser Thr Thr Ala Phe
 105 110 115

gca aca gta ctt tta gcc ctg att cgg atc gtg ttc atc atg ctg tac 499
 Ala Thr Val Leu Leu Ala Leu Ile Pro Ile Val Phe Ile Met Leu Tyr
 120 125 130

gtg atg aaa att ggt cct gaa tcc tgg cac gca cca aca cct cgc caa 547
 Val Met Lys Ile Gly Pro Glu Ser Trp His Ala Pro Thr Pro Arg Gln
 135 140 145

ctt cag cga aag cgc atg atc gaa ctg cgt gaa aag gaa aaa ctc cgc 595
 Leu Gln Arg Lys Arg Met Ile Glu Leu Arg Glu Lys Glu Lys Leu Arg
 150 155 160 165

gac atg gag ctc aaa gcc cag cgc aag gaa cgc acc cac gca tta acc 643
 Asp Met Glu Leu Lys Ala Gln Arg Lys Glu Arg Thr His Ala Leu Thr
 170 175 180

aac cgc gcg ttg gat gct gct gaa act gct ttc aac acc aag ccc tgg 691
 Asn Arg Ala Leu Asp Ala Ala Glu Thr Ala Phe Asn Thr Lys Pro Trp
 185 190 195

aag aag aac aaa tagggctttt gaagtgtgtc gcg 726
 Lys Lys Asn Lys
 200

<210> 1218
 <211> 201
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 1218
 Met Gly Glu Gln Phe Pro Gly Asp Lys Asn Ile Arg Val Ser Asp Thr
 1 5 10

Glu Arg Ser Ala Ala Leu Ala Ala Leu Gly Gln Phe Tyr Ala Glu Gly
 20 25 30

Arg Leu Ser Leu Glu Glu Thr Asp Asp Arg Cys Glu Ala Val Ala Asp
 35 40 45

Ala Lys Thr Arg Gly Asp Leu Asn Ala Ile Phe Tyr Asp Leu Pro Asn
 50 55 60

Gln Gln Ile Ala Val Val Asp Arg Ser Glu Gln Thr Tyr Thr Ala Thr
 65 70 75 80

Glu Val Ala Glu Leu His Arg Lys Gly Ala Arg Pro Arg Ala Gly Ile
 85 90 95

Leu Gly Leu Thr Thr Val Leu Ala Ile Thr Gly Thr Ala Ala Phe Ala
 100 105 110

Ser Thr Thr Ala Phe Ala Thr Val Leu Leu Ala Leu Ile Pro Ile Val
 115 120 125

Phe Ile Met Leu Tyr Val Met Lys Ile Gly Pro Glu Ser Trp His Ala
 130 135 140

Pro Thr Pro Arg Gln Leu Gln Arg Lys Arg Met Ile Glu Leu Arg Glu
 145 150 155 160

Lys Glu Lys Leu Arg Asp Met Glu Leu Lys Ala Gln Arg Lys Glu Arg
 165 170
 Thr His Ala Leu Thr Asn Arg Ala Leu Asp Ala Ala Glu Thr Ala Phe
 180 185 190
 Asn Thr Lys Pro Trp Lys Lys Asn Lys
 195 200

<210> 1219
 <211> 726
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(703)
 <223> FRXA02555

<400> 1219
 gttttatcgc tatttaatac aggcctaccc ccactacccc cattcagttc agggaaatccc 60
 cggatttaaa acaattaaaa accctctaga atgagacatt atg ggc gaa caa ttt 115
 Met Gly Glu Gln Phe
 1 5
 cca ggc gat aaa aac atc cga gtc agc gac acc gaa aga tca gca gca 163
 Pro Gly Asp Lys Asn Ile Arg Val Ser Asp Thr Glu Arg Ser Ala Ala
 10 15 20
 cta gca gca ctc ggc cag ttc tac gca gaa ggt cgc ctc tcc cta gaa 211
 Leu Ala Ala Leu Gly Gln Phe Tyr Ala Glu Gly Arg Leu Ser Leu Glu
 25 30 35
 gaa acc gac gac cgc tgc gaa gcc gtc gcc gac gcc aaa acc cgc ggc 259
 Glu Thr Asp Asp Arg Cys Glu Ala Val Ala Asp Ala Lys Thr Arg Gly
 40 45 50
 gac ctc aac gcc atc ttc tac gat ctg ccc aac caa caa atc gca gtc 307
 Asp Leu Asn Ala Ile Phe Tyr Asp Leu Pro Asn Gln Gln Ile Ala Val
 55 60 65
 gtc gac cgc tcc gaa caa acc tac aca gcc acc gaa gtt gcc gaa ctc 355
 Val Asp Arg Ser Glu Gln Thr Tyr Thr Ala Thr Glu Val Ala Glu Leu
 70 75 80 85
 cac cgc aaa ggc gca cgc cca cgc gcc gga atc ctc gga ctc acc aca 403
 His Arg Lys Gly Ala Arg Pro Arg Ala Gly Ile Leu Gly Leu Thr Thr
 90 95 100
 gtt tta gcc atc acc ggt acc gct gct ttc gcc agc acc aca gct ttt 451
 Val Leu Ala Ile Thr Gly Thr Ala Ala Phe Ala Ser Thr Thr Ala Phe
 105 110 115
 gca aca gta ctt tta gcc ctg att ccg atc gtg ttc atc atg ctg tac 499
 Ala Thr Val Leu Leu Ala Leu Ile Pro Ile Val Phe Ile Met Leu Tyr
 120 125 130
 gtg atg aaa att ggt cct gaa tcc tgg cac gca cca aca cct cgc caa 547
 Val Met Lys Ile Gly Pro Glu Ser Trp His Ala Pro Thr Pro Arg Gln

135

140

145

ctt cag cga aag cgc atg atc gaa ctg cgt gaa aag gaa aaa ctc cgc 595
 Leu Gln Arg Lys Arg Met Ile Glu Leu Arg Glu Lys Glu Lys Leu Arg
 150 155 160 165

gac atg gag ctc aaa gcc cag cgc aag gaa cgc acc cac gca tta acc 643
 Asp Met Glu Leu Lys Ala Gln Arg Lys Glu Arg Thr His Ala Leu Thr
 170 175 180

aac cgc gcg ttg gat gct gct gaa act gct ttc aac acc aag ccc tgg 691
 Asn Arg Ala Leu Asp Ala Ala Glu Thr Ala Phe Asn Thr Lys Pro Trp
 185 190 195

aag aag aac aaa tagggctttt gaagtgtgtc gcg 726
 Lys Lys Asn Lys
 200

<210> 1220

<211> 201

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1220

Met Gly Glu Gln Phe Pro Gly Asp Lys Asn Ile Arg Val Ser Asp Thr
 1 5 10 15

Glu Arg Ser Ala Ala Leu Ala Ala Leu Gly Gln Phe Tyr Ala Glu Gly
 20 25 30

Arg Leu Ser Leu Glu Glu Thr Asp Asp Arg Cys Glu Ala Val Ala Asp
 35 40 45

Ala Lys Thr Arg Gly Asp Leu Asn Ala Ile Phe Tyr Asp Leu Pro Asn
 50 55 60

Gln Gln Ile Ala Val Val Asp Arg Ser Glu Gln Thr Tyr Thr Ala Thr
 65 70 75 80

Glu Val Ala Glu Leu His Arg Lys Gly Ala Arg Pro Arg Ala Gly Ile
 85 90 95

Leu Gly Leu Thr Thr Val Leu Ala Ile Thr Gly Thr Ala Ala Phe Ala
 100 105 110

Ser Thr Thr Ala Phe Ala Thr Val Leu Leu Ala Leu Ile Pro Ile Val
 115 120 125

Phe Ile Met Leu Tyr Val Met Lys Ile Gly Pro Glu Ser Trp His Ala
 130 135 140

Pro Thr Pro Arg Gln Leu Gln Arg Lys Arg Met Ile Glu Leu Arg Glu
 145 150 155 160

Lys Glu Lys Leu Arg Asp Met Glu Leu Lys Ala Gln Arg Lys Glu Arg
 165 170 175

Thr His Ala Leu Thr Asn Arg Ala Leu Asp Ala Ala Glu Thr Ala Phe
 180 185 190

Asn Thr Lys Pro Trp Lys Lys Asn Lys
195 200

<210> 1221

<211> 1125

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1102)

<223> RXN02564

<400> 1221

acaccacagt gaagcgggtga cgtgaatcac ccaagcactt aggcataaaa cattcaagag 60

ctgtgtgtcc aaaagtccga ccgagaggga ttcccccaaa atg gcc gaa gta gga 115
Met Ala Glu Val Gly
1 5

gca gaa ccc gca ggg tct gca caa tcc aaa act aaa caa ttt gtt gta 163
Ala Glu Pro Ala Gly Ser Ala Gln Ser Lys Thr Lys Gln Phe Val Val
10 15 20

ggt acc gca gcg gtg gtc atc act gca atc gct gcg ttt ttc tcc atc 211
Gly Thr Ala Ala Val Val Ile Thr Ala Ile Ala Ala Phe Phe Ser Ile
25 30 35

cag tct gca tcc ggt ggc gag gat att cgt tcc aac atg acg ctg att 259
Gln Ser Ala Ser Gly Gly Glu Asp Ile Arg Ser Asn Met Thr Leu Ile
40 45 50

gct cct gca gct gca ggt gga ggt tgg gat act ttc caa cgt gag cag 307
Ala Pro Ala Ala Ala Gly Gly Gly Trp Asp Thr Phe Gln Arg Glu Gln
55 60 65

cag cag tct atg cgc gtg aat aag atc gtg aac aat att cag gtg gtc 355
Gln Gln Ser Met Arg Val Asn Lys Ile Val Asn Asn Ile Gln Val Val
70 75 80 85

aac atc cct gga gct ggt gga acc att gca ctt ggc aaa ctg tct acc 403
Asn Ile Pro Gly Ala Gly Gly Thr Ile Ala Leu Gly Lys Leu Ser Thr
90 95 100

atg act gca ccg aac acc ttg atg gtg ggt gga acg ggg cat atc gca 451
Met Thr Ala Pro Asn Thr Leu Met Val Gly Gly Thr Gly His Ile Ala
105 110 115

gca caa att caa ttc gat acc cct gcg aaa atc cag gat gtc acc cca 499
Ala Gln Ile Gln Phe Asp Thr Pro Ala Lys Ile Gln Asp Val Thr Pro
120 125 130

att gct cgt gtg gtg gaa gag ttc gac atc atc acc gtg cca gcg gat 547
Ile Ala Arg Val Val Glu Glu Phe Asp Ile Ile Thr Val Pro Ala Asp
135 140 145

tct cca tac aac acc ctt gaa gag ctg att gaa ggt tgg aag gca gat 595
Ser Pro Tyr Asn Thr Leu Glu Glu Leu Ile Glu Gly Trp Lys Ala Asp
150 155 160 165

cca gca gga gtg tcc tgg acc ggt ggt ggt tcc ttt gac cag ctt gtt 643
Pro Ala Gly Val Ser Trp Thr Gly Gly Gly Ser Phe Asp Gln Leu Val
170 175 180

atg aca gaa att gca ctg tct gca ggt ata gat cct aag caa acc acc 691
Met Thr Glu Ile Ala Leu Ser Ala Gly Ile Asp Pro Lys Gln Thr Thr
185 190 195

ttt att cct tct gat ggt ggt ggc gaa gcg att cag gcg cta ctg aac 739
Phe Ile Pro Ser Asp Gly Gly Gly Glu Ala Ile Gln Ala Leu Leu Asn
200 205 210

gga acc gca aag gca tca act ggt ggt ttt gct gat atg tat ccg cag 787
Gly Thr Ala Lys Ala Ser Thr Gly Gly Phe Ala Asp Met Tyr Pro Gln
215 220 225

gta gaa gcc ggt cga ttg aag gtt ttg gga att gct gca gaa gaa cgc 835
Val Glu Ala Gly Arg Leu Lys Val Leu Gly Ile Ala Ala Glu Glu Arg
230 235 240 245

ctt cca ggt tct gac att cca acg cta gtg gaa caa ggc tat gac gtg 883
Leu Pro Gly Ser Asp Ile Pro Thr Leu Val Glu Gln Gly Tyr Asp Val
250 255 260

acc ttg acc aac tgg cgt gcc atg ttc gct cct cct ggt ttg agc gat 931
Thr Leu Thr Asn Trp Arg Ala Met Phe Ala Pro Pro Gly Leu Ser Asp
265 270 275

gat caa att gcg gaa ctt cga gca atc gtt gcg gag tct gtg gag act 979
Asp Gln Ile Ala Glu Leu Arg Ala Ile Val Ala Glu Ser Val Glu Thr
280 285 290

gct gaa tgg cag tcc gcg gtg gaa cga aac tac tgg atg aac gcc tca 1027
Ala Glu Trp Gln Ser Ala Val Glu Arg Asn Tyr Trp Met Asn Ala Ser
295 300 305

ctt gaa ggc gaa gaa ctc gac cag ttt gtt gaa gat gaa att gac cga 1075
Leu Glu Gly Glu Glu Leu Asp Gln Phe Val Glu Asp Glu Ile Asp Arg
310 315 320 325

att gat cag cta ttc aag gag atg ggc tagtgaacgt cactgaacaa 1122
Ile Asp Gln Leu Phe Lys Glu Met Gly
330

tcc 1125

<210> 1222
<211> 334
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 1222
Met Ala Glu Val Gly Ala Glu Pro Ala Gly Ser Ala Gln Ser Lys Thr
1 5 10 15
Lys Gln Phe Val Val Gly Thr Ala Ala Val Val Ile Thr Ala Ile Ala
20 25 30
Ala Phe Phe Ser Ile Gln Ser Ala Ser Gly Gly Glu Asp Ile Arg Ser
35 40 45

Asn Met Thr Leu Ile Ala Pro Ala Ala Ala Gly Gly Gly Trp Asp Thr
 50 55 60
 Phe Gln Arg Glu Gln Gln Gln Ser Met Arg Val Asn Lys Ile Val Asn
 65 70 75 80
 Asn Ile Gln Val Val Asn Ile Pro Gly Ala Gly Gly Thr Ile Ala Leu
 85 90 95
 Gly Lys Leu Ser Thr Met Thr Ala Pro Asn Thr Leu Met Val Gly Gly
 100 105 110
 Thr Gly His Ile Ala Ala Gln Ile Gln Phe Asp Thr Pro Ala Lys Ile
 115 120 125
 Gln Asp Val Thr Pro Ile Ala Arg Val Val Glu Glu Phe Asp Ile Ile
 130 135 140
 Thr Val Pro Ala Asp Ser Pro Tyr Asn Thr Leu Glu Glu Leu Ile Glu
 145 150 155 160
 Gly Trp Lys Ala Asp Pro Ala Gly Val Ser Trp Thr Gly Gly Gly Ser
 165 170 175
 Phe Asp Gln Leu Val Met Thr Glu Ile Ala Leu Ser Ala Gly Ile Asp
 180 185 190
 Pro Lys Gln Thr Thr Phe Ile Pro Ser Asp Gly Gly Gly Glu Ala Ile
 195 200 205
 Gln Ala Leu Leu Asn Gly Thr Ala Lys Ala Ser Thr Gly Gly Phe Ala
 210 215 220
 Asp Met Tyr Pro Gln Val Glu Ala Gly Arg Leu Lys Val Leu Gly Ile
 225 230 235 240
 Ala Ala Glu Glu Arg Leu Pro Gly Ser Asp Ile Pro Thr Leu Val Glu
 245 250 255
 Gln Gly Tyr Asp Val Thr Leu Thr Asn Trp Arg Ala Met Phe Ala Pro
 260 265 270
 Pro Gly Leu Ser Asp Asp Gln Ile Ala Glu Leu Arg Ala Ile Val Ala
 275 280 285
 Glu Ser Val Glu Thr Ala Glu Trp Gln Ser Ala Val Glu Arg Asn Tyr
 290 295 300
 Trp Met Asn Ala Ser Leu Glu Gly Glu Glu Leu Asp Gln Phe Val Glu
 305 310 315 320
 Asp Glu Ile Asp Arg Ile Asp Gln Leu Phe Lys Glu Met Gly
 325 330

<210> 1223

<211> 775

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(775)

<223> FRXA02564

<400> 1223

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cttgtgtgtcc aaaagtccga ccgagaggga tccccccaaa atg gcc gaa gta gga 115
 Met Ala Glu Val Gly
 1 5

gca gaa ccc gca ggg tct gca caa tcc aaa act aaa caa ttt gtt gta 163
 Ala Glu Pro Ala Gly Ser Ala Gln Ser Lys Thr Lys Gln Phe Val Val
 10 15 20

ggt acc gca gcg gtg gtc atc act gca atc gct gcg ttt ttc tcc atc 211
 Gly Thr Ala Ala Val Val Ile Thr Ala Ala Phe Phe Ser Ile
 25 30 35

cag tct gca tcc ggt ggc gag gat att cgt tcc aac atg acg ctg att 259
 Gln Ser Ala Ser Gly Gly Glu Asp Ile Arg Ser Asn Met Thr Leu Ile
 40 45 50

gct cct gca gct gca ggt gga ggt tgg gat act ttc caa cgt gag cag 307
 Ala Pro Ala Ala Ala Gly Gly Trp Asp Thr Phe Gln Arg Glu Gln
 55 60 65

cag cag tct atg cgc gtg aat aag atc gtg aac aat att cag gtg gtc 355
 Gln Gln Ser Met Arg Val Asn Lys Ile Val Asn Asn Ile Gln Val Val
 70 75 80 85

aac atc cct gga gct ggt gga acc att gca ctt ggc aaa ctg tct acc 403
 Asn Ile Pro Gly Ala Gly Gly Thr Ile Ala Leu Gly Lys Leu Ser Thr
 90 95 100

atg act gca ccg aac acc ttg atg gtg ggt gga acg ggg cat atc gca 451
 Met Thr Ala Pro Asn Thr Leu Met Val Gly Gly Thr Gly His Ile Ala
 105 110 115

gca caa att caa ttc gat acc cct gcg aaa atc cag gat gtc acc cca 499
 Ala Gln Ile Gln Phe Asp Thr Pro Ala Lys Ile Gln Asp Val Thr Pro
 120 125 130

att gct cgt gtg gtg gaa gag ttc gac atc atc acc gtg cca gcg gat 547
 Ile Ala Arg Val Val Glu Glu Phe Asp Ile Ile Thr Val Pro Ala Asp
 135 140 145

tct cca tac aac acc ctt gaa gag ctg att gaa ggt tgg aag gca gat 595
 Ser Pro Tyr Asn Thr Leu Glu Glu Leu Ile Glu Gly Trp Lys Ala Asp
 150 155 160 165

cca gca gga gtg tcc tgg acc ggt ggt ggt tcc ttt gac cag ctt gtt 643
 Pro Ala Gly Val Ser Trp Thr Gly Gly Gly Ser Phe Asp Gln Leu Val
 170 175 180

atg aca gaa att gca ctg tct gca ggt ata gat cct aag caa acc acc 691
 Met Thr Glu Ile Ala Leu Ser Ala Gly Ile Asp Pro Lys Gln Thr Thr
 185 190 195

ttt att cct tct gat ggt ggt ggc gaa gcg att cag gcg cta ctg aac 739

Phe Ile Pro Ser Asp Gly Gly Gly Glu Ala Ile Gln Ala Leu Leu Asn
 200 205 210

gga acc gca aag gca tca act ggt ggt ttt gct gat 775
 Gly Thr Ala Lys Ala Ser Thr Gly Gly Phe Ala Asp
 215 220 225

<210> 1224

<211> 225

<212> PRT

<213> Corynebacterium glutamicum

<400> 1224

Met Ala Glu Val Gly Ala Glu Pro Ala Gly Ser Ala Gln Ser Lys Thr
 1 5 10 15

Lys Gln Phe Val Val Gly Thr Ala Ala Val Val Ile Thr Ala Ile Ala
 20 25 30

Ala Phe Phe Ser Ile Gln Ser Ala Ser Gly Gly Glu Asp Ile Arg Ser
 35 40 45

Asn Met Thr Leu Ile Ala Pro Ala Ala Ala Gly Gly Gly Trp Asp Thr
 50 55 60

Phe Gln Arg Glu Gln Gln Gln Ser Met Arg Val Asn Lys Ile Val Asn
 65 70 75 80

Asn Ile Gln Val Val Asn Ile Pro Gly Ala Gly Gly Thr Ile Ala Leu
 85 90 95

Gly Lys Leu Ser Thr Met Thr Ala Pro Asn Thr Leu Met Val Gly Gly
 100 105 110

Thr Gly His Ile Ala Ala Gln Ile Gln Phe Asp Thr Pro Ala Lys Ile
 115 120 125

Gln Asp Val Thr Pro Ile Ala Arg Val Val Glu Glu Phe Asp Ile Ile
 130 135 140

Thr Val Pro Ala Asp Ser Pro Tyr Asn Thr Leu Glu Glu Leu Ile Glu
 145 150 155 160

Gly Trp Lys Ala Asp Pro Ala Gly Val Ser Trp Thr Gly Gly Gly Ser
 165 170 175

Phe Asp Gln Leu Val Met Thr Glu Ile Ala Leu Ser Ala Gly Ile Asp
 180 185 190

Pro Lys Gln Thr Thr Phe Ile Pro Ser Asp Gly Gly Gly Glu Ala Ile
 195 200 205

Gln Ala Leu Leu Asn Gly Thr Ala Lys Ala Ser Thr Gly Gly Phe Ala
 210 215 220

Asp
 225

<210> 1225

<211> 1753

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1753)

<223> RXN02568

<400> 1225

ccagctacga tatggaattt caccaaatgc gaactaccct aaataccaaa gacagacagt 60

gacagccctt togagaatgc agcaagagac gacacctcct atg gac ggc acc tcg 115
 Met Asp Gly Thr Ser
 1 5

cca cag aac aaa att tcc acc act ccc cca gcg cca gga aat gct att 163
 Pro Gln Asn Lys Ile Ser Thr Thr Pro Pro Ala Pro Gly Asn Ala Ile
 10 15 20

cct gca cct gga ggc gcc att cct aca cca gcg aaa act gag cag gac 211
 Pro Ala Pro Gly Gly Ala Ile Pro Thr Pro Ala Lys Thr Glu Gln Asp
 25 30 35

gca gta cct cca act gtg gcg gcg aaa cta ccc gta cct gga agt tct 259
 Ala Val Pro Pro Thr Val Ala Ala Lys Leu Pro Val Pro Gly Ser Ser
 40 45 50

att cca gca ccc ggt aga gca ttg cca act cca gtg gct ccg gga ggt 307
 Ile Pro Ala Pro Gly Arg Ala Leu Pro Thr Pro Val Ala Pro Gly Gly
 55 60 65

tcc gtc cca gct ccg aga gcg tcc gca cct gcg gtt cct aac gtt cct 355
 Ser Val Pro Ala Pro Arg Ala Ser Ala Pro Ala Val Pro Asn Val Pro
 70 75 80 85

gca gct ccc ggc gct gct gtt cca gct ccg gga atc tcg atc ccg gca 403
 Ala Ala Pro Gly Ala Ala Val Pro Ala Pro Gly Ile Ser Ile Pro Ala
 90 95 100

gca cct agt gcc cca ggc agt gca att cca aca cca ggc aca gca atc 451
 Ala Pro Ser Ala Pro Gly Ser Ala Ile Pro Thr Pro Gly Thr Ala Ile
 105 110 115

cct gtg cct gga agt gca act cct gtc cca gca cct ggg gtt agt gca 499
 Pro Val Pro Gly Ser Ala Thr Pro Val Pro Ala Pro Gly Val Ser Ala
 120 125 130

cct ggc gca agc gtt cca agc att cca gta cca gga tct gtc acc cca 547
 Pro Gly Ala Ser Val Pro Ser Ile Pro Val Pro Gly Ser Val Thr Pro
 135 140 145

cct gca cca gga att tcc gca cct ggc ggt gca ctt ccg act cct ggc 595
 Pro Ala Pro Gly Ile Ser Ala Pro Gly Gly Ala Leu Pro Thr Pro Gly
 150 155 160 165

agt gcg ccc cca aca cct ggc ggt gcc ctt ccg act cca gag gca 643
 Ser Ala Pro Pro Thr Pro Gly Gly Ala Leu Pro Thr Pro Gly Glu Ala
 170 175 180

ctt ccc gtt ccc gga gca cct ggt gca ccc gga gca tcc gga atc cca 691

Leu	Pro	Val	Pro	Gly	Ala	Pro	Gly	Ala	Pro	Gly	Ala	Ser	Gly	Ile	Pro	
			185					190					195			
agt	cct	ggc	ctt	cca	acc	cca	ggt	gtc	cca	act	ccc	gga	gct	tcc	tta	739
Ser	Pro	Gly	Leu	Pro	Thr	Pro	Gly	Val	Pro	Thr	Pro	Gly	Ala	Ser	Leu	
		200					205				210					
cca	gtc	cca	gga	gca	cca	gac	gca	cct	gga	acc	cca	agc	att	ccc	gca	787
Pro	Val	Pro	Gly	Ala	Pro	Asp	Ala	Pro	Gly	Thr	Pro	Ser	Ile	Pro	Ala	
		215				220				225						
gct	ccc	ggc	att	caa	gca	cca	gga	att	cca	gca	gca	cca	gga	gcc	cct	835
Ala	Pro	Gly	Ile	Gln	Ala	Pro	Gly	Ile	Pro	Ala	Ala	Pro	Gly	Ala	Pro	
		230			235					240				245		
gcc	caa	gct	gct	gct	cac	gca	aag	cca	gta	ttc	caa	gat	gca	gag	aaa	883
Ala	Gln	Ala	Ala	Ala	His	Ala	Lys	Pro	Val	Phe	Gln	Asp	Ala	Glu	Lys	
				250					255				260			
cga	cct	cgc	aca	gat	gaa	gct	gga	aat	gcg	aag	aag	gaa	ctg	ccg	ctg	931
Arg	Pro	Arg	Thr	Asp	Glu	Ala	Gly	Asn	Ala	Lys	Lys	Glu	Leu	Pro	Leu	
			265					270					275			
aga	gtt	cgg	ttg	gcg	cag	cca	att	aca	cgt	aag	cag	tgg	gca	atg	act	979
Arg	Val	Arg	Leu	Ala	Gln	Pro	Ile	Thr	Arg	Lys	Gln	Trp	Ala	Met	Thr	
		280					285					290				
ctt	ggt	gtc	ctg	gtt	ctc	gga	gca	att	gtc	gtg	gct	gca	atc	gcg	gtg	1027
Leu	Gly	Val	Leu	Val	Leu	Gly	Ala	Ile	Val	Val	Ala	Ala	Ile	Ala	Val	
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gtc	ctt	gcc	aaa	tgg	gcg	ttt	acc	acg	gag	tgg	ttg	cag	gac	ttc	gtc	1075
Val	Leu	Ala	Lys	Trp	Ala	Phe	Thr	Thr	Glu	Trp	Leu	Gln	Asp	Phe	Val	
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gag	aag	tat	ccg	ggt	aaa	tat	gac	aac	ccc	gaa	ggt	gcg	cca	gta	gga	1123
Glu	Lys	Tyr	Pro	Gly	Lys	Tyr	Asp	Asn	Pro	Glu	Gly	Ala	Pro	Val	Gly	
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att	cca	acg	tgg	ctg	agt	tgg	cag	cac	ttc	ttc	aac	atg	ttc	ttc	atg	1171
Ile	Pro	Thr	Trp	Leu	Ser	Trp	Gln	His	Phe	Phe	Asn	Met	Phe	Phe	Met	
			345					350					355			
gtg	ttg	att	atc	aag	acg	ggc	att	gag	atc	aat	aga	acc	cgc	agg	cca	1219
Val	Leu	Ile	Ile	Lys	Thr	Gly	Ile	Glu	Ile	Asn	Arg	Thr	Arg	Arg	Pro	
		360				365					370					
aag	ggt	tat	tgg	acg	ccg	aaa	aag	ggt	ggc	aag	aag	atc	tcc	ttg	acg	1267
Lys	Gly	Tyr	Trp	Thr	Pro	Lys	Lys	Gly	Gly	Lys	Lys	Ile	Ser	Leu	Thr	
		375				380				385						
ttg	tgg	atc	cac	ctg	gtt	ttg	gat	ttg	ttg	tgg	atc	atc	aac	ggg	gcg	1315
Leu	Trp	Ile	His	Leu	Val	Leu	Asp	Leu								

	425	430	435	
	tat gtg tcg ttg gat tgg cgg act gag aat ggt tgg gcg aat tac aac			1459
	Tyr Val Ser Leu Asp Trp Pro Thr Glu Asn Gly Trp Ala Asn Tyr Asn			
	440	445	450	
	agt ttg cag gag ctg acg tac ttc ttc act gtc ttt att gcg gca ccg			1507
	Ser Leu Gln Glu Leu Thr Tyr Phe Phe Thr Val Phe Ile Ala Ala Pro			
	455	460	465	
	ttg tcg att gtg tct ggt ttc cgg atg tcg agt tac tgg cct aag aac			1555
	Leu Ser Ile Val Ser Gly Phe Arg Met Ser Ser Tyr Trp Pro Lys Asn			
	470	475	480	485
	aat gcg acg atg aat aag ttg atc ccc atc ggg ttt gct cgt gcg ctg			1603
	Asn Ala Thr Met Asn Lys Leu Ile Pro Ile Gly Phe Ala Arg Ala Leu			
	490	495	500	
	cac atg cca gtg atg gtg tat tac atc gtg ttc att tgt atc cac gtg			1651
	His Met Pro Val Met Val Tyr Tyr Ile Val Phe Ile Cys Ile His Val			
	505	510	515	
	ttc ttg gtg ttg gcg acc ggc gcg ttg cgc aat ttc aac cat atg tat			1699
	Phe Leu Val Leu Ala Thr Gly Ala Leu Arg Asn Phe Asn His Met Tyr			
	520	525	530	
	gca ggt caa gac gtt gtg aac tgg gtt ggt ttt ggt tgg ttc gtg gcg			1747
	Ala Gly Gln Asp Val Val Asn Trp Val Gly Phe Gly Trp Phe Val Ala			
	535	540	545	
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	Ser Leu			
	550			
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	<211> 551			
	<212> PRT			
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	<400> 1226			
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	Lys Thr Glu Gln Asp Ala Val Pro Pro Thr Val Ala Ala Lys Leu Pro			
	35 40 45			
	Val Pro Gly Ser Ser Ile Pro Ala Pro Gly Arg Ala Leu Pro Thr Pro			
	50 55 60			
	Val Ala Pro Gly Gly Ser Val Pro Ala Pro Arg Ala Ser Ala Pro Ala			
	65 70 75 80			
	Val Pro Asn Val Pro Ala Ala Pro Gly Ala Ala Val Pro Ala Pro Gly			
	85 90 95			
	Ile Ser Ile Pro Ala Ala Pro Ser Ala Pro Gly Ser Ala Ile Pro Thr			
	100 105 110			

Pro Gly Thr Ala Ile Pro Val Pro Gly Ser Ala Thr Pro Val Pro Ala
 115 120 125
 Pro Gly Val Ser Ala Pro Gly Ala Ser Val Pro Ser Ile Pro Val Pro
 130 135 140
 Gly Ser Val Thr Pro Pro Ala Pro Gly Ile Ser Ala Pro Gly Gly Ala
 145 150 155 160
 Leu Pro Thr Pro Gly Ser Ala Pro Pro Thr Pro Gly Gly Ala Leu Pro
 165 170 175
 Thr Pro Gly Glu Ala Leu Pro Val Pro Gly Ala Pro Gly Ala Pro Gly
 180 185 190
 Ala Ser Gly Ile Pro Ser Pro Gly Leu Pro Thr Pro Gly Val Pro Thr
 195 200 205
 Pro Gly Ala Ser Leu Pro Val Pro Gly Ala Pro Asp Ala Pro Gly Thr
 210 215 220
 Pro Ser Ile Pro Ala Ala Pro Gly Ile Gln Ala Pro Gly Ile Pro Ala
 225 230 235 240
 Ala Pro Gly Ala Pro Ala Gln Ala Ala His Ala Lys Pro Val Phe
 245 250 255
 Gln Asp Ala Glu Lys Arg Pro Arg Thr Asp Glu Ala Gly Asn Ala Lys
 260 265 270
 Lys Glu Leu Pro Leu Arg Val Arg Leu Ala Gln Pro Ile Thr Arg Lys
 275 280 285
 Gln Trp Ala Met Thr Leu Gly Val Leu Val Leu Gly Ala Ile Val Val
 290 295 300
 Ala Ala Ile Ala Val Val Leu Ala Lys Trp Ala Phe Thr Thr Glu Trp
 305 310 315 320
 Leu Gln Asp Phe Val Glu Lys Tyr Pro Gly Lys Tyr Asp Asn Pro Glu
 325 330 335
 Gly Ala Pro Val Gly Ile Pro Thr Trp Leu Ser Trp Gln His Phe Phe
 340 345 350
 Asn Met Phe Phe Met Val Leu Ile Ile Lys Thr Gly Ile Glu Ile Asn
 355 360 365
 Arg Thr Arg Arg Pro Lys Gly Tyr Trp Thr Pro Lys Lys Gly Gly Lys
 370 375 380
 Lys Ile Ser Leu Thr Leu Trp Ile His Leu Val Leu Asp Leu Leu Trp
 385 390 395 400
 Ile Ile Asn Gly Ala Val Phe Ile Ile Leu Leu Phe Ala Thr Gly Gln
 405 410 415
 Trp Met Arg Ile Val Pro Thr Ser Trp Asp Val Phe Pro Asn Ala Leu
 420 425 430

Ser Ala Gly Leu Gln Tyr Val Ser Leu Asp Trp Pro Thr Glu Asn Gly
435 440 445

Trp Ala Asn Tyr Asn Ser Leu Gln Glu Leu Thr Tyr Phe Phe Thr Val
450 455 460

Phe Ile Ala Ala Pro Leu Ser Ile Val Ser Gly Phe Arg Met Ser Ser
465 470 475 480

Tyr Trp Pro Lys Asn Asn Ala Thr Met Asn Lys Leu Ile Pro Ile Gly
485 490 495

Phe Ala Arg Ala Leu His Met Pro Val Met Val Tyr Tyr Ile Val Phe
500 505 510

Ile Cys Ile His Val Phe Leu Val Leu Ala Thr Gly Ala Leu Arg Asn
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Phe Asn His Met Tyr Ala Gly Gln Asp Val Val Asn Trp Val Gly Phe
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Gly Trp Phe Val Ala Ser Leu
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<211> 1359

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(1359)

<223> FRXA02568

<400> 1227

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aca gca atc cct gtg cct gga agt gca act cct gtc cca gca cct ggc 96
Thr Ala Ile Pro Val Pro Gly Ser Ala Thr Pro Val Pro Ala Pro Gly
20 25 30

gtt agt gca cct ggc gca agc gtt cca agc att cca gta cca gga tct 144
Val Ser Ala Pro Gly Ala Ser Val Pro Ser Ile Pro Val Pro Gly Ser
35 40 45

gtc acc cca cct gca cca gga att tcc gca cct ggc ggt gca ctt ccg 192
Val Thr Pro Pro Ala Pro Gly Ile Ser Ala Pro Gly Gly Ala Leu Pro
50 55 60

act cct ggc agt gcg ccc cca aca cct ggc ggt gcc ctt ccg act cca 240
Thr Pro Gly Ser Ala Pro Pro Thr Pro Gly Gly Ala Leu Pro Thr Pro
65 70 75 80

ggt gag gca ctt ccc gtt ccc gga gca cct ggt gca ccc gga gca tcc 288
Gly Glu Ala Leu Pro Val Pro Gly Ala Pro Gly Ala Pro Gly Ala Ser
85 90 95

gga atc cca agt cct ggc ctt cca acc cca ggt gtc cca act ccc gga 336

Gly	Ile	Pro	Ser	Pro	Gly	Leu	Pro	Thr	Pro	Gly	Val	Pro	Thr	Pro	Gly	
			100					105					110			
gct	tcc	tta	cca	gtc	cca	gga	gca	cca	gac	gca	cct	gga	acc	cca	agc	384
Ala	Ser	Leu	Pro	Val	Pro	Gly	Ala	Pro	Asp	Ala	Pro	Gly	Thr	Pro	Ser	
		115					120					125				
att	ccc	gca	gct	ccc	ggc	att	caa	gca	cca	gga	att	cca	gca	gca	cca	432
Ile	Pro	Ala	Ala	Pro	Gly	Ile	Gln	Ala	Pro	Gly	Ile	Pro	Ala	Ala	Pro	
		130					135				140					
gga	gcc	cct	gcc	caa	gct	gct	gct	cac	gca	aag	cca	gta	ttc	caa	gat	480
Gly	Ala	Pro	Ala	Gln	Ala	Ala	Ala	His	Ala	Lys	Pro	Val	Phe	Gln	Asp	
		145			150					155					160	
gca	gag	aaa	cga	cct	cgc	aca	gat	gaa	gct	gga	aat	gcg	aag	aag	gaa	528
Ala	Glu	Lys	Arg	Pro	Arg	Thr	Asp	Glu	Ala	Lys	Ala	Asn	Ala	Lys	Lys	
			165						170					175		
ctg	ccg	ctg	aga	gtt	cgg	ttg	gcg	cag	cca	att	aca	cgt	aag	cag	tgg	576
Leu	Pro	Leu	Arg	Val	Arg	Leu	Ala	Gln	Pro	Ile	Thr	Arg	Lys	Gln	Trp	
			180					185					190			
gca	atg	act	ctt	ggc	gtc	ctg	gtt	ctc	gga	gca	att	gtc	gtg	gct	gca	624
Ala	Met	Thr	Leu	Gly	Val	Leu	Val	Leu	Gly	Ala	Ile	Val	Val	Ala	Ala	
			195				200					205				
atc	gcg	gtg	gtc	ctt	gcc	aaa	tgg	gcg	ttt	acc	acg	gag	tgg	ttg	cag	672
Ile	Ala	Val	Val	Leu	Ala	Lys	Trp	Ala	Phe	Thr	Thr	Glu	Trp	Leu	Gln	
		210				215					220					
gac	ttc	gtc	gag	aag	tat	ccg	ggc	aaa	tat	gac	aac	ccc	gaa	ggc	gcg	720
Asp	Phe	Val	Glu	Lys	Tyr	Pro	Gly	Lys	Tyr	Asp	Asn	Pro	Glu	Gly	Ala	
		225			230					235				240		
cca	gta	gga	att	cca	acg	tgg	ctg	agt	tgg	cag	cac	ttc	ttc	aac	atg	768
Pro	Val	Gly	Ile	Pro	Thr	Trp	Leu	Ser	Trp	Gln	His	Phe	Phe	Asn	Met	
				245					250					255		
ttc	ttc	atg	gtg	ttg	att	atc	aag	acg	ggc	att	gag	atc	aat	aga	acc	816
Phe	Phe	Met	Val	Leu	Ile	Ile	Lys	Thr	Gly	Ile	Glu	Ile	Asn	Arg	Thr	
		260					265					270				
cgc	agg	cca	aag	ggc	tat	tgg	acg	ccg	aaa	aag	ggc	gac	aag	aag	atc	864
Arg	Arg	Pro	Lys	Gly	Tyr	Trp	Thr	Pro	Lys	Lys	Gly	Gly	Lys	Lys	Ile	
		275				280					285					
tcc	ttg	acg	ttg	tgg	atc	cac	ctg	gtt	ttg	gat	ttg	ttg	tgg	atc	atc	912
Ser	Leu	Thr	Leu	Trp	Ile	His	Leu	Val	Leu	Asp	Leu	Leu	Trp	Ile	Ile	
		290				295					300					
aac	ggc	gcg	gtg	ttc	atc	att	ttg	ttg	ttc	gcg	acg	ggc	cag	tgg	atg	960
Asn	Gly	Ala	Val	Phe	Ile	Ile	Leu	Leu	Phe	Ala	Thr	Gly	Gln	Trp	Met	
		305			310					315				320		
cgc	att	gtt	cca	acc	agt	tgg	gat	gtg	ttc	ccg	aac	gcg	ctg	agt	gct	1008
Arg	Ile	Val	Pro	Thr	Ser	Trp	Asp	Val	Phe	Pro	Asn	Ala	Leu	Ser	Ala	
				325					330					335		
ggc	ttg	cag	tat	gtg	tcg	ttg	gat	tgg	ccg	act	gag	aat	ggc	tgg	gcg	1056
Gly	Leu	Gln	Tyr	Val	Ser	Leu	Asp	Trp	Pro	Thr	Glu	Asn	Gly	Trp	Ala	

340	345	350	
aat tac aac agt ttg cag gag ctg acg tac ttc ttc act gtc ttt att			1104
Asn Tyr Asn Ser Leu Gln Glu Leu Thr Tyr Phe Phe Thr Val Phe Ile			
355	360	365	
gcg gca ccg ttg tcg att gtg tct ggt ttc cgg atg tcg agt tac tgg			1152
Ala Ala Pro Leu Ser Ile Val Ser Gly Phe Arg Met Ser Ser Tyr Trp			
370	375	380	
cct aag aac aat gcg acg atg aat aag ttg atc ccc atc ggg ttt gct			1200
Pro Lys Asn Asn Ala Thr Met Asn Lys Leu Ile Pro Ile Gly Phe Ala			
385	390	395	400
cgt gcg ctg cac atg cca gtg atg gtg tat tac atc gtg ttc att tgt			1248
Arg Ala Leu His Met Pro Val Met Val Tyr Tyr Ile Val Phe Ile Cys			
405	410	415	
atc cac gtg ttc ttg gtg ttg gcg acc ggc gcg ttg cgc aat ttc aac			1296
Ile His Val Phe Leu Val Leu Ala Thr Gly Ala Leu Arg Asn Phe Asn			
420	425	430	
cat atg tat gca ggt caa gac gtt gtg aac tgg gtt ggt ttt ggt tgg			1344
His Met Tyr Ala Gly Gln Asp Val Val Asn Trp Val Gly Phe Gly Trp			
435	440	445	
ttc gtg gcg tcg ttg			1359
Phe Val Ala Ser Leu			
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Val Ser Ala Pro Gly Ala Ser Val Pro Ser Ile Pro Val Pro Gly Ser			
35	40	45	
Val Thr Pro Pro Ala Pro Gly Ile Ser Ala Pro Gly Gly Ala Leu Pro			
50	55	60	
Thr Pro Gly Ser Ala Pro Pro Thr Pro Gly Gly Ala Leu Pro Thr Pro			
65	70	75	80
Gly Glu Ala Leu Pro Val Pro Gly Ala Pro Gly Ala Pro Gly Ala Ser			
85	90	95	
Gly Ile Pro Ser Pro Gly Leu Pro Thr Pro Gly Val Pro Thr Pro Gly			
100	105	110	
Ala Ser Leu Pro Val Pro Gly Ala Pro Asp Ala Pro Gly Thr Pro Ser			
115	120	125	


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Ile Pro Ala Ala Pro Gly Ile Gln Ala Pro Gly Ile Pro Ala Ala Pro
130          135          140

Gly Ala Pro Ala Gln Ala Ala Ala His Ala Lys Pro Val Phe Gln Asp
145          150          155          160

Ala Glu Lys Arg Pro Arg Thr Asp Glu Ala Gly Asn Ala Lys Lys Glu
          165          170          175

Leu Pro Leu Arg Val Arg Leu Ala Gln Pro Ile Thr Arg Lys Gln Trp
          180          185          190

Ala Met Thr Leu Gly Val Leu Val Leu Gly Ala Ile Val Val Ala Ala
          195          200          205

Ile Ala Val Val Leu Ala Lys Trp Ala Phe Thr Thr Glu Trp Leu Gln
          210          215          220

Asp Phe Val Glu Lys Tyr Pro Gly Lys Tyr Asp Asn Pro Glu Gly Ala
225          230          235          240

Pro Val Gly Ile Pro Thr Trp Leu Ser Trp Gln His Phe Phe Asn Met
          245          250          255

Phe Phe Met Val Leu Ile Ile Lys Thr Gly Ile Glu Ile Asn Arg Thr
          260          265          270

Arg Arg Pro Lys Gly Tyr Trp Thr Pro Lys Lys Gly Gly Lys Lys Ile
          275          280          285

Ser Leu Thr Leu Trp Ile His Leu Val Leu Asp Leu Leu Trp Ile Ile
          290          295          300

Asn Gly Ala Val Phe Ile Ile Leu Leu Phe Ala Thr Gly Gln Trp Met
305          310          315          320

Arg Ile Val Pro Thr Ser Trp Asp Val Phe Pro Asn Ala Leu Ser Ala
          325          330          335

Gly Leu Gln Tyr Val Ser Leu Asp Trp Pro Thr Glu Asn Gly Trp Ala
          340          345          350

Asn Tyr Asn Ser Leu Gln Glu Leu Thr Tyr Phe Phe Thr Val Phe Ile
          355          360          365

Ala Ala Pro Leu Ser Ile Val Ser Gly Phe Arg Met Ser Ser Tyr Trp
          370          375          380

Pro Lys Asn Asn Ala Thr Met Asn Lys Leu Ile Pro Ile Gly Phe Ala
385          390          395          400

Arg Ala Leu His Met Pro Val Met Val Tyr Tyr Ile Val Phe Ile Cys
          405          410          415

Ile His Val Phe Leu Val Leu Ala Thr Gly Ala Leu Arg Asn Phe Asn
          420          425          430

His Met Tyr Ala Gly Gln Asp Val Val Asn Trp Val Gly Phe Gly Trp
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Phe Val Ala Ser Leu

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<211> 720

<212> DNA

<213> *Corynebacterium glutamicum*

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<221> CDS

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<223> RXN02593

<400> 1229

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aca acg atc acc gtt ttc tct ccc acc cac tcc ccc gca caa atc cgc 163
Thr Thr Ile Thr Val Phe Ser Pro Thr His Ser Pro Ala Gln Ile Arg
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gaa acc atc ctc agc gcc gcg aaa gaa gac gac gtg gac ttc ctc gga 211
Glu Thr Ile Leu Ser Ala Ala Lys Glu Asp Asp Val Asp Phe Leu Gly
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gtc ccc ttt acc cac ccc aga aac gtc acc atc gaa gtc gac gac gaa 259
Val Pro Phe Thr His Pro Arg Asn Val Thr Ile Glu Val Asp Asp Glu
                        40 45 50

ctg atc aac gac tgc tta ggc tgg ctc gac gac gtg gca ctc gcc tcc 307
Leu Ile Asn Asp Cys Leu Gly Trp Leu Asp Asp Val Ala Leu Ala Ser
                        55 60 65

ggc ctg ggc atc caa tac aac gac gaa gtg ctc cgc tac ggc gac gaa 355
Gly Leu Gly Ile Gln Tyr Asn Asp Glu Val Leu Arg Tyr Gly Asp Glu
                        70 75 80 85

gac att tcc ttt acc gtc caa acc aaa aat gac gat gac gcc cgc atc 403
Asp Ile Ser Phe Thr Val Gln Thr Lys Asn Asp Asp Ala Arg Ile
                        90 95 100

ggc gcc tcc cgc ctt gga ctc gag cac cag ttg aac gtc att gcc ggg 451
Gly Ala Ser Arg Leu Gly Leu Glu His Gln Leu Asn Val Ile Ala Gly
                        105 110 115

ggc tct gga gat tcc ggg gat tcc ggg gat tat ttg aag att gca cac 499
Gly Ser Gly Asp Ser Gly Asp Ser Gly Asp Tyr Leu Lys Ile Ala His
                        120 125 130

ttc gac cta gac aac ccc gcc gac gag tcc tcc tac atc ttc gcg cgc 547
Phe Asp Leu Asp Asn Pro Ala Asp Glu Ser Ser Tyr Ile Phe Ala Arg
                        135 140 145

agc ctc gca gaa gta gac ggc tgg acc cta gaa ttc ggc gtc gca gga 595
Ser Leu Ala Glu Val Asp Gly Trp Thr Leu Glu Phe Gly Val Ala Gly
                        150 155 160 165

gta aaa aac acc acc att gtt tcc tcc atc gac gat gcc atc acc acc 643

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Val Lys Asn Thr Thr Ile Val Ser Ser Ile Asp Asp Ala Ile Thr Thr
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att ttg cga tgg atg aac ggc gaa gac atc cgc gac ctc aac tgg acc 691
Ile Leu Arg Trp Met Asn Gly Glu Asp Ile Arg Asp Leu Asn Trp Thr
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<211> 199

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1230

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Val Asp Phe Leu Gly Val Pro Phe Thr His Pro Arg Asn Val Thr Ile
      35                      40                      45

Glu Val Asp Asp Glu Leu Ile Asn Asp Cys Leu Gly Trp Leu Asp Asp
      50                      55                      60

Val Ala Leu Ala Ser Gly Leu Gly Ile Gln Tyr Asn Asp Glu Val Leu
      65                      70                      75                      80

Arg Tyr Gly Asp Glu Asp Ile Ser Phe Thr Val Gln Thr Lys Asn Asp
      85                      90                      95

Asp Asp Ala Arg Ile Gly Ala Ser Arg Leu Gly Leu Glu His Gln Leu
      100                      105                      110

Asn Val Ile Ala Gly Gly Ser Gly Asp Ser Gly Asp Ser Gly Asp Tyr
      115                      120                      125

Leu Lys Ile Ala His Phe Asp Leu Asp Asn Pro Ala Asp Glu Ser Ser
      130                      135                      140

Tyr Ile Phe Ala Arg Ser Leu Ala Glu Val Asp Gly Trp Thr Leu Glu
      145                      150                      155                      160

Phe Gly Val Ala Gly Val Lys Asn Thr Thr Ile Val Ser Ser Ile Asp
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Asp Ala Ile Thr Thr Ile Leu Arg Trp Met Asn Gly Glu Asp Ile Arg
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Asp Leu Asn Trp Thr Arg Ala
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<211> 336

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(313)

<223> FRXA02593

<400> 1231

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Leu Lys Ile Ala His
1 5

ttc gac cta gac aac ccc gcc gac gag tcc tcc tac atc ttc gcg cgc 163
Phe Asp Leu Asp Asn Pro Ala Asp Glu Ser Ser Tyr Ile Phe Ala Arg
10 15 20

agc ctc gca gaa gta gac ggc tgg acc cta gaa ttc ggc gtc gca gga 211
Ser Leu Ala Glu Val Asp Gly Trp Thr Leu Glu Phe Gly Val Ala Gly
25 30 35

gta aaa aac acc acc att gtt tcc tcc atc gac gat gcc atc acc acc 259
Val Lys Asn Thr Thr Ile Val Ser Ser Ile Asp Asp Ala Ile Thr Thr
40 45 50

att ttg cga tgg atg aac ggc gaa gac atc cgc gac ctc aac tgg acc 307
Ile Leu Arg Trp Met Asn Gly Glu Asp Ile Arg Asp Leu Asn Trp Thr
55 60 65

cgc gca taaatggcct catttccgga gct 336
Arg Ala
70

<210> 1232

<211> 71

<212> PRT

<213> Corynebacterium glutamicum

<400> 1232

Leu Lys Ile Ala His Phe Asp Leu Asp Asn Pro Ala Asp Glu Ser Ser
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Tyr Ile Phe Ala Arg Ser Leu Ala Glu Val Asp Gly Trp Thr Leu Glu
20 25 30

Phe Gly Val Ala Gly Val Lys Asn Thr Thr Ile Val Ser Ser Ile Asp
35 40 45

Asp Ala Ile Thr Thr Ile Leu Arg Trp Met Asn Gly Glu Asp Ile Arg
50 55 60

Asp Leu Asn Trp Thr Arg Ala
65 70

<210> 1233

<211> 447

<212> DNA

<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(424)
<223> FRXA02594

<400> 1233
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catagggtta ttcagtctag ctgcttttaa acaagccata atg gaa gcc atg gcc 115
                                         Met Glu Ala Met Ala
                                         1                               5

aca acg atc acc gtt ttc tct ccc acc cac tcc ccc gca caa atc cgc 163
Thr Thr Ile Thr Val Phe Ser Pro Thr His Ser Pro Ala Gln Ile Arg
                        10                        15                        20

gaa acc atc ctc agc gcc gcg aaa gaa gac gac gtg gac ttc ctc gga 211
Glu Thr Ile Leu Ser Ala Ala Lys Glu Asp Asp Val Asp Phe Leu Gly
                        25                        30                        35

gtc ccc ttt acc cac ccc aga aac gtc acc atc gaa gtc gac gac gaa 259
Val Pro Phe Thr His Pro Arg Asn Val Thr Ile Glu Val Asp Asp Glu
                        40                        45                        50

ctg atc aac gac tgc tta ggc tgg ctc gac gac gtg gca ctc gcc tcc 307
Leu Ile Asn Asp Cys Leu Gly Trp Leu Asp Asp Val Ala Leu Ala Ser
                        55                        60                        65

ggc ctg ggc atc caa tac aac gac gaa gtg ctc cgc tac ggc gac gaa 355
Gly Leu Gly Ile Gln Tyr Asn Asp Glu Val Leu Arg Tyr Gly Asp Glu
                        70                        75                        80                        85

gac att tcc ttt acc gtc caa acc aaa aat gac gat gac gcc cgc atc 403
Asp Ile Ser Phe Thr Val Gln Thr Lys Asn Asp Asp Ala Arg Ile
                        90                        95                        100

ggc gcc tcc cgc ctt gga ctc tagcaccagt tgaacgtcat tgc 447
Gly Ala Ser Arg Leu Gly Leu
                        105

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<210> 1234
<211> 108
<212> PRT
<213> Corynebacterium glutamicum

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<400> 1234
Met Glu Ala Met Ala Thr Thr Ile Thr Val Phe Ser Pro Thr His Ser
  1                               5                               10                               15

Pro Ala Gln Ile Arg Glu Thr Ile Leu Ser Ala Ala Lys Glu Asp Asp
  20                               25                               30

Val Asp Phe Leu Gly Val Pro Phe Thr His Pro Arg Asn Val Thr Ile
  35                               40                               45

Glu Val Asp Asp Glu Leu Ile Asn Asp Cys Leu Gly Trp Leu Asp Asp
  50                               55                               60

Val Ala Leu Ala Ser Gly Leu Gly Ile Gln Tyr Asn Asp Glu Val Leu

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gaa cac ggc atc tcc gcc gaa aaa caa gac acc atc cgc tac gaa cta 547
Glu His Gly Ile Ser Ala Glu Lys Gln Asp Thr Ile Arg Tyr Glu Leu
135 140 145

gaa aaa ctc aac gac aac aca tcc cta tcc cga gcc tca ctc cgc aaa 595
 Glu Lys Leu Asn Asp Asn Thr Ser Leu Ser Arg Ala Ser Leu Arg Lys
 150 155 160 165

cta gca atg cag gaa gcc acc agc cga acc ccc gaa gac cta cgc aac 643
 Leu Ala Met Gln Glu Ala Thr Ser Arg Thr Pro Glu Asp Leu Arg Asn
 170 175 180

tgg acc cgc aac aaa gtt atc cgc ata aac ccc acc gcc aaa gac cca 691
 Trp Thr Arg Asn Lys Val Ile Arg Ile Asn Pro Thr Ala Lys Asp Pro
 185 190 195

ctc gcc gca gta aag aaa cgc tcc tta agc atc gga cgc caa gac cac 739
 Leu Ala Ala Val Lys Lys Arg Ser Leu Ser Ile Gly Arg Gln Asp His
 200 205 210

gac ggc gga gcc aaa gca tcc ctc tat tta gat gcc aaa ggt cta gcc 787
 Asp Gly Gly Ala Lys Ala Ser Leu Tyr Leu Asp Ala Lys Gly Leu Ala
 215 220 225

ctg ctc aaa tca ctg atg tct aaa gcc aag ccg ggg cat ttg ctt gaa 835
 Leu Leu Lys Ser Leu Met Ser Lys Ala Lys Pro Gly His Leu Leu Glu
 230 235 240 245

gac tct ttg gcg gag gat aaa cgt acg aaa ccg caa cgc caa tac gat 883
 Asp Ser Leu Ala Glu Asp Lys Arg Thr Lys Pro Gln Arg Gln Tyr Asp
 250 255 260

gcc ttc gcc gac atc ctc cac cgc gca cac agc gat ctc ctc ccc gca 931
 Ala Phe Ala Asp Ile Leu His Arg Ala His Ser Asp Leu Leu Pro Ala
 265 270 275

cga tcc gga gtg ggc acc atc ctc gtc tcc ctc tcc gcc aaa gac gta 979
 Arg Ser Gly Val Gly Thr Ile Leu Val Ser Leu Ser Ala Lys Asp Val
 280 285 290

aca aac ctc aaa gca tgc ggc ccc gac cac cgc tac ccc acc agc acc 1027
 Thr Asn Leu Lys Ala Ser Gly Pro Asp His Arg Tyr Pro Thr Ser Thr
 295 300 305

ggc ata aaa ctc aca ccg ctt gag atc ctg cga ctc ggt gca gcc aaa 1075
 Gly Ile Lys Leu Thr Pro Leu Glu Ile Leu Arg Leu Gly Ala Ala Lys
 310 315 320 325

tat gac ttc gtg acc gtc ctc gac tcc gaa tcc ggc cgt ccg ctg cac 1123
 Tyr Asp Phe Val Thr Val Leu Asp Ser Glu Ser Gly Arg Pro Leu His
 330 335 340

ctg gca cgc act caa cgc acc gcc agc ctg tat caa cgc cta gcc ctc 1171
 Leu Ala Arg Thr Gln Arg Thr Ala Ser Leu Tyr Gln Arg Leu Ala Leu
 345 350 355

ttc gcc tcc gaa ctc gtc tgc acc cgc gaa ggc tgc gac tcc ccc ttc 1219
 Phe Ala Ser Glu Leu Val Cys Thr Arg Glu Gly Cys Asp Ser Pro Phe
 360 365 370

gaa gac aac gaa ata cac cac atc aga tcc tgg cta gac ggc ggc ccc 1267
 Glu Asp Asn Glu Ile His His Ile Arg Ser Trp Leu Asp Gly Gly Pro
 375 380 385

aca gac ata gaa aac atc acc aac atc tgc ccc cac gac cac gga aac 1315
 Thr Asp Ile Glu Asn Ile Thr Asn Ile Cys Pro His Asp His Gly Asn
 390 395 400 405

aac aac gac caa cgc gac ggc aaa gac aac atg ggg cac atg aac ata 1363
 Asn Asn Asp Gln Arg Asp Gly Lys Asp Asn Met Gly His Met Asn Ile
 410 415 420

gat ccc aca acc ggg cgc gtc gga tat caa ccc gcc gac cgc cga aaa 1411
 Asp Pro Thr Thr Gly Arg Val Gly Tyr Gln Pro Ala Asp Arg Arg Lys
 425 430 435

ccc atg cgg ttt aac aac acc gca gcc gca gca gaa tca gga gga gca 1459
 Pro Met Arg Phe Asn Asn Thr Ala Ala Ala Ala Glu Ser Gly Gly Ala
 440 445 450

cag gcc agg acc taagttttta gcgcgccaaa aag 1494
 Gln Ala Arg Thr
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<210> 1236

<211> 457

<212> PRT

<213> Corynebacterium glutamicum

<400> 1236

Met Gln Glu Ile His Thr Ile Met Lys His Met Asp Ala Leu Ile Ala
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Asp Pro Ser Ala Ala Ala Phe Lys Ala Thr Leu Pro Phe Ala Glu Leu
 20 25 30

Leu Glu Lys Leu His Asn Lys Lys Ala Leu Phe Asp Ala Ala Leu Ala
 35 40 45

Lys Ser Ala Glu Arg Ala Asp Ala Gly Arg Ile Ile Gly Lys Thr Ser
 50 55 60

His Ile Asp Ala Leu Ala Tyr Leu Leu Asp Ile Ser Lys Ser Glu Ala
 65 70 75 80

Phe Arg Arg Thr Lys Arg Ala Glu Glu His Tyr Gly Asn Pro Ser Pro
 85 90 95

Glu Pro Ser Ser Glu Glu Leu Ala Lys Glu Thr Pro Glu Glu Lys Leu
 100 105 110

Ala Arg Glu Glu Lys Glu Lys Gln Asp Leu Ala Glu Gln Ala Glu Ala
 115 120 125

Asn Arg Ile Ala Arg Glu His Gly Ile Ser Ala Glu Lys Gln Asp Thr
 130 135 140

Ile Arg Tyr Glu Leu Glu Lys Leu Asn Asp Asn Thr Ser Leu Ser Arg
 145 150 155 160

Ala Ser Leu Arg Lys Leu Ala Met Gln Glu Ala Thr Ser Arg Thr Pro
 165 170 175

Glu Asp Leu Arg Arg Asn Trp Thr Arg Asn Lys Val Ile Arg Ile Asn Pro

180										185										190										
Thr	Ala	Lys	Asp	Pro	Leu	Ala	Ala	Val	Lys	Lys	Arg	Ser	Leu	Ser	Ile															
		195						200					205																	
Gly	Arg	Gln	Asp	His	Asp	Gly	Gly	Ala	Lys	Ala	Ser	Leu	Tyr	Leu	Asp															
		210				215					220																			
Ala	Lys	Gly	Leu	Ala	Leu	Leu	Lys	Ser	Leu	Met	Ser	Lys	Ala	Lys	Pro															
		225			230					235					240															
Gly	His	Leu	Leu	Glu	Asp	Ser	Leu	Ala	Glu	Asp	Lys	Arg	Thr	Lys	Pro															
			245						250					255																
Gln	Arg	Gln	Tyr	Asp	Ala	Phe	Ala	Asp	Ile	Leu	His	Arg	Ala	His	Ser															
			260					265					270																	
Asp	Leu	Leu	Pro	Ala	Arg	Ser	Gly	Val	Gly	Thr	Ile	Leu	Val	Ser	Leu															
		275					280					285																		
Ser	Ala	Lys	Asp	Val	Thr	Asn	Leu	Lys	Ala	Ser	Gly	Pro	Asp	His	Arg															
		290				295					300																			
Tyr	Pro	Thr	Ser	Thr	Gly	Ile	Lys	Leu	Thr	Pro	Leu	Glu	Ile	Leu	Arg															
		305			310					315				320																
Leu	Gly	Ala	Ala	Lys	Tyr	Asp	Phe	Val	Thr	Val	Leu	Asp	Ser	Glu	Ser															
			325					330					335																	
Gly	Arg	Pro	Leu	His	Leu	Ala	Arg	Thr	Gln	Arg	Thr	Ala	Ser	Leu	Tyr															
			340				345					350																		
Gln	Arg	Leu	Ala	Leu	Phe	Ala	Ser	Glu	Leu	Val	Cys	Thr	Arg	Glu	Gly															
		355				360					365																			
Cys	Asp	Ser	Pro	Phe	Glu	Asp	Asn	Glu	Ile	His	His	Ile	Arg	Ser	Trp															
		370			375					380																				
Leu	Asp	Gly	Gly	Pro	Thr	Asp	Ile	Glu	Asn	Ile	Thr	Asn	Ile	Cys	Pro															
		385			390				395					400																
His	Asp	His	Gly	Asn	Asn	Asn	Asp	Gln	Arg	Asp	Gly	Lys	Asp	Asn	Met															
			405					410						415																
Gly	His	Met	Asn	Ile	Asp	Pro	Thr	Thr	Gly	Arg	Val	Gly	Tyr	Gln	Pro															
		420					425						430																	
Ala	Asp	Arg	Arg	Lys	Pro	Met	Arg	Phe	Asn	Asn	Thr	Ala	Ala	Ala	Ala															
		435				440						445																		
Glu	Ser	Gly	Gly	Ala	Gln	Ala	Arg	Thr																						
		450			455																									

<210> 1237

<211> 1494

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1471)

<223> FRXA02606

<400> 1237

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cttcggtgtg gtgaaaaaca gaaaaggagg ggaaaaacaa atg  caa  gaa  atc  cac    115
               Met  Gln  Glu  Ile  His
               1                                5

acc  atc  atg  aaa  cac  atg  gac  gcg  ctc  atc  gcc  gac  cgg  tcc  gcc  gcc    163
Thr  Ile  Met  Lys  His  Met  Asp  Ala  Leu  Ile  Ala  Asp  Pro  Ser  Ala  Ala
               10                                15                                20

gca  ttc  aaa  gca  aca  ctc  ccc  ttc  gcc  gaa  ctc  ctc  gaa  aag  ctc  cac    211
Ala  Phe  Lys  Ala  Thr  Leu  Pro  Phe  Ala  Glu  Leu  Leu  Glu  Lys  Leu  His
               25                                30                                35

aac  aaa  aaa  gcg  ctt  ttc  gac  gcc  gcc  ctc  gcc  aaa  tcc  gcc  gag  cgc    259
Asn  Lys  Lys  Ala  Leu  Phe  Asp  Ala  Ala  Leu  Ala  Lys  Ser  Ala  Glu  Arg
               40                                45                                50

gcc  gat  gcc  gga  cgc  atc  atc  gga  aaa  acc  tcc  cac  atc  gat  gcc  ctc    307
Ala  Asp  Ala  Gly  Arg  Ile  Ile  Gly  Lys  Thr  Ser  His  Ile  Asp  Ala  Leu
               55                                60                                65

gcg  tac  ctt  ctc  gac  atc  tcc  aaa  tcc  gaa  gca  ttc  cga  cgc  aca  aaa    355
Ala  Tyr  Leu  Leu  Asp  Ile  Ser  Lys  Ser  Glu  Ala  Phe  Arg  Arg  Thr  Lys
               70                                75                                80                                85

cgc  gcc  gaa  gaa  cac  tac  gcc  aac  cca  agc  cgg  gaa  ccc  agt  tca  gaa    403
Arg  Ala  Glu  Glu  His  Tyr  Gly  Asn  Pro  Ser  Pro  Glu  Pro  Ser  Ser  Glu
               90                                95                                100

gaa  ctc  gcg  aaa  gaa  acc  ccc  gaa  gag  aag  cta  gcc  aga  gaa  gaa  aaa    451
Glu  Leu  Ala  Lys  Glu  Thr  Pro  Glu  Glu  Lys  Leu  Ala  Arg  Glu  Glu  Lys
               105                                110                                115

gag  aaa  caa  gac  cta  gcc  gaa  caa  gca  gaa  gcc  aac  cgc  atc  gcc  cgc    499
Glu  Lys  Glu  Asp  Leu  Ala  Glu  Gln  Ala  Glu  Ala  Asn  Arg  Ile  Ala  Arg
               120                                125                                130

gaa  cac  gcc  atc  tcc  gcc  gaa  aaa  caa  gac  acc  atc  cgc  tac  gaa  cta    547
Glu  His  Gly  Ile  Ser  Ala  Glu  Lys  Gln  Asp  Thr  Ile  Arg  Tyr  Glu  Leu
               135                                140                                145

gaa  aaa  ctc  aac  gac  aac  aca  tcc  cta  tcc  cga  gcc  tca  ctc  cgc  aaa    595
Glu  Lys  Leu  Asn  Asp  Asn  Thr  Ser  Leu  Ser  Arg  Ala  Ser  Leu  Arg  Lys
               150                                155                                160

cta  gca  atg  cag  gaa  gcc  acc  agc  cga  acc  ccc  gaa  gac  cta  cgc  aac    643
Leu  Ala  Met  Gln  Glu  Ala  Thr  Ser  Arg  Thr  Pro  Glu  Asp  Leu  Arg  Asn
               170                                175                                180

tgg  acc  cgc  aac  aaa  gtt  atc  cgc  ata  aac  ccc  acc  gcc  aaa  gac  cca    691
Trp  Thr  Arg  Asn  Lys  Val  Ile  Arg  Ile  Asn  Pro  Thr  Ala  Lys  Asp  Pro
               185                                190                                195

ctc  gcc  gca  gta  aag  aaa  cgc  tcc  tta  agc  atc  gga  cgc  caa  gac  cac    739
Leu  Ala  Ala  Val  Lys  Lys  Arg  Ser  Leu  Ser  Ile  Gly  Arg  Gln  Asp  His
               200                                205                                210

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gac ggc gga gcc aaa gca tcc ctc tat tta gat gcc aaa ggt cta gcc Asp Gly Gly Ala Lys Ala Ser Leu Tyr Leu Asp Ala Lys Gly Leu Ala 215 220	787
ctg ctc aaa tca ctg atg tct aaa gcc aag ccg ggg cat ttg ctt gaa Leu Leu Lys Ser Leu Met Ser Lys Ala Lys Pro Gly His Leu Leu Glu 230 235 240 245	835
gac tct ttg gcg gag gat aaa cgt acg aaa ccg caa cgc caa tac gat Asp Ser Leu Ala Glu Asp Lys Arg Thr Lys Pro Gln Arg Gln Tyr Asp 250 255 260	883
gcc ttc gcc gac atc ctc cac cgc gca cac agc gat ctc ctc ccc gca Ala Phe Ala Asp Ile Leu His Arg Ala His Ser Asp Leu Leu Pro Ala 265 270 275	931
cga tcc gga gtg ggc acc atc ctc gtc tcc ctc tcc gcc aaa gac gta Arg Ser Gly Val Gly Thr Ile Leu Val Ser Leu Ser Ala Lys Asp Val 280 285 290	979
aca aac ctc aaa gca tgc ggc ccc gac cac cgc tac ccc acc agc acc Thr Asn Leu Lys Ala Ser Gly Pro Asp His Arg Tyr Pro Thr Ser Thr 295 300 305	1027
ggc ata aaa ctc aca ccg ctt gag atc ctg cga cte ggt gca gcc aaa Gly Ile Lys Leu Thr Pro Leu Glu Ile Leu Arg Leu Gly Ala Ala Lys 310 315 320 325	1075
tat gac ttc gtg acc gtc ctc gac tcc gaa tcc ggc cgt ccg ctg cac Tyr Asp Phe Val Thr Val Leu Asp Ser Glu Ser Gly Arg Pro Leu His 330 335 340	1123
ctg gca cgc act caa cgc acc gcc agc ctg tat caa cgc cta gcc ctc Leu Ala Arg Thr Gln Arg Thr Ala Ser Leu Tyr Gln Arg Leu Ala Leu 345 350 355	1171
ttc gcc tcc gaa ctc gtc tgc acc cgc gaa ggc tgc gac tcc ccc ttc Phe Ala Ser Glu Leu Val Cys Thr Arg Glu Gly Cys Asp Ser Pro Phe 360 365 370	1219
gaa gac aac gaa ata cac cac atc aga tcc tgg cta gac ggc ggc ccc Glu Asp Asn Glu Ile His His Ile Arg Ser Trp Leu Asp Gly Gly Pro 375 380 385	1267
aca gac ata gaa aac atc acc aac atc tgc ccc cac gac cac gga aac Thr Asp Ile Glu Asn Ile Thr Asn Ile Cys Pro His Asp His Gly Asn 390 395 400 405	1315
aac aac gac caa cgc gac ggc aaa gac aac atg ggg cac atg aac ata Asn Asn Asp Gln Arg Asp Gly Lys Asp Asn Met Gly His Met Asn Ile 410 415 420	1363
gat ccc aca acc ggg cgc gtc gga tat caa ccc gcc gac cgc cga aaa Asp Pro Thr Thr Gly Arg Val Gly Tyr Gln Pro Ala Asp Arg Arg Lys 425 430 435	1411
ccc atg cgg ttt aac aac acc gca gcc gca gca gaa tca gga gga gca Pro Met Arg Phe Asn Asn Thr Ala Ala Ala Ala Glu Ser Gly Gly Ala 440 445 450	1459

cag gcc agg acc taagttttta ggcgcgcaaaa aag
 Gln Ala Arg Thr
 455

1494

<210> 1238
 <211> 457
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1238
 Met Gln Glu Ile His Thr Ile Met Lys His Met Asp Ala Leu Ile Ala
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 Asp Pro Ser Ala Ala Ala Phe Lys Ala Thr Leu Pro Phe Ala Glu Leu
 20 25 30
 Leu Glu Lys Leu His Asn Lys Lys Ala Leu Phe Asp Ala Ala Leu Ala
 35 40 45
 Lys Ser Ala Glu Arg Ala Asp Ala Gly Arg Ile Ile Gly Lys Thr Ser
 50 55 60
 His Ile Asp Ala Leu Ala Tyr Leu Leu Asp Ile Ser Lys Ser Glu Ala
 65 70 75 80
 Phe Arg Arg Thr Lys Arg Ala Glu Glu His Tyr Gly Asn Pro Ser Pro
 85 90 95
 Glu Pro Ser Ser Glu Glu Leu Ala Lys Glu Thr Pro Glu Glu Lys Leu
 100 105 110
 Ala Arg Glu Glu Lys Glu Lys Gln Asp Leu Ala Glu Gln Ala Glu Ala
 115 120 125
 Asn Arg Ile Ala Arg Glu His Gly Ile Ser Ala Glu Lys Gln Asp Thr
 130 135 140
 Ile Arg Tyr Glu Leu Glu Lys Leu Asn Asp Asn Thr Ser Leu Ser Arg
 145 150 155 160
 Ala Ser Leu Arg Lys Leu Ala Met Gln Glu Ala Thr Ser Arg Thr Pro
 165 170 175
 Glu Asp Leu Arg Asn Trp Thr Arg Asn Lys Val Ile Arg Ile Asn Pro
 180 185 190
 Thr Ala Lys Asp Pro Leu Ala Ala Val Lys Lys Arg Ser Leu Ser Ile
 195 200 205
 Gly Arg Gln Asp His Asp Gly Gly Ala Lys Ala Ser Leu Tyr Leu Asp
 210 215 220
 Ala Lys Gly Leu Ala Leu Leu Lys Ser Leu Met Ser Lys Ala Lys Pro
 225 230 235 240
 Gly His Leu Leu Glu Asp Ser Leu Ala Glu Asp Lys Arg Thr Lys Pro
 245 250 255
 Gln Arg Gln Tyr Asp Ala Phe Ala Asp Ile Leu His Arg Ala His Ser
 260 265 270

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Asp Leu Leu Pro Ala Arg Ser Gly Val Gly Thr Ile Leu Val Ser Leu
    275                      280                      285

Ser Ala Lys Asp Val Thr Asn Leu Lys Ala Ser Gly Pro Asp His Arg
    290                      295                      300

Tyr Pro Thr Ser Thr Gly Ile Lys Leu Thr Pro Leu Glu Ile Leu Arg
    305                      310                      315                      320

Leu Gly Ala Ala Lys Tyr Asp Phe Val Thr Val Leu Asp Ser Glu Ser
                325                      330                      335

Gly Arg Pro Leu His Leu Ala Arg Thr Gln Arg Thr Ala Ser Leu Tyr
    340                      345                      350

Gln Arg Leu Ala Leu Phe Ala Ser Glu Leu Val Cys Thr Arg Glu Gly
    355                      360                      365

Cys Asp Ser Pro Phe Glu Asp Asn Glu Ile His His Ile Arg Ser Trp
    370                      375                      380

Leu Asp Gly Gly Pro Thr Asp Ile Glu Asn Ile Thr Asn Ile Cys Pro
    385                      390                      395                      400

His Asp His Gly Asn Asn Asn Asp Gln Arg Asp Gly Lys Asp Asn Met
                405                      410                      415

Gly His Met Asn Ile Asp Pro Thr Thr Gly Arg Val Gly Tyr Gln Pro
                420                      425                      430

Ala Asp Arg Arg Lys Pro Met Arg Phe Asn Asn Thr Ala Ala Ala Ala
    435                      440                      445

Glu Ser Gly Gly Ala Gln Ala Arg Thr
    450                      455

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<210> 1239

<211> 1050

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1027)

<223> RXN02610

<400> 1239

ccagctcatc gtgcaggac gcaccagcgt gaaggaagat caagcagcgg aaatttctac 60

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gctgctgaag gaatctgcgg atcggacgta ttgttaaccg atg agg aaa acc atc    115
                Met Arg Lys Thr Ile
                1                      5

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acc gtt att gct gta ttg atc gtc ctc gcc tta atc ggc gtg ggc atc    163
Thr Val Ile Ala Val Leu Ile Val Leu Ala Leu Ile Gly Val Gly Ile
                10                      15                      20

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gtg cag tat gtg aac aca tcc gat gac tca gat ttc att ggc cag cct    211
Val Gln Tyr Val Asn Thr Ser Asp Asp Ser Asp Phe Ile Gly Gln Pro

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	ggc gag cca acc ggt acc gaa acc acg gaa cca ccg gtt caa cct gat			259
	Gly Glu Pro Thr Gly Thr Glu Thr Glu Pro Pro Val Gln Pro Asp			
	40	45	50	
	tgg tgc cct gcg gta gaa gtc att gcc gcg ccg ggt acg tgg gag tgc			307
	Trp Cys Pro Ala Val Glu Val Ile Ala Ala Pro Gly Thr Trp Glu Ser			
	55	60	65	
	gct gct aat gat gat ccg atc aac ccg acc gct aat ccg ctg tca ttc			355
	Ala Ala Asn Asp Asp Pro Ile Asn Pro Thr Ala Asn Pro Leu Ser Phe			
	70	75	80	85
	atg ttg agc atc act cag cca ctg cag gag cgt tat tct gcg gat gac			403
	Met Leu Ser Ile Thr Gln Pro Leu Gln Glu Arg Tyr Ser Ala Asp Asp			
	90	95	100	
	gtc aag gtg tgg acg ctg ccg tac act gcg cag ttc cgc aac atc aac			451
	Val Lys Val Trp Thr Leu Pro Tyr Thr Ala Gln Phe Arg Asn Ile Asn			
	105	110	115	
	tgc caa aat gag atg tcc tat gat gat tgc cgc aat gaa gcc acc gcg			499
	Ser Gln Asn Glu Met Ser Tyr Asp Asp Ser Arg Asn Glu Gly Thr Ala			
	120	125	130	
	aag atg aat gag gaa ctg atc aac act cac aat gag tgc cct gcc acg			547
	Lys Met Asn Glu Glu Leu Ile Asn Thr His Asn Glu Cys Pro Ala Thr			
	135	140	145	
	gag ttc atc atc gtt ggt ttc tcc cag ggt gcg gtc att gcg gcc gat			595
	Glu Phe Ile Ile Val Gly Phe Ser Gln Gly Ala Val Ile Ala Gly Asp			
	150	155	160	165
	gtg gct gct cag atc ggt tca gag caa ggt gtt att cca gct gac agc			643
	Val Ala Ala Gln Ile Gly Ser Glu Gln Gly Val Ile Pro Ala Asp Ser			
	170	175	180	
	gtc agg ggt gtc gcc ctg atc gct gac ggt cgc cgg gag cct ggt gtg			691
	Val Arg Gly Val Ala Leu Ile Ala Asp Gly Arg Arg Glu Pro Gly Val			
	185	190	195	
	ggc cag ttc cca gcc acg ttt gtg gat gcc atc gcc gcg gag gtt act			739
	Gly Gln Phe Pro Gly Thr Phe Val Asp Gly Ile Gly Ala Glu Val Thr			
	200	205	210	
	ctg cag cct ttg aac ttg ctg gtg cag ccg att gtt ccg gcc gca acc			787
	Leu Gln Pro Leu Asn Leu Leu Val Gln Pro Ile Val Pro Gly Ala Thr			
	215	220	225	
	atg cgt gcc ggg cgc gcg gcc ggt ttc ggt gtg ctc aac gac ccg gtg			835
	Met Arg Gly Gly Arg Ala Gly Gly Phe Gly Val Leu Asn Asp Arg Val			
	230	235	240	245
	cag gat att tgt gct cca aat gat gcg atc tgt gat gct ccg gtg aat			883
	Gln Asp Ile Cys Ala Pro Asn Asp Ala Ile Cys Asp Ala Pro Val Asn			
	250	255	260	
	gtc gcc aac gcc ctt gat cgt gcg ttg gcc atg gtc tcc gcc aac ggt			931
	Val Gly Asn Ala Leu Asp Arg Ala Leu Ala Met Val Ser Ala Asn Gly			
	265	270	275	

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gtg cac gcg ctc tac gcc acc aat ccg gat gtt ttc cca ggc aca acc 979
Val His Ala Leu Tyr Ala Thr Asn Pro Asp Val Phe Pro Gly Thr Thr
      280                      285                      290

acc aat gcg tgg gtt gtg gat tgg gcg acc aac ctc atc gac aac gga 1027
Thr Asn Ala Trp Val Val Asp Trp Ala Thr Asn Leu Ile Asp Asn Gly
      295                      300                      305

taaagctttt tcgcttttcg acg 1050

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<210> 1240

<211> 309

<212> FRT

<213> *Corynebacterium glutamicum*

<400> 1240

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Met Arg Lys Thr Ile Thr Val Ile Ala Val Leu Ile Val Leu Ala Leu
 1          5          10          15

Ile Gly Val Gly Ile Val Gln Tyr Val Asn Thr Ser Asp Asp Ser Asp
      20          25          30

Phe Ile Gly Gln Pro Gly Glu Pro Thr Gly Thr Glu Thr Thr Glu Pro
      35          40          45

Pro Val Gln Pro Asp Trp Cys Pro Ala Val Glu Val Ile Ala Ala Pro
      50          55          60

Gly Thr Trp Glu Ser Ala Ala Asn Asp Asp Pro Ile Asn Pro Thr Ala
      65          70          75          80

Asn Pro Leu Ser Phe Met Leu Ser Ile Thr Gln Pro Leu Gln Glu Arg
      85          90          95

Tyr Ser Ala Asp Asp Val Lys Val Trp Thr Leu Pro Tyr Thr Ala Gln
      100          105          110

Phe Arg Asn Ile Asn Ser Gln Asn Glu Met Ser Tyr Asp Asp Ser Arg
      115          120          125

Asn Glu Gly Thr Ala Lys Met Asn Glu Glu Leu Ile Asn Thr His Asn
      130          135          140

Glu Cys Pro Ala Thr Glu Phe Ile Ile Val Gly Phe Ser Gln Gly Ala
      145          150          155          160

Val Ile Ala Gly Asp Val Ala Ala Gln Ile Gly Ser Glu Gln Gly Val
      165          170          175

Ile Pro Ala Asp Ser Val Arg Gly Val Ala Leu Ile Ala Asp Gly Arg
      180          185          190

Arg Glu Pro Gly Val Gly Gln Phe Pro Gly Thr Phe Val Asp Gly Ile
      195          200          205

Gly Ala Glu Val Thr Leu Gln Pro Leu Asn Leu Leu Val Gln Pro Ile
      210          215          220

Val Pro Gly Ala Thr Met Arg Gly Gly Arg Ala Gly Gly Phe Gly Val

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<210> 1241
<211> 1050
<212> DNA
<213> Corynebacterium glutamicum
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[illegible]

105	110	115	
tcg caa aat gag atg tcc tat	gat gat tcg cgc aat gaa ggc acc gcg	499	
Ser Gln Asn Glu Met Ser Tyr	Asp Asp Ser Arg Asn Glu Gly Thr Ala		
120	125 130		
aag atg aat gag gaa ctg atc	aac act cac aat gag tgc cct gcc acg	547	
Lys Met Asn Glu Glu Leu	Asn Thr His Asn Glu Cys Pro Ala Thr		
135	140 145		
gag ttc atc atc gtt ggt ttc	tcc cag ggt gcg gtc att gcg ggc gat	595	
Glu Phe Ile Ile Val Gly Phe	Ser Gln Gly Ala Val Ile Ala Gly Asp		
150	155 160		
gtg gct gct cag atc ggt tca	gag caa ggt gtt att cca gct gac agc	643	
Val Ala Ala Gln Ile Gly Ser	Glu Gln Gly Val Ile Pro Ala Asp Ser		
170	175 180		
gtc agg ggt gtc gcc ctg atc	gct gac ggt cgc cgg gag cct ggt gtg	691	
Val Arg Gly Val Ala Leu Ile	Ala Asp Gly Arg Arg Glu Pro Gly Val		
185	190 195		
ggc cag ttc cca ggc acg ttt	gtg gat ggc atc ggc gcg gag gtt act	739	
Gly Gln Phe Pro Gly Thr Phe	Val Asp Gly Ile Gly Ala Glu Val Thr		
200	205 210		
ctg cag cct ttg aac ttg ctg	gtg cag ccg att gtt ccg gcc gca acc	787	
Leu Gln Pro Leu Asn Leu Leu	Val Gln Pro Ile Val Pro Gly Ala Thr		
215	220 225		
atg cgt ggc ggg cgc gcg ggc	ggt ttc ggt gtg ctc aac gac cgg gtg	835	
Met Arg Gly Gly Arg Ala Gly	Gly Phe Gly Val Leu Asn Asp Arg Val		
230	235 240		
cag gat att tgt gct cca aat	gat gcg atc tgt gat gct ccg gtg aat	883	
Gln Asp Ile Cys Ala Pro	Asn Asp Ala Ile Cys Asp Ala Pro Val Asn		
250	255 260		
gtc ggc aac gcc ctt gat cgt	gcg ttg gcc atg gtc tcc gcc aac ggt	931	
Val Gly Asn Ala Leu Asp Arg	Ala Leu Ala Met Val Ser Ala Asn Gly		
265	270 275		
gtg cac gcg ctc tac gcc acc	aat ccg gat gtt ttc cca ggc aca acc	979	
Val His Ala Leu Tyr Ala Thr	Asn Pro Asp Val Phe Pro Gly Thr Thr		
280	285 290		
acc aat gcg tgg gtt gtg gat	tgg gcg acc aac ctc atc gac aac gga	1027	
Thr Asn Ala Trp Val Val Asp	Trp Ala Thr Asn Leu Ile Asp Asn Gly		
295	300 305		
taaagctttt tcgcttttcg acg		1050	

<210> 1242

<211> 309

<212> PRT

<213> Corynebacterium glutamicum

<400> 1242

Met Arg Lys Thr Ile Thr Val Ile Ala Val Leu Ile Val Leu Ala Leu

1

5

10

15

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Ile Gly Val Gly Ile Val Gln Tyr Val Asn Thr Ser Asp Asp Ser Asp
      20                      25                      30

Phe Ile Gly Gln Pro Gly Glu Pro Thr Gly Thr Glu Thr Thr Glu Pro
      35                      40                      45

Pro Val Gln Pro Asp Trp Cys Pro Ala Val Glu Val Ile Ala Ala Pro
      50                      55                      60

Gly Thr Trp Glu Ser Ala Ala Asn Asp Asp Pro Ile Asn Pro Thr Ala
      65                      70                      75                      80

Asn Pro Leu Ser Phe Met Leu Ser Ile Thr Gln Pro Leu Gln Glu Arg
      85                      90                      95

Tyr Ser Ala Asp Asp Val Lys Val Trp Thr Leu Pro Tyr Thr Ala Gln
      100                     105                     110

Phe Arg Asn Ile Asn Ser Gln Asn Glu Met Ser Tyr Asp Asp Ser Arg
      115                     120                     125

Asn Glu Gly Thr Ala Lys Met Asn Glu Glu Leu Ile Asn Thr His Asn
      130                     135                     140

Glu Cys Pro Ala Thr Glu Phe Ile Ile Val Gly Phe Ser Gln Gly Ala
      145                     150                     155                     160

Val Ile Ala Gly Asp Val Ala Ala Gln Ile Gly Ser Glu Gln Gly Val
      165                     170                     175

Ile Pro Ala Asp Ser Val Arg Gly Val Ala Leu Ile Ala Asp Gly Arg
      180                     185                     190

Arg Glu Pro Gly Val Gly Gln Phe Pro Gly Thr Phe Val Asp Gly Ile
      195                     200                     205

Gly Ala Glu Val Thr Leu Gln Pro Leu Asn Leu Leu Val Gln Pro Ile
      210                     215                     220

Val Pro Gly Ala Thr Met Arg Gly Gly Arg Ala Gly Gly Phe Gly Val
      225                     230                     235                     240

Leu Asn Asp Arg Val Gln Asp Ile Cys Ala Pro Asn Asp Ala Ile Cys
      245                     250                     255

Asp Ala Pro Val Asn Val Gly Asn Ala Leu Asp Arg Ala Leu Ala Met
      260                     265                     270

Val Ser Ala Asn Gly Val His Ala Leu Tyr Ala Thr Asn Pro Asp Val
      275                     280                     285

Phe Pro Gly Thr Thr Thr Asn Ala Trp Val Val Asp Trp Ala Thr Asn
      290                     295                     300

Leu Ile Asp Asn Gly
305

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<210> 1243

<211> 1419

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1396)

<223> RXN02624

<400> 1243

accgcggtcag atccgacgtc gccggccaaa accgcgaagca cctgcgcgaaa cgccacagaa 60

ggcagctcag caatcaaaagt tgctgcgttt ccttccaacc gtg ctg att ccg cat 115
 Val Leu Ile Pro His
 1 5

ggc gtg gcg gtg ctt ttg gtt att att ctc gcc gta gcc tcc cta atg 163
 Gly Val Ala Val Leu Leu Val Ile Ile Leu Ala Val Ala Ser Leu Met
 10 15 20

ttc acc aat tct tca atg gtg aat ctt tcg gca acg att gca cag ctg 211
 Phe Thr Asn Ser Ser Met Val Asn Leu Ser Ala Thr Ile Ala Gln Leu
 25 30 35

tgg ctt tcc cta aat ctc ggt gcg gtg gac gcc agt ggg gaa gtg atc 259
 Trp Leu Ser Leu Asn Leu Gly Ala Val Asp Gly Ser Gly Glu Val Ile
 40 45 50

tca gta ctg ccc acg ctt ccc gcc ttt ata ttc ctc tgg gcc atc gcc 307
 Ser Val Leu Pro Thr Leu Pro Gly Phe Ile Phe Leu Trp Ala Ile Ala
 55 60 65

gcg cgc atc cac cgc gca gtc aaa gat cgt gtc agc atc gcc gac tta 355
 Ala Arg Ile His Arg Ala Val Lys Asp Arg Val Ser Ile Ala Asp Leu
 70 75 80 85

ggc gtc ctc gca gca ctc gtc ctc gcc atc ccg ctt gcg ctc acc gcc 403
 Gly Val Leu Ala Ala Leu Val Leu Gly Ile Pro Leu Ala Leu Thr Ala
 90 95 100

atc gca gcg ttc atg ctt ttc gac gcc tcc agc gtc ctc aac gtc gag 451
 Ile Ala Ala Phe Met Leu Phe Asp Ala Ser Ser Val Leu Asn Val Glu
 105 110 115

gtc ccg cca atc acg cgc ctc cta cgc gtg atg ttg ttc cac ctc agc 499
 Val Pro Pro Ile Thr Arg Leu Leu Arg Val Met Leu Phe His Leu Ser
 120 125 130

gcc ctc ttc ctc gcc atg ggg cca cgc ctg tgg cag gcg ttg gcg cgc 547
 Ala Leu Phe Leu Gly Met Gly Pro Arg Leu Trp Gln Ala Leu Ala Arg
 135 140 145

cgc tac ggt gct cca gaa tgg ctt atc gac gcc atc acc caa gct ttc 595
 Arg Tyr Gly Ala Pro Glu Trp Leu Ile Asp Ala Ile Thr Gln Ala Phe
 150 155 160 165

cgc ttc ctc atc gca ttt gga aca gtc tcc ttg gtt tcc gtg ctc gtg 643
 Arg Phe Leu Ile Ala Phe Gly Thr Val Ser Leu Val Ser Val Leu Val
 170 175 180

atg acc gcg atc aac cac agt gca ttc acc gcg acc atg cag ggt tac 691
 Met Thr Ala Ile Asn His Ser Ala Phe Thr Ala Thr Met Gln Gly Tyr

185										190										195										
gac Asp	gac Asp	tcc Ser	gcc Ala	tct Ser	gtt Val	gtg Val	gcc Ala	ttg Leu	atc Ile	gtc Val	ctg Leu	agc Ser	att Ile	ctg Leu	tat Tyr	739														
ctg Leu	ccc Pro	aac Asn	atg Met	atg Met	atc Ile	ttt Phe	gcg Ala	atg Met	ggc Gly	aat Asn	ctg Leu	atc Ile	ggc Gly	tca Ser	ccc Pro	787														
ctt 230	tac Tyr	ttc Phe	ggt Gly	gac Asp	gcc 235	tcc Ser	atc Ile	agc Ser	gtc Val	ttc Phe	agc Ser	gtg Val	cat His	tcc Val	ggt 245	835														
cca Pro	ttg Leu	cca Pro	cgc Pro	ctt Leu	ccc 250	atc Ile	ctc Leu	gca Ala	gct Ala	ctc Leu	ccc Pro	agc Ser	gaa Glu	gcc Ala	ctc Leu	883														
tca Ser	tggt Trp	gca Ala	gtg Val	gcc Ala	tta Leu	ctg Leu	gtc Val	atc Ile	cct Pro	gca Ala	att Ile	att Ile	gcc Ala	acc Thr	tggt Trp	931														
gtc Val	tggt Cys	gtg Val	aga Arg	aac Asn	ccc Pro	atg Met	cgc Arg	ctt Leu	gcc Ala	gtg Val	aac Asn	aca Thr	aca Thr	gca Ala	gca Ala	979														
gtc Val	att Ile	tca Ser	gca Ala	ctg Leu	tgt Cys	ttc Phe	ctc Leu	gtc Val	ctg Leu	gca Ala	gtt Val	ttc Phe	gcc Ala	ggc Gly	gga Gly	1027														
acc 310	ttg Leu	ggc Gly	gta Val	tac Tyr	aac Asn	tac Tyr	gtc Val	gga Gly	ctc Leu	aac Asn	ctc Leu	ctg Leu	gcg Ala	tca Ser	ggt Val	1075														
ggc Gly	cta Leu	ggt Val	ttc Phe	gtc Val	tat Tyr	ttc Phe	gcc Ala	ctc Leu	ggt Val	gga Gly	ctc Leu	ctc Leu	atc Ile	gcc Ala	gga Gly	1123														
atc Ile	gac Asp	aag Lys	ctg Leu	cgc Arg	aac Asn	cct Pro	gta Val	gaa Glu	ggt Val	aag Lys	tct Ser	gtt Val	aag Lys	gct Ala	gtg Val	1171														
gct Ala	ggt Val	gtg Val	gag Glu	ccc Pro	gag Glu	cct Pro	gaa Glu	gaa Glu	ggt Val	gaa Glu	gag Glu	gac Asp	gaa Glu	gag Glu	gag Glu	1219														
cat His	ggt Val	gaa Glu	gaa Glu	gaa Glu	gta Val	gat Asp	gag Glu	gag Glu	gaa Glu	gag Glu	gaa Glu	ggt Val	gag Glu	gaa Glu	ggg Gly	1267														
gta Val	gaa Glu	gag Glu	gtc Val	gaa Glu	gaa Glu	gac Asp	gac Asp	gca Ala	gag Glu	gat Asp	cct Pro	gaa Glu	gag Glu	aat Asn	cct Pro	1315														
gaa Glu	gag Glu	gaa Glu	gaa Glu	tcc Ser	gac Asp	gaa Glu	gaa Glu	att Ile	gag Glu	aca Thr	gaa Glu	act Thr	gag Glu	gct Ala	gaa Glu	1363														
gaa Glu	acc Thr	aat Asn	gat Asp	ggt Gly	tcc Ser	gag Glu	gcc Ala	gaa Ala	gac Asp	cgt Arg	taacatactct	gttg	gtgaatt	1416																

ctg

1419

<210> 1244

<211> 432

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1244

Val Leu Ile Pro His Gly Val Ala Val Leu Leu Val Ile Ile Leu Ala
 1 5 10 15

Val Ala Ser Leu Met Phe Thr Asn Ser Ser Met Val Asn Leu Ser Ala
 20 25 30

Thr Ile Ala Gln Leu Trp Leu Ser Leu Asn Leu Gly Ala Val Asp Gly
 35 40 45

Ser Gly Glu Val Ile Ser Val Leu Pro Thr Leu Pro Gly Phe Ile Phe
 50 55 60

Leu Trp Ala Ile Ala Ala Arg Ile His Arg Ala Val Lys Asp Arg Val
 65 70 75 80

Ser Ile Ala Asp Leu Gly Val Leu Ala Ala Leu Val Leu Gly Ile Pro
 85 90 95

Leu Ala Leu Thr Ala Ile Ala Ala Phe Met Leu Phe Asp Ala Ser Ser
 100 105 110

Val Leu Asn Val Glu Val Pro Pro Ile Thr Arg Leu Leu Arg Val Met
 115 120 125

Leu Phe His Leu Ser Ala Leu Phe Leu Gly Met Gly Pro Arg Leu Trp
 130 135 140

Gln Ala Leu Ala Arg Arg Tyr Gly Ala Pro Glu Trp Leu Ile Asp Ala
 145 150 155 160

Ile Thr Gln Ala Phe Arg Phe Leu Ile Ala Phe Gly Thr Val Ser Leu
 165 170 175

Val Ser Val Leu Val Met Thr Ala Ile Asn His Ser Ala Phe Thr Ala
 180 185 190

Thr Met Gln Gly Tyr Asp Asp Ser Ala Ser Val Val Ala Leu Ile Val
 195 200 205

Leu Ser Ile Leu Tyr Leu Pro Asn Met Met Ile Phe Ala Met Gly Asn
 210 215 220

Leu Ile Gly Ser Pro Leu Tyr Phe Gly Asp Ala Ser Ile Ser Val Phe
 225 230 235 240

Ser Val His Ser Val Pro Leu Pro Pro Leu Pro Ile Leu Ala Ala Leu
 245 250 255

Pro Ser Glu Ala Leu Ser Trp Ala Val Ala Leu Leu Val Ile Pro Ala
 260 265 270

Ile	Ile	Ala	Thr	Trp	Val	Cys	Val	Arg	Asn	Pro	Met	Arg	Leu	Ala	Val
275							280					285			
Asn	Thr	Thr	Ala	Ala	Val	Ile	Ser	Ala	Leu	Cys	Phe	Leu	Val	Leu	Ala
290						295				300					
Val	Phe	Ala	Gly	Gly	Thr	Leu	Gly	Val	Tyr	Asn	Tyr	Val	Gly	Leu	Asn
305					310					315					320
Leu	Leu	Ala	Ser	Val	Gly	Leu	Val	Phe	Val	Tyr	Phe	Ala	Leu	Val	Gly
				325					330					335	
Leu	Leu	Ile	Ala	Gly	Ile	Asp	Lys	Leu	Arg	Asn	Pro	Val	Glu	Val	Lys
		340						345					350		
Ser	Val	Lys	Ala	Val	Ala	Val	Val	Glu	Pro	Glu	Pro	Glu	Glu	Val	Glu
		355					360					365			
Glu	Asp	Glu	Glu	Glu	His	Val	Glu	Glu	Glu	Val	Asp	Glu	Glu	Glu	Glu
	370					375					380				
Glu	Val	Glu	Glu	Gly	Val	Glu	Glu	Val	Glu	Glu	Asp	Asp	Ala	Glu	Asp
385					390					395					400
Pro	Glu	Glu	Asn	Pro	Glu	Glu	Glu	Glu	Ser	Asp	Glu	Glu	Ile	Glu	Thr
			405						410				415		
Glu	Thr	Glu	Ala	Glu	Glu	Thr	Asn	Asp	Gly	Ser	Glu	Ala	Glu	Asp	Arg
		420						425					430		

<210> 1245

<211> 737

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

 $\langle 222 \rangle \quad (1) \dots (714)$

<223> FRXA02624

<400> 1245

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Gln Gly Tyr Asp Asp Ser Ala Ser Val Val Ala Leu Ile Val Leu Ser
1 5 10 15

att ctg tat ctg ccc aac atg atg atc ttt gcg atg ggc aat ctg atc 96
Ile Leu Tyr Leu Pro Asn Met Met Ile Phe Ala Met Gly Asn Leu Ile
20 25 30

ggc tca ccc ctt tac ttc ggt gac gcc tcc atc agc gtc ttc agc gtg 144
Gly Ser Pro Leu Tyr Phe Gly Asp Ala Ser Ile Ser Val Phe Ser Val
35 40 45

cat tcc gtt cca ttg cca cgg ctt ccc atc ctc gca gct ctc ccc agc 192
His Ser Val Pro Leu Pro Pro Leu Pro Ile Leu Ala Ala Leu Pro Ser
50 55 60

gaa gcc ctc tca tgg gca gtg gcc tta ctg gtc atc cct gca att att 240
 Glu Ala Leu Ser Trp Ala Val Ala Leu Leu Val Ile Pro Ala Ile Ile 80
 65 70 75

 gcc acc tgg gtc tgc gtg aga aac ccc atg cgc ctt gcc gtg aac aca 288
 Ala Thr Trp Val Cys Val Arg Asn Pro Met Arg Leu Ala Val Asn Thr 95
 85 90

 aca gca gca gtc att tca gca ctg tgt ttc ctc gtc ctg gca gtt ttc 336
 Thr Ala Ala Val Ile Ser Ala Leu Cys Phe Leu Val Leu Ala Val Phe 110
 100 105

 gcc ggc gga acc ttg ggc gta tac aac tac gtc gga ctc aac ctc ctg 384
 Ala Gly Gly Thr Leu Gly Val Tyr Asn Tyr Val Gly Leu Asn Leu Leu 125
 115 120

 gcg tca gtt ggc cta gtt ttc gtc tat ttc gcc ctc gtt gga ctc ctc 432
 Ala Ser Val Gly Leu Val Phe Val Tyr Phe Ala Leu Val Gly Leu Leu 140
 130 135

 atc gcc gga atc gac aag ctg cgc aac cct gta gaa gtt aag tct gtt 480
 Ile Ala Gly Ile Asp Lys Leu Arg Asn Pro Val Glu Val Lys Ser Val 160
 145 150 155

 aag gct gtg gct gtt gtg gag ccc gag cct gaa gaa gtt gaa gag gac 528
 Lys Ala Val Ala Val Val Glu Pro Glu Glu Glu Val Glu Glu Asp 175
 165 170

 gaa gag gag cat gtt gaa gaa gaa gta gat gag gag gaa gag gaa gtt 576
 Glu Glu Glu His Val Glu Glu Glu Val Asp Glu Glu Glu Glu Val 190
 180 185

 gag gaa ggg gta gaa gag gtc gaa gaa gac gac gca gag gat cct gaa 624
 Glu Glu Gly Val Glu Glu Val Glu Glu Asp Asp Ala Glu Asp Pro Glu 205
 195 200

 gag aat cct gaa gag gaa gaa tcc gac gaa gaa att gag aca gaa act 672
 Glu Asn Pro Glu Glu Glu Ser Asp Glu Glu Ile Glu Thr Glu Thr 220
 210 215

 gag gct gaa gaa acc aat gat ggt tcc gag gcc gaa gac cgt 714
 Glu Ala Glu Glu Thr Asn Asp Gly Ser Glu Ala Glu Asp Arg 235
 225 230

 taacatatct gttgtgaatt ctg 737

<210> 1246

<211> 238

<212> PR7

<213> Corynebacterium glutamicum

<400> 1246

Gln Gly Tyr Asp Asp Ser Ala Ser Val Val Ala Leu Ile Val Leu Ser
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Ile Leu Tyr Leu Pro Asn Met Met Ile Phe Ala Met Gly Asn Leu Ile
 20 25 30

Gly Ser Pro Leu Tyr Phe Gly Asp Ala Ser Ile Ser Val Phe Ser Val
 35 40 45

His Ser Val Pro Leu Pro Pro Leu Pro Ile Leu Ala Ala Leu Pro Ser
50 55 60

Glu Ala Leu Ser Trp Ala Val Ala Leu Leu Val Ile Pro Ala Ile Ile
65 70 75 80

Ala Thr Trp Val Cys Val Arg Asn Pro Met Arg Leu Ala Val Asn Thr
85 90 95

Thr Ala Ala Val Ile Ser Ala Leu Cys Phe Leu Val Leu Ala Val Phe
100 105 110

Ala Gly Gly Thr Leu Gly Val Tyr Asn Tyr Val Gly Leu Asn Leu Leu
115 120 125

Ala Ser Val Gly Leu Val Phe Val Tyr Phe Ala Leu Val Gly Leu Leu
130 135 140

Ile Ala Gly Ile Asp Lys Leu Arg Asn Pro Val Glu Val Lys Ser Val
145 150 155 160

Lys Ala Val Ala Val Val Glu Pro Glu Pro Glu Glu Val Glu Glu Asp
165 170 175

Glu Glu Glu His Val Glu Glu Glu Val Asp Glu Glu Glu Glu Val
180 185 190

Glu Glu Gly Val Glu Glu Val Glu Glu Asp Asp Ala Glu Asp Pro Glu
195 200 205

Glu Asn Pro Glu Glu Glu Glu Ser Asp Glu Glu Ile Glu Thr Glu Thr
210 215 220

Glu Ala Glu Glu Thr Asn Asp Gly Ser Glu Ala Glu Asp Arg
225 230 235

<210> 1247

<211> 1128

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1105)

<223> RXN02626

<400> 1247

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agatgttggg aagttcttca cgctatcagt tagggagcac atg agt act caa gtt 115
Met Ser Thr Gln Val
1 5

gaa ctc aaa aca ccg aaa tcg gaa gac cgg gca gca tat atc gct gca 163
Glu Leu Lys Thr Pro Lys Ser Glu Asp Arg Ala Ala Tyr Ile Ala Ala
10 15 20

ttg gga ttc ccg gtc ttg gtc atc att ggc ggc atc atc gga ttc aca 211
Leu Gly Phe Pro Val Leu Val Ile Ile Gly Gly Ile Ile Gly Phe Thr

	25	30	35	
	gcc tgc gat gtt gtg ctc aat att tct tgc tgg gtc aat cct ttg ctg			259
	Ala Ser Asp Val Val Leu Asn Ile Ser Ser Trp Val Asn Pro Leu Leu			
	40	45	50	
	ggc atc atc atg ttc tcc atg ggc ctg acc ttg aag cca gtt gac ttc			307
	Gly Ile Ile Met Phe Ser Met Gly Leu Thr Leu Lys Pro Val Asp Phe			
	55	60	65	
	gcc ctt gtt gct aaa cgc cca ctc cca gtt ctt atc ggc gtg atc gcc			355
	Ala Leu Val Ala Lys Arg Pro Leu Pro Val Leu Ile Gly Val Ile Ala			
	70	75	80	85
	cag ttt gtc atc atg ccc ctg atc gca ttg ctg gtg gtc tgg gtt ttg			403
	Gln Phe Val Ile Met Pro Leu Ile Ala Leu Leu Val Val Trp Val Leu			
	90	95	100	
	cag ctg cct gcg gaa att gcg gcc ggt gtc atc ttg gtt ggt tgt gca			451
	Gln Leu Pro Ala Glu Ile Ala Ala Gly Val Ile Leu Val Gly Cys Ala			
	105	110	115	
	cct ggc gga act tcc tcc aac gtg gtg tct tac ctg tcc cgt ggt gat			499
	Pro Gly Gly Thr Ser Ser Asn Val Val Ser Tyr Leu Ser Arg Gly Asp			
	120	125	130	
	gtt gcg ctg tct gtc acc atg act tcc atc tcc acg ctg ctt gct cca			547
	Val Ala Leu Ser Val Thr Met Thr Ser Ile Ser Thr Leu Leu Ala Pro			
	135	140	145	
	att ttc act cca ctg ctt acc ctg tgg ctg gcg ggg caa tac atg cca			595
	Ile Phe Thr Pro Leu Leu Thr Leu Trp Leu Ala Gly Gln Tyr Met Pro			
	150	155	160	165
	ctt aat gcc gct gat atg gct gta tcc atc gtc caa gtt gtg ctg atc			643
	Leu Asn Ala Ala Asp Met Ala Val Ser Ile Val Gln Val Val Leu Ile			
	170	175	180	
	cca gtc gtg ggc gga ctt gtt gtg cgg ttg atc ttc ccg aca ctc att			691
	Pro Val Val Gly Gly Leu Val Val Arg Leu Ile Phe Pro Thr Leu Ile			
	185	190	195	
	ggc aag gtt ttg cct ctt ttg cca tgg att tca gtc att gcg att tca			739
	Gly Lys Val Leu Pro Leu Leu Pro Trp Ile Ser Val Ile Ala Ile Ser			
	200	205	210	
	ttg atc gtt gcc atc gtg gtc gct ggt tca agg gat aaa atc ctc gaa			787
	Leu Ile Val Ala Ile Val Val Ala Gly Ser Arg Asp Lys Ile Leu Glu			
	215	220	225	
	gca gga ctg ctc gtg ctg gct gcc gtg att att cac aac acc ctc ggc			835
	Ala Gly Leu Leu Val Leu Ala Ala Val Ile Ile His Asn Thr Leu Gly			
	230	235	240	245
	tac tcc ctg gga tac ctc gct gcg aaa ttc act ggg cag cct gct gca			883
	Tyr Ser Leu Gly Tyr Leu Ala Ala Lys Phe Thr Gly Gln Pro Ala Ala			
	250	255	260	
	gct cga cgc act acc gcg att gag gtc ggt atg caa aac tcc ggc ctc			931
	Ala Arg Arg Thr Thr Ala Ile Glu Val Gly Met Gln Asn Ser Gly Leu			
	265	270	275	

gca gat gga ctc gca tcc cag tac atg tca cca atg tct gct ctg cca 979
 Ala Asp Gly Leu Ala Ser Gln Tyr Met Ser Pro Met Ser Ala Leu Pro
 280 285 290

ggc gct atc ttc tct gtc tgg cac aac ctt tcc gga gca ctt ctt gct 1027
 Gly Ala Ile Phe Ser Val Trp His Asn Leu Ser Gly Ala Leu Leu Ala
 295 300 305

gca ttg tgc agg gcg tcc gat aag agg gct gcg gag aag gtg gct tca 1075
 Ala Leu Cys Arg Ala Ser Asp Lys Arg Ala Ala Glu Lys Val Ala Ser
 310 315 320 325

gaa aag gct gcc tcg gag aag gcc gct tcc taaaaggcctt cgctcctaaa 1125
 Glu Lys Ala Ala Ser Glu Lys Ala Ala Ser
 330 335

act 1128

<210> 1248

<211> 335

<212> PRT

<213> Corynebacterium glutamicum

<400> 1248

Met Ser Thr Gln Val Glu Leu Lys Thr Pro Lys Ser Glu Asp Arg Ala
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Ala Tyr Ile Ala Ala Leu Gly Phe Pro Val Leu Val Ile Ile Gly Gly
 20 25 30

Ile Ile Gly Phe Thr Ala Ser Asp Val Val Leu Asn Ile Ser Ser Trp
 35 40 45

Val Asn Pro Leu Leu Gly Ile Ile Met Phe Ser Met Gly Leu Thr Leu
 50 55 60

Lys Pro Val Asp Phe Ala Leu Val Ala Lys Arg Pro Leu Pro Val Leu
 65 70 75 80

Ile Gly Val Ile Ala Gln Phe Val Ile Met Pro Leu Ile Ala Leu Leu
 85 90 95

Val Val Trp Val Leu Gln Leu Pro Ala Glu Ile Ala Ala Gly Val Ile
 100 105 110

Leu Val Gly Cys Ala Pro Gly Gly Thr Ser Ser Asn Val Val Ser Tyr
 115 120 125

Leu Ser Arg Gly Asp Val Ala Leu Ser Val Thr Met Thr Ser Ile Ser
 130 135 140

Thr Leu Leu Ala Pro Ile Phe Thr Pro Leu Leu Thr Leu Trp Leu Ala
 145 150 155 160

Gly Gln Tyr Met Pro Leu Asn Ala Ala Asp Met Ala Val Ser Ile Val
 165 170 175

Gln Val Val Leu Ile Pro Val Val Gly Gly Leu Val Val Arg Leu Ile
 180 185 190

Phe Pro Thr Leu Ile Gly Lys Val Leu Pro Leu Leu Pro Trp Ile Ser
195 200 205

Val Ile Ala Ile Ser Leu Ile Val Ala Ile Val Val Ala Gly Ser Arg
210 215 220

Asp Lys Ile Leu Glu Ala Gly Leu Leu Val Leu Ala Ala Val Ile Ile
225 230 235 240

His Asn Thr Leu Gly Tyr Ser Leu Gly Tyr Leu Ala Ala Lys Phe Thr
245 250 255

Gly Gln Pro Ala Ala Ala Arg Arg Thr Thr Ala Ile Glu Val Gly Met
260 265 270

Gln Asn Ser Gly Leu Ala Asp Gly Leu Ala Ser Gln Tyr Met Ser Pro
275 280 285

Met Ser Ala Leu Pro Gly Ala Ile Phe Ser Val Trp His Asn Leu Ser
290 295 300

Gly Ala Leu Leu Ala Ala Leu Cys Arg Ala Ser Asp Lys Arg Ala Ala
305 310 315 320

Glu Lys Val Ala Ser Glu Lys Ala Ala Ser Glu Lys Ala Ala Ser
325 330 335

<210> 1249

<211> 963

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(940)

<223> RXN02656

<400> 1249

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ttgatctcgg cttttctaac ctaggataaa ggtaacagct atg att ttc ggc gta 115
Met Ile Phe Gly Val
1 5

ctc gca tac ttg gga tgg ggc atg ttc ccg gcc ttt ttc cca cta ctt 163
Leu Ala Tyr Leu Gly Trp Gly Met Phe Pro Ala Phe Phe Pro Leu Leu
10 15 20

ctt ccg gca gga ccg ttc gaa att tta gcg cat ccg atc cta tgg act 211
Leu Pro Ala Gly Pro Phe Glu Ile Leu Ala His Arg Ile Leu Trp Thr
25 30 35

gct gta tta atg atg att atc att agt ttc acg tcg gga tgg aaa gag 259
Ala Val Leu Met Met Ile Ile Ile Ser Phe Thr Ser Gly Trp Lys Glu
40 45 50

ctt aag tcc gct gat cgc ggt aca tgg tta cgc att ata ttg tca tcg 307
Leu Lys Ser Ala Asp Arg Gly Thr Trp Leu Arg Ile Ile Leu Ser Ser
55 60 65

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ttg ttt att gcc ggg aac tgg ctg atc tat gtc atc gct gtc aat tct 355
Leu Phe Ile Ala Gly Asn Trp Leu Ile Tyr Val Ile Ala Val Asn Ser
70 75 80 85

ggg caa gtt act gaa gcc gct ctc gga tac ttt att aac ccc ctg tta 403
Gly Gln Val Thr Glu Ala Ala Leu Gly Tyr Phe Ile Asn Pro Leu Leu
90 95 100

agt gtc gtg ctt ggc att gtg ttc ttc aaa gaa cag tta cga aaa ctg 451
Ser Val Val Leu Leu Gly Ile Val Phe Phe Lys Glu Gln Leu Arg Lys Leu
105 110 115

caa att agt gcg gtg gtt att gct gct gcg ggg gtt ttg gta cta aca 499
Gln Ile Ser Ala Val Val Ile Ala Ala Ala Gly Val Leu Val Leu Thr
120 125 130

ttt cta ggt gat aag cca ccg tat tta gcg ata aca cta gca ttt aca 547
Phe Leu Gly Asp Lys Pro Pro Tyr Leu Ala Ile Thr Leu Ala Phe Thr
135 140 145

ttc ggc atc tat gga gcg ttg aaa aaa caa gtc aag atg tct gct gct 595
Phe Gly Ile Tyr Gly Ala Leu Lys Lys Gln Val Lys Met Ser Ala Ala
150 155 160 165

agt tct ttg tgc gct gaa act tta gta ctg ctg ccc atc gca gtc ata 643
Ser Ser Leu Cys Ala Glu Thr Leu Val Leu Leu Pro Ile Ala Val Ile
170 175 180

tac ctg att ggg ctc gaa gct tcc ggt cac agt acc ttt ttc aac aat 691
Tyr Leu Ile Gly Leu Glu Ala Ser Gly His Ser Thr Phe Phe Asn Asn
185 190 195

ggc agt ggg cac atg gcg tta tta atc tgc tcg ggt ttg gtc aca gcc 739
Gly Ser Gly His Met Ala Leu Leu Ile Cys Ser Gly Leu Val Thr Ala
200 205 210

gtc ccg ctg ttg atg ttt gca ttg gcc gcc aag gca ata cct ctt tcc 787
Val Pro Leu Leu Met Phe Ala Leu Ala Ala Lys Ala Ile Pro Leu Ser
215 220 225

act gtc ggc atg ctg caa tat ctg acc cca acg atg cag atg ctg tgg 835
Thr Val Gly Met Leu Gln Tyr Leu Thr Pro Thr Met Gln Met Leu Trp
230 235 240 245

gca ttg ttt gtg gtc aac gaa tca gta gaa cca atg cgt tgg ttc gga 883
Ala Leu Phe Val Val Asn Glu Ser Val Glu Pro Met Arg Trp Phe Gly
250 255 260

ttc gtt ttc att tgg atc gca gtt act att tac atc aca gat agc cta 931
Phe Val Phe Ile Trp Ile Ala Val Thr Ile Tyr Ile Thr Asp Ser Leu
265 270 275

ctt aag aag taggtaatag cagtattgat atg 963
Leu Lys Lys
280

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<210> 1250

<211> 280

<212> PRT

<213> Corynebacterium glutamicum

<400> 1250

Met Ile Phe Gly Val Leu Ala Tyr Leu Gly Trp Gly Met Phe Pro Ala
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Phe Phe Pro Leu Leu Leu Pro Ala Gly Pro Phe Glu Ile Leu Ala His
 20 25 30

Arg Ile Leu Trp Thr Ala Val Leu Met Met Ile Ile Ser Phe Thr
 35 40 45

Ser Gly Trp Lys Glu Leu Lys Ser Ala Asp Arg Gly Thr Trp Leu Arg
 50 55 60

Ile Ile Leu Ser Ser Leu Phe Ile Ala Gly Asn Trp Leu Ile Tyr Val
 65 70 75 80

Ile Ala Val Asn Ser Gly Gln Val Thr Glu Ala Ala Leu Gly Tyr Phe
 85 90 95

Ile Asn Pro Leu Leu Ser Val Val Leu Gly Ile Val Phe Phe Lys Glu
 100 105 110

Gln Leu Arg Lys Leu Gln Ile Ser Ala Val Val Ile Ala Ala Ala Gly
 115 120 125

Val Leu Val Leu Thr Phe Leu Gly Asp Lys Pro Pro Tyr Leu Ala Ile
 130 135 140

Thr Leu Ala Phe Thr Phe Gly Ile Tyr Gly Ala Leu Lys Lys Gln Val
 145 150 155 160

Lys Met Ser Ala Ala Ser Ser Leu Cys Ala Glu Thr Leu Val Leu Leu
 165 170 175

Pro Ile Ala Val Ile Tyr Leu Ile Gly Leu Glu Ala Ser Gly His Ser
 180 185 190

Thr Phe Phe Asn Asn Gly Ser Gly His Met Ala Leu Leu Ile Cys Ser
 195 200 205

Gly Leu Val Thr Ala Val Pro Leu Leu Met Phe Ala Leu Ala Ala Lys
 210 215 220

Ala Ile Pro Leu Ser Thr Val Gly Met Leu Gln Tyr Leu Thr Pro Thr
 225 230 235 240

Met Gln Met Leu Trp Ala Leu Phe Val Val Asn Glu Ser Val Glu Pro
 245 250 255

Met Arg Trp Phe Gly Phe Val Phe Ile Trp Ile Ala Val Thr Ile Tyr
 260 265 270

Ile Thr Asp Ser Leu Leu Lys Lys
 275 280

<210> 1251

<211> 756

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(733)

<223> RXN02673

<400> 1251

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aacgccgaga cataatgaag tcatttacaa gcgccgccgc atg gca gcg ctc cta 115
 Met Ala Ala Leu Leu
 1 5

gtt ctg ctc gtc gtg att gcc ttg att atc tgg gca gtc gtc gcg ctt 163
 Val Leu Leu Val Val Ile Ala Leu Ile Ile Trp Ala Val Val Ala Leu
 10 15 20

cga ggt gga tca tcg gag cct gag gaa gag cag cca aat aat gct gta 211
 Arg Gly Gly Ser Ser Glu Pro Glu Glu Glu Gln Pro Asn Asn Ala Val
 25 30 35

gtg acc tcc tca atg gaa tct tcc gcg acg tct agt tct tct tct aaa 259
 Val Thr Ser Ser Met Glu Ser Ser Ala Thr Ser Ser Ser Ser Lys
 40 45 50

gaa tcc acg act gaa gcc acc aca gaa gaa gag act tcc agt gct gaa 307
 Glu Ser Thr Thr Glu Ala Thr Thr Glu Glu Glu Thr Ser Ser Ala Glu
 55 60 65

cca acc gca aca tcc tcc gtt gca gca gat gca aaa aag acc tgt gag 355
 Pro Thr Ala Thr Ser Ser Val Ala Ala Asp Ala Lys Lys Thr Cys Glu
 70 75 80 85

ctt agt gac ttg gtg att tcc gca agc act aat cag ccg act ttc tca 403
 Leu Ser Asp Leu Val Ile Ser Ala Ser Thr Asn Gln Pro Thr Phe Ser
 90 95 100

ggt tct gcg cag cca gaa tta ttt atg gct gtg cat aat ccg act gct 451
 Gly Ser Ala Gln Pro Glu Leu Phe Met Ala Val His Asn Pro Thr Ala
 105 110 115

gtt gat tgc gaa att gac ctc gag gag aac aaa ctc cgt ttc gag gta 499
 Val Asp Cys Glu Ile Asp Leu Glu Glu Asn Lys Leu Arg Phe Glu Val
 120 125 130

tac aat ctc gcg acc aac gca cga atc tgg tct gat gtc gac tgc aac 547
 Tyr Asn Leu Ala Thr Asn Ala Arg Ile Trp Ser Asp Val Asp Cys Asn
 135 140 145

cct gca gtt gaa gac gcc acg agc gtg ttc cct gcc gcc gag gat cgc 595
 Pro Ala Val Glu Asp Gly Thr Ser Val Phe Pro Ala Gly Glu Asp Arg
 150 155 160 165

tac ttc cag gca aca tgg tct cgt acc act tca gcg cca aac cag tgc 643
 Tyr Phe Gln Ala Thr Trp Ser Arg Thr Thr Ser Ala Pro Asn Gln Cys
 170 175 180

aac aac cgc act gat gtc ccc gcc ggt gcc tac tac ttg cac act gtt 691
 Asn Asn Arg Thr Asp Val Pro Ala Gly Gly Tyr Tyr Leu His Thr Val
 185 190 195

gtc ggt aat aac cct tca cca gcg gtg acc ttt aac cta act 733
 Val Gly Asn Asn Pro Ser Pro Ala Val Thr Phe Asn Leu Thr
 200 205 210

taaacggcca agtcggtcgg tga 756

<210> 1252

<211> 211

<212> PRT

<213> Corynebacterium glutamicum

<400> 1252

Met Ala Ala Leu Leu Val Leu Leu Val Val Ile Ala Leu Ile Ile Trp
 1 5 10 15

Ala Val Val Ala Leu Arg Gly Gly Ser Ser Glu Pro Glu Glu Glu Gln
 20 25 30

Pro Asn Asn Ala Val Val Thr Ser Ser Met Glu Ser Ser Ala Thr Ser
 35 40 45

Ser Ser Ser Ser Lys Glu Ser Thr Thr Glu Ala Thr Thr Glu Glu Glu
 50 55 60

Thr Ser Ser Ala Glu Pro Thr Ala Thr Ser Ser Val Ala Ala Asp Ala
 65 70 75 80

Lys Lys Thr Cys Glu Leu Ser Asp Leu Val Ile Ser Ala Ser Thr Asn
 85 90 95

Gln Pro Thr Phe Ser Gly Ser Ala Gln Pro Glu Leu Phe Met Ala Val
 100 105 110

His Asn Pro Thr Ala Val Asp Cys Glu Ile Asp Leu Glu Glu Asn Lys
 115 120 125

Leu Arg Phe Glu Val Tyr Asn Leu Ala Thr Asn Ala Arg Ile Trp Ser
 130 135 140

Asp Val Asp Cys Asn Pro Ala Val Glu Asp Gly Thr Ser Val Phe Pro
 145 150 155 160

Ala Gly Glu Asp Arg Tyr Phe Gln Ala Thr Trp Ser Arg Thr Thr Ser
 165 170 175

Ala Pro Asn Gln Cys Asn Asn Arg Thr Asp Val Pro Ala Gly Gly Tyr
 180 185 190

Tyr Leu His Thr Val Val Gly Asn Asn Pro Ser Pro Ala Val Thr Phe
 195 200 205

Asn Leu Thr
 210

<210> 1253

<211> 756

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(733)

<223> FRXA02673

<400> 1253

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aacgccgaga cataatgaag tcatttacaa ggcgccgcgcg atg gca gcg ctc cta 115
 Met Ala Ala Leu Leu
 1 5

gtt ctg ctc gtc gtg att gcc ttg att atc tgg gca gtc gtc gcg ctt 163
 Val Leu Leu Val Val Ile Ala Leu Ile Ile Trp Ala Val Val Ala Leu
 10 15 20

cga ggt gga tca tcg gag cct gag gaa gag cag cca aat aat gct gta 211
 Arg Gly Gly Ser Ser Glu Pro Glu Glu Glu Gln Pro Asn Asn Ala Val
 25 30 35

gtg acc tcc tca atg gaa tct tcc gcg acg tct agt tct tct tct aaa 259
 Val Thr Ser Ser Met Glu Ser Ser Ala Thr Ser Ser Ser Ser Ser Lys
 40 45 50

gaa tcc acg act gaa gcc acc aca gaa gaa gag act tcc agt gct gaa 307
 Glu Ser Thr Thr Glu Ala Thr Thr Glu Glu Glu Thr Ser Ser Ala Glu
 55 60 65

cca acc gca aca tcc tcc gtt gca gca gat gca aaa aag acc tgt gag 355
 Pro Thr Ala Thr Ser Ser Val Ala Ala Asp Ala Lys Lys Thr Cys Glu
 70 75 80 85

ctt agt gac ttg gtg att tcc gca agc act aat cag ccg act ttc tca 403
 Leu Ser Asp Leu Val Ile Ser Ala Ser Thr Asn Gln Pro Thr Phe Ser
 90 95 100

ggc tct gcg cag cca gaa tta ttt atg gct gtg cat aat cag act gct 451
 Gly Ser Ala Gln Pro Glu Leu Phe Met Ala Val His Asn Pro Thr Ala
 105 110 115

gtt gat tgc gaa att gac ctc gag gag aac aaa ctc cgt ttc gag gta 499
 Val Asp Cys Glu Ile Asp Leu Glu Glu Asn Lys Leu Arg Phe Glu Val
 120 125 130

tac aat ctc gcg acc aac gca cga atc tgg tct gat gtc gac tgc aac 547
 Tyr Asn Leu Ala Thr Asn Ala Arg Ile Trp Ser Asp Val Asn Cys Asn
 135 140 145

cct gca gtt gaa gac ggc acg agc gtg ttc cct gcc gcc gag gat cgc 595
 Pro Ala Val Glu Asp Gly Thr Ser Val Phe Pro Ala Gly Glu Asp Arg
 150 155 160 165

tac ttc cag gca aca tgg tct cgt acc act tca gcg cca aac cag tgc 643
 Tyr Phe Gln Ala Thr Trp Ser Arg Thr Thr Ser Ala Pro Asn Gln Cys
 170 175 180

aac aac cgc act gat gtc ccc gcc ggt gcc tac tac ttg cac act gtg 691
 Asn Asn Arg Thr Asp Val Pro Ala Gly Gly Tyr Tyr Leu His Thr Val
 185 190 195

gtc ggt aat aac cct tca cca gcg gtg acc ttt aac cta act 733
Val Gly Asn Asn Pro Ser Pro Ala Val Thr Phe Asn Leu Thr
200 205 210

taaacggcca agtccgtcgg tga 756

<210> 1254

$\langle 211 \rangle$ 211

<212> PRT

<213> Corynebacterium glutamicum

<400> 1254

Met Ala Ala Leu Leu Val Leu Leu Val Val Ile Ala Leu Ile Ile Trp
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Ala Val Val Ala Leu Arg Gly Gly Ser Ser Glu Pro Glu Glu Glu Gln
20 25 30

Pro Asn Asn Ala Val Val Thr Ser Ser Met Glu Ser Ser Ala Thr Ser
35 40 45

Ser Ser Ser Ser Lys Glu Ser Thr Thr Glu Ala Thr Thr Glu Glu Glu
50 55 60

Thr Ser Ser Ala Glu Pro Thr Ala Thr Ser Ser Val Ala Ala Asp Ala
65 70 75 80

Lys Lys Thr Cys Glu Leu Ser Asp Leu Val Ile Ser Ala Ser Thr Asn
85 90 95

Gln Pro Thr Phe Ser Gly Ser Ala Gln Pro Glu Leu Phe Met Ala Val
100 105 110

His Asn Pro Thr Ala Val Asp Cys Glu Ile Asp Leu Glu Glu Asn Lys
115 120 125

Leu Arg Phe Glu Val Tyr Asn Leu Ala Thr Asn Ala Arg Ile Trp Ser
130 135 140

Asp Val Asp Cys Asn Pro Ala Val Glu Asp Gly Thr Ser Val Phe Pro
145 150 155 160

Ala Gly Glu Asp Arg Tyr Phe Gln Ala Thr Trp Ser Arg Thr Thr Ser
165 170 175

Ala Pro Asn Gln Cys Asn Asn Arg Thr Asp Val Pro Ala Gly Gly Tyr
180 185 190

Tyr Leu His Thr Val Val Gly Asn Asn Pro Ser Pro Ala Val Thr Phe
195 200 205

Asn Leu Thr
210

<210> 1255

<211> 1407

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1384)

<223> RXN02680

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tttcactttt ttgagaagtt ttacttttat attagttctc atg cgc ctc aac aaa 115
 Met Arg Leu Asn Lys
 1 5

cga ctc cca gcg gca ctc tcc gga ctg ctg ctc tct gct gcc ctt ctt 163
 Arg Leu Pro Ala Ala Leu Ser Gly Leu Leu Leu Ser Ala Ala Leu Leu
 10 15 20

gcc gga tgc tcc act tct gga acc gcc gag acc acg aca aca acc gtt 211
 Ala Gly Cys Ser Thr Ser Gly Thr Ala Glu Thr Thr Thr Thr Val
 25 30 35

tca tct gct gcg gca tca aca acc act tcc acc tcc tct gct tgg tct 259
 Ser Ser Ala Ala Ala Ser Thr Thr Thr Ser Thr Ser Ala Ser Ser
 40 45 50

tcc tct tcc tcc tcc tct tcc tcc tct tcc tcc gac tca agc acc acc 307
 Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Asp Ser Ser Thr Thr
 55 60 65

gcc gaa acc atc tcc aac acc gcg gaa gct gcc caa gct ttc ttg tcc 355
 Ala Glu Thr Ile Ser Asn Thr Ala Glu Ala Ala Gln Ala Phe Leu Ser
 70 75 80 85

acc ctg tcc acc gaa gaa caa gac gcc gta ctc tac gac tac gac gcc 403
 Thr Leu Ser Thr Glu Glu Gln Asp Ala Val Leu Tyr Asp Tyr Asp Ala
 90 95 100

gaa gaa aag tcc acc ggc tgg tct aac ttc cca gtc acc ttc gtg cag 451
 Glu Glu Lys Ser Thr Gly Trp Ser Asn Phe Pro Val Thr Phe Val Gln
 105 110 115

cgt tcc ggc gtg aac ctc acc gac ctc act gag gaa cag caa gca gct 499
 Arg Ser Gly Val Asn Leu Thr Asp Leu Thr Glu Glu Gln Ala Ala
 120 125 130

gcc ctc aac gtg ctg aag aac ctg ctc aac gac gac gcc tac caa atg 547
 Ala Leu Asn Val Leu Lys Asn Leu Leu Asn Asp Asp Ala Tyr Gln Met
 135 140 145

atc gaa gac atc atg gct agc gat cag tac ctc aac gac gaa agc aac 595
 Ile Glu Asp Ile Met Ala Ser Asp Gln Tyr Leu Asn Asp Glu Ser Asn
 150 155 160 165

acc acc gag gat tcc ctc ggc cag tac tac atc gca ttc ttc ggc gat 643
 Thr Thr Glu Asp Ser Leu Gly Gln Tyr Tyr Ile Ala Phe Phe Gly Asp
 170 175 180

cca agc agc gac tcc gac tgg tcc atc caa ttc ggc gga cac cac atc 691
 Pro Ser Ser Asp Ser Asp Trp Ser Ile Gln Phe Gly Gly His His Ile
 185 190 195

ggc atc aac acc acc ttc tcc gac ggt gcc atc acc ttc gcc cca acc 739

Gly	Ile	Asn	Thr	Thr	Phe	Ser	Asp	Gly	Ala	Ile	Thr	Phe	Ala	Pro	Thr		
		200					205					210					
cac	ctt	ggc	acc	cag	cct	tcc	gag	tgg	acc	aac	gag	gac	ggc	gaa	acc	787	
His	Leu	Gly	Thr	Gln	Pro	Ser	Glu	Trp	Thr	Asn	Glu	Asp	Gly	Glu	Thr		
	215					220				225							
gtt	gca	gca	cta	agc	aac	atg	tac	gaa	acc	gcc	ttc	gcc	ttc	tac	gac	835	
Val	Ala	Ala	Leu	Ser	Asn	Met	Tyr	Glu	Thr	Ala	Phe	Ala	Phe	Tyr	Asp		
	230				235					240				245			
agc	ctc	ggc	gaa	gag	cag	caa	gca	cag	ctc	tac	cag	ggt	gaa	gag	ttg	883	
Ser	Leu	Ala	Glu	Glu	Gln	Gln	Ala	Gln	Leu	Tyr	Gln	Gly	Glu	Glu	Leu		
			250					255						260			
gat	tcc	atg	gtg	tgc	gca	ccg	ggc	agc	acg	tgc	gac	tac	cca	acc	ggc	931	
Asp	Ser	Met	Val	Cys	Ala	Pro	Gly	Ser	Thr	Cys	Asp	Tyr	Pro	Thr	Gly		
			265				270						275				
acc	ggc	ttg	aaa	ggc	tct	gac	ctc	acc	gat	gag	caa	aaa	gaa	ttg	ctc	979	
Thr	Gly	Leu	Lys	Gly	Ser	Asp	Leu	Thr	Asp	Glu	Gln	Lys	Glu	Leu	Leu		
		280					285					290					
atc	gat	gtc	atc	gca	aac	tgg	gtt	ggc	ctc	gcc	gat	gag	gaa	acc	acc	1027	
Ile	Asp	Val	Ile	Ala	Asn	Trp	Val	Gly	Leu	Ala	Asp	Glu	Glu	Thr	Thr		
	295					300					305						
gaa	act	gaa	ctc	gat	gcc	atc	cgc	gaa	acc	ctg	gat	gac	acc	tac	atc	1075	
Glu	Thr	Glu	Leu	Asp	Ala	Ile	Arg	Glu	Thr	Leu	Asp	Asp	Thr	Tyr	Ile		
	310				315					320				325			
aac	tgg	tcc	ggc	gcc	acc	gag	tac	gac	acc	tcc	acc	ggc	gac	ggc	atc	1123	
Asn	Trp	Ser	Gly	Ala	Thr	Glu	Tyr	Asp	Thr	Ser	Thr	Gly	Asp	Gly	Ile		
			330					335						340			
tac	ttc	cag	atc	agt	ggc	cca	aag	gtc	tac	att	gag	ttc	gct	aac	cag	1171	
Tyr	Phe	Gln	Ile	Ser	Gly	Pro	Lys	Val	Tyr	Ile	Glu	Phe	Ala	Asn	Gln		
			345					350					355				
caa	ggt	tct	gca	ggt	gcc	gac	atc	gac	ggt	gtc	atc	acc	gct	gga	tgg	1219	
Gln	Gly	Ser	Ala	Gly	Ala	Asp	Ile	Asp	Gly	Val	Ile	Thr	Ala	Gly	Trp		
		360				365						370					
ggc	cac	att	cac	acc	atc	tac	cgc	gac	cca	acc	aat	gac	tac	gct	aac	1267	
Gly	His	Ile	His	Thr	Ile	Tyr	Arg	Asp	Pro	Thr	Asn	Asp	Tyr	Ala	Asn		
		375				380					385						
tcc	gta	act	cag	gaa	gca	gcc	agc	gga	atg	atg	ggc	ggc	ggc	cct	ggc	1315	
Ser	Val	Thr	Gln	Glu	Ala	Ala	Ser	Gly	Met	Met	Gly	Gly	Gly	Pro	Gly		
	390				395					400				405			
ggt	aat	ggt	ggc	gag	atg	cct	agc	ggt	gac	atg	cct	act	ggt	gag	atg	1363	
Gly	Asn	Gly	Gly	Glu	Met	Pro	Ser	Gly	Asp	Met	Pro	Thr	Gly	Glu	Met		
			410					415					420				
cct	tct	ggc	gct	cca	tca	aac	taacgccatt	taagaggccg	aac							1407	
Pro	Ser	Gly	Ala	Pro	Ser	Asn											
			425														

<210> 1256

<211> 428

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1256

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 1 5 10 15

Ser Ala Ala Leu Leu Ala Gly Cys Ser Thr Ser Gly Thr Ala Glu Thr
 20 25 30

Thr Thr Thr Thr Val Ser Ser Ala Ala Ala Ser Thr Thr Thr Ser Thr
 35 40 45

Ser Ser Ala Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
 50 55 60

Asp Ser Ser Thr Thr Ala Glu Thr Ile Ser Asn Thr Ala Glu Ala Ala
 65 70 75 80

Gln Ala Phe Leu Ser Thr Leu Ser Thr Glu Glu Gln Asp Ala Val Leu
 85 90 95

Tyr Asp Tyr Asp Ala Glu Glu Lys Ser Thr Gly Trp Ser Asn Phe Pro
 100 105 110

Val Thr Phe Val Gln Arg Ser Gly Val Asn Leu Thr Asp Leu Thr Glu
 115 120 125

Glu Gln Gln Ala Ala Ala Leu Asn Val Leu Lys Asn Leu Leu Asn Asp
 130 135 140

Asp Ala Tyr Gln Met Ile Glu Asp Ile Met Ala Ser Asp Gln Tyr Leu
 145 150 155 160

Asn Asp Glu Ser Asn Thr Thr Glu Asp Ser Leu Gly Gln Tyr Tyr Ile
 165 170 175

Ala Phe Phe Gly Asp Pro Ser Ser Asp Ser Asp Trp Ser Ile Gln Phe
 180 185 190

Gly Gly His His Ile Gly Ile Asn Thr Thr Phe Ser Asp Gly Ala Ile
 195 200 205

Thr Phe Ala Pro Thr His Leu Gly Thr Gln Pro Ser Glu Trp Thr Asn
 210 215 220

Glu Asp Gly Glu Thr Val Ala Ala Leu Ser Asn Met Tyr Glu Thr Ala
 225 230 235 240

Phe Ala Phe Tyr Asp Ser Leu Ala Glu Glu Gln Gln Ala Gln Leu Tyr
 245 250 255

Gln Gly Glu Glu Leu Asp Ser Met Val Cys Ala Pro Gly Ser Thr Cys
 260 265 270

Asp Tyr Pro Thr Gly Thr Gly Leu Lys Gly Ser Asp Leu Thr Asp Glu
 275 280 285

Gln Lys Glu Leu Leu Ile Asp Val Ile Ala Asn Trp Val Gly Leu Ala
 290 295 300

Asp Glu Glu Thr Thr Glu Thr Glu Leu Asp Ala Ile Arg Glu Thr Leu
305 310 315 320

Asp Asp Thr Tyr Ile Asn Trp Ser Gly Ala Thr Glu Tyr Asp Thr Ser
325 330 335

Thr Gly Asp Gly Ile Tyr Phe Gln Ile Ser Gly Pro Lys Val Tyr Ile
340 345 350

Glu Phe Ala Asn Gln Gln Gly Ser Ala Gly Ala Asp Ile Asp Gly Val
355 360 365

Ile Thr Ala Gly Trp Gly His Ile His Thr Ile Tyr Arg Asp Pro Thr
370 375 380

Asn Asp Tyr Ala Asn Ser Val Thr Gln Glu Ala Ala Ser Gly Met Met
385 390 395 400

Gly Gly Gly Pro Gly Gly Asn Gly Gly Glu Met Pro Ser Gly Asp Met
405 410 415

Pro Thr Gly Glu Met Pro Ser Gly Ala Pro Ser Asn
420 425

<210> 1257

<211> 1407

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1384)

<223> FRXA02680

<400> 1257
aataccagggt caacacacac aggaaccggt cagaaacott ccagattgct cactttttta 60

tttcactttt ttgagaagtt ttacttttat attagttctc atg cgc ctc aac aaa 115
Met Arg Leu Asn Lys
1 5

cga ctc cca gcg gca ctc tcc gga ctg ctg ctc tct gct gcc ctt ctt 163
Arg Leu Pro Ala Ala Leu Ser Gly Leu Leu Leu Ser Ala Ala Leu Leu
10 15 20

gcc gga tgc tcc act tct gga acc gcc gag acc acg aca aca acc gtt 211
Ala Gly Cys Ser Thr Ser Gly Thr Ala Glu Thr Thr Thr Thr Thr Val
25 30 35

tca tct gct gcg gca tca aca acc act tcc acc tcc tct gct tgg tct 259
Ser Ser Ala Ala Ala Ser Thr Thr Thr Ser Thr Ser Ala Ser Ser
40 45 50

tcc tct tcc tcc tcc tct tcc tcc tct tcc tcc gac tca agc acc acc 307
Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Asp Ser Ser Thr Thr
55 60 65

gcc gaa acc atc tcc aac acc gcg gaa gct gcc caa gct ttc ttg tcc 355
Ala Glu Thr Ile Ser Asn Thr Ala Glu Ala Ala Gln Ala Phe Leu Ser

70	75	80	85	
acc ctg tcc acc gaa gaa caa gac gcc gta ctc tac gac tac gac gcc	403			
Thr Leu Ser Thr	Glu Glu Gln Asp Ala Val Leu Tyr Asp Tyr Asp Ala	90	95	100
gaa gaa aag tcc acc ggc tgg tct aac ttc cca gtc acc ttc gtg cag	451			
Glu Glu Lys Ser Thr	Gly Trp Ser Asn Phe Pro Val Thr Phe Val Gln	105	110	115
cgt tcc ggc gtg aac ctc acc gac ctc act gag gaa cag caa gca gct	499			
Arg Ser Gly Val Asn Leu Thr	Asp Leu Thr Glu Glu Gln Gln Ala Ala	120	125	130
gcc ctc aac gtg ctg aag aac ctg ctc aac gac gac gcc tac caa atg	547			
Ala Leu Asn Val Leu Lys Asn Leu Leu Asn Asp Asp Ala Tyr Gln Met	135	140	145	
atc gaa gac atc atg gct agc gat cag tac ctc aac gac gaa agc aac	595			
Ile Glu Asp Ile Met Ala Ser Asp Gln Tyr Leu Asn Asp Glu Ser Asn	150	155	160	165
acc acc gag gat tcc ctc ggc cag tac tac atc gca ttc ttc ggc gat	643			
Thr Thr Glu Asp Ser Leu Gly Gln Tyr Tyr Ile Ala Phe Phe Gly Asp	170	175	180	
cca agc agc gac tcc gac tgg tcc atc caa ttc ggc gga cac cac atc	691			
Pro Ser Ser Asp Ser Asp Trp Ser Ile Gln Phe Gly Gly His His Ile	185	190	195	
ggc atc aac acc acc ttc tcc gac ggt gcc atc acc ttc gcc cca acc	739			
Gly Ile Asn Thr Thr Phe Ser Asp Gly Ala Ile Thr Phe Ala Pro Thr	200	205	210	
cac ctt ggc acc cag cct tcc gag tgg acc aac gag gac ggc gaa acc	787			
His Leu Gly Thr Gln Pro Ser Glu Trp Thr Asn Glu Asp Gly Glu Thr	215	220	225	
gtt gca gca cta agc aac atg tac gaa acc gcc ttc gcc ttc tac gac	835			
Val Ala Ala Leu Ser Asn Met Tyr Glu Thr Ala Phe Ala Phe Tyr Asp	230	235	240	245
agc ctc gcc gaa gag cag caa gca cag ctc tac cag ggt gaa gag ttg	883			
Ser Leu Ala Glu Glu Gln Gln Ala Gln Leu Tyr Gln Gly Glu Glu Leu	250	255	260	
gat tcc atg gtg tgc gca cgc ggc agc acg tgc gac tac cca acc ggc	931			
Asp Ser Met Val Cys Ala Pro Gly Ser Thr Cys Asp Tyr Pro Thr Gly	265	270	275	
acc ggc ttg aaa ggc tct gac ctc acc gat gag caa aaa gaa ttg ctc	979			
Thr Gly Leu Lys Gly Ser Asp Leu Thr Asp Glu Gln Lys Glu Leu Leu	280	285	290	
atc gat gtc atc gca aac tgg gtt ggc ctc gcc gat gag gaa acc acc	1027			
Ile Asp Val Ile Ala Asn Trp Val Gly Leu Ala Asp Glu Glu Thr Thr	295	300	305	
gaa act gaa ctc gat gcc atc cgc gaa acc ctg gat gac acc tac atc	1075			
Glu Thr Glu Leu Asp Ala Ile Arg Glu Thr Leu Asp Asp Thr Tyr Ile	310	315	320	325

aac tgg tcc ggc gcc acc gag tac gac acc tcc acc ggc gac ggc atc 1123
 Asn Trp Ser Gly Ala Thr Glu Tyr Asp Thr Ser Thr Gly Asp Gly Ile
 330 335 340

tac ttc cag atc agt ggc cca aag gtc tac att gag ttc gct aac cag 1171
 Tyr Phe Gln Ile Ser Gly Pro Lys Val Tyr Ile Glu Phe Ala Asn Gln
 345 350 355

caa ggt tct gca ggt gcc gac atc gac ggt gtc atc acc gct gga tgg 1219
 Gln Gly Ser Ala Gly Ala Asp Ile Asp Gly Val Ile Thr Ala Gly Trp
 360 365 370

ggc cac att cac acc atc tac cgc gac cca acc aat gac tac gct aac 1267
 Gly His Ile His Thr Ile Tyr Arg Asp Pro Thr Asn Asp Tyr Ala Asn
 375 380 385

tcc gta act cag gaa gca gcc agc gga atg atg ggc ggc ggc cct ggt 1315
 Ser Val Thr Gln Glu Ala Ala Ser Gly Met Met Gly Gly Gly Pro Gly
 390 395 400 405

ggt aat ggt ggc gag atg cct agc ggt gac atg cct act ggt gag atg 1363
 Gly Asn Gly Gly Glu Met Pro Ser Gly Asp Met Pro Thr Gly Glu Met
 410 415 420

cct tct ggc gct cca tca aac taacgccatt taagaggcgc aac 1407
 Pro Ser Gly Ala Pro Ser Asn
 425

<210> 1258
 <211> 428
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1258
 Met Arg Leu Asn Lys Arg Leu Pro Ala Ala Leu Ser Gly Leu Leu Leu
 1 5 10 15

Ser Ala Ala Leu Leu Ala Gly Cys Ser Thr Ser Gly Thr Ala Glu Thr
 20 25 30

Thr Thr Thr Thr Val Ser Ser Ala Ala Ala Ser Thr Thr Thr Ser Thr
 35 40 45

Ser Ser Ala Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
 50 55 60

Asp Ser Ser Thr Thr Ala Glu Thr Ile Ser Asn Thr Ala Glu Ala Ala
 65 70 75 80

Gln Ala Phe Leu Ser Thr Leu Ser Thr Glu Glu Gln Asp Ala Val Leu
 85 90 95

Tyr Asp Tyr Asp Ala Glu Glu Lys Ser Thr Gly Trp Ser Asn Phe Pro
 100 105 110

Val Thr Phe Val Gln Arg Ser Gly Val Asn Leu Thr Asp Leu Thr Glu
 115 120 125

Glu Gln Gln Ala Ala Ala Leu Asn Val Leu Lys Asn Leu Leu Asn Asp

130 135 140
 Asp Ala Tyr Gln Met Ile Glu Asp Ile Met Ala Ser Asp Gln Tyr Leu
 145 150 155 160
 Asn Asp Glu Ser Asn Thr Thr Glu Asp Ser Leu Gly Gln Tyr Tyr Ile
 165 170 175
 Ala Phe Phe Gly Asp Pro Ser Ser Asp Ser Asp Trp Ser Ile Gln Phe
 180 185 190
 Gly Gly His His Ile Gly Ile Asn Thr Thr Phe Ser Asp Gly Ala Ile
 195 200 205
 Thr Phe Ala Pro Thr His Leu Gly Thr Gln Pro Ser Glu Trp Thr Asn
 210 215 220
 Glu Asp Gly Glu Thr Val Ala Ala Leu Ser Asn Met Tyr Glu Thr Ala
 225 230 235 240
 Phe Ala Phe Tyr Asp Ser Leu Ala Glu Glu Gln Gln Ala Gln Leu Tyr
 245 250 255
 Gln Gly Glu Glu Leu Asp Ser Met Val Cys Ala Pro Gly Ser Thr Cys
 260 265 270
 Asp Tyr Pro Thr Gly Thr Gly Leu Lys Gly Ser Asp Leu Thr Asp Glu
 275 280 285
 Gln Lys Glu Leu Leu Ile Asp Val Ile Ala Asn Trp Val Gly Leu Ala
 290 295 300
 Asp Glu Glu Thr Thr Glu Thr Glu Leu Asp Ala Ile Arg Glu Thr Leu
 305 310 315
 Asp Asp Thr Tyr Ile Asn Trp Ser Gly Ala Thr Glu Tyr Asp Thr Ser
 325 330 335
 Thr Gly Asp Gly Ile Tyr Phe Gln Ile Ser Gly Pro Lys Val Tyr Ile
 340 345 350
 Glu Phe Ala Asn Gln Gln Gly Ser Ala Gly Ala Asp Ile Asp Gly Val
 355 360 365
 Ile Thr Ala Gly Trp Gly His Ile His Thr Ile Tyr Arg Asp Pro Thr
 370 375 380
 Asn Asp Tyr Ala Asn Ser Val Thr Gln Glu Ala Ala Ser Gly Met Met
 385 390 395
 Gly Gly Gly Pro Gly Gly Asn Gly Gly Glu Met Pro Ser Gly Asp Met
 405 410 415
 Pro Thr Gly Glu Met Pro Ser Gly Ala Pro Ser Asn
 420 425

<210> 1259

<211> 549

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(526)

<223> FRXA02679

<400> 1259

caccattacc accagggcgc ccgcccacatca ttccgctggc tgcttectga gttacggagt 60

tagcgtatgc attggttggg tcgcggtaga tgggtgtgaat gtg gcc cca tcc agc 115
Val Ala Pro Ser Ser
1 5

ggt gat gac acc gtc gat gtc ggc acc tgc aga acc ttg ctg gtt agc 163
Gly Asp Asp Thr Val Asp Val Gly Thr Cys Arg Thr Leu Leu Val Ser
10 15 20

gaa ctc aat gta gac ctt tgg gcc act gat ctg gaa gta gat gcc gtc 211
Glu Leu Asn Val Asp Leu Trp Ala Thr Asp Leu Glu Val Asp Ala Val
25 30 35

gcc ggt gga ggt gtc gta ctc ggt ggc gcc gga cca gtt gat gta ggt 259
Ala Gly Gly Gly Val Val Leu Gly Gly Ala Gly Pro Val Asp Val Gly
40 45 50

gtc atc cag ggt ttc gcg gat ggc atc gag ttc agt ttc ggt ggt ttc 307
Val Ile Gln Gly Phe Ala Asp Gly Ile Glu Phe Ser Phe Gly Gly Phe
55 60 65

ctc atc ggc gag gcc aac cca gtt tgc gat gac atc gat gag caa ttc 355
Leu Ile Gly Glu Ala Asn Pro Val Cys Asp Ile Asp Glu Gln Phe
70 75 80 85

ttt ttg ctc atc ggt gag gtc aga gcc ttt caa gcc ggt gcc ggt tgg 403
Phe Leu Leu Ile Gly Glu Val Arg Ala Phe Gln Ala Gly Ala Gly Trp
90 95 100

gta gtc gca cgt gct gcc cgg tgc gca cac cat gga atc caa ctc ttc 451
Val Val Ala Arg Ala Ala Arg Cys Ala His His Gly Ile Gln Leu Phe
105 110 115

acc ctg gta gag ctg tgc ttg ctg ctc ttc ggc gag gct gtc gta gaa 499
Thr Leu Val Glu Leu Cys Leu Leu Leu Phe Gly Glu Ala Val Val Glu
120 125 130

ggc gaa ggc ggt ttc gta cat gtt gct tagtgctgca acggtttcgc 546
Gly Glu Gly Gly Phe Val His Val Ala
135 140

cgt 549

<210> 1260

<211> 142

<212> PRT

<213> Corynebacterium glutamicum

<400> 1260

Val Ala Pro Ser Ser Gly Asp Asp Thr Val Asp Val Gly Thr Cys Arg
1 5 10 15

```

Thr Leu Leu Val Ser Glu Leu Asn Val Asp Leu Trp Ala Thr Asp Leu
      20                25                30

Glu Val Asp Ala Val Ala Gly Gly Gly Val Val Leu Gly Gly Ala Gly
      35                40                45

Pro Val Asp Val Gly Val Ile Gln Gly Phe Ala Asp Gly Ile Glu Phe
      50                55                60

Ser Phe Gly Gly Phe Leu Ile Gly Glu Ala Asn Pro Val Cys Asp Asp
      65                70                75                80

Ile Asp Glu Gln Phe Phe Leu Leu Ile Gly Glu Val Arg Ala Phe Gln
      85                90                95

Ala Gly Ala Gly Trp Val Val Ala Arg Ala Ala Arg Cys Ala His His
      100               105               110

Gly Ile Gln Leu Phe Thr Leu Val Glu Leu Cys Leu Leu Phe Gly
      115               120               125

Glu Ala Val Val Glu Gly Glu Gly Gly Phe Val His Val Ala
      130               135               140

```

<210> 1261

<211> 567

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(544)

<223> FRXA02681

<400> 1261

cgaggctgtc gtagaaggcg aagcggttt cgtacatgtt gcttagtgct gcaacggttt 60

```

cgccgtcctc gttggtccac tcggaaggct ggggtgccaaag  gtg ggt tgg ggc gaa  115
                                     Val Gly Trp Gly Glu
                                     1                    5

```

```

ggt gat ggc acc gtc gga gaa ggt ggt gtt gat gcc gat gtg gtg tcc  163
Gly Asp Gly Thr Val Gly Glu Gly Gly Val Asp Ala Asp Val Val Ser
      10                15                20

```

```

gcc gaa ttg gat gga cca gtc gga gtc gct gct tgg atc gcc gaa gaa  211
Ala Glu Leu Asp Gly Pro Val Gly Val Ala Ala Trp Ile Ala Glu Glu
      25                30                35

```

```

tgc gat gta gta ctg gcc gag gga atc ctc ggt ggt gtt gct ttc gtc  259
Cys Asp Val Val Leu Ala Glu Gly Ile Leu Gly Gly Val Ala Phe Val
      40                45                50

```

```

gtt gag gta ctg atc gct agc cat gat gtc ttc gat cat ttg gta ggc  307
Val Glu Val Leu Ile Ala Ser His Asp Val Phe Asp His Leu Val Gly
      55                60                65

```

```

gtc gtc gtt gag cag gtt ctt cag cac gtt gag ggc agc tgc ttg ctg  355
Val Val Val Glu Gln Val Leu Gln His Val Glu Gly Ser Cys Leu Leu
      70                75                80                85

```

```

ttc ctc agt gag gtc ggt gag gtt cac gcc gga acg ctg cac gaa ggt 403
Phe Leu Ser Glu Val Gly Glu Val His Ala Gly Thr Leu His Glu Gly
          90                      95                      100

gac tgg gaa gtt aga cca gcc ggt gga ctt ttc ttc ggc gtc gta gtc 451
Asp Trp Glu Val Arg Pro Ala Gly Gly Leu Phe Phe Gly Val Val Val
          105                      110                      115

gta gag tac ggc gtc ttg ttc ttc ggt gga cag ggt gga caa gaa agc 499
Val Glu Tyr Gly Val Leu Phe Phe Gly Gly Gln Gly Gly Gln Glu Ser
          120                      125                      130

ttg ggc agc ttc cgc ggt gtt gga gat ggt ttc ggc ggt ggt gct 544
Leu Gly Ser Phe Arg Gly Val Gly Asp Gly Phe Gly Gly Gly Ala
          135                      140                      145

tgagtcggag gaagaggagg aag 567

```

<210> 1262

<211> 148

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1262

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Val Gly Trp Gly Glu Gly Asp Gly Thr Val Gly Glu Gly Gly Val Asp
  1                      5                      10                      15

```

```

Ala Asp Val Val Ser Ala Glu Leu Asp Gly Pro Val Gly Val Ala Ala
  20                      25                      30

```

```

Trp Ile Ala Glu Glu Cys Asp Val Val Leu Ala Glu Gly Ile Leu Gly
  35                      40                      45

```

```

Gly Val Ala Phe Val Val Glu Val Leu Ile Ala Ser His Asp Val Phe
  50                      55                      60

```

```

Asp His Leu Val Gly Val Val Val Glu Gln Val Leu Gln His Val Glu
  65                      70                      75                      80

```

```

Gly Ser Cys Leu Leu Phe Leu Ser Glu Val Gly Glu Val His Ala Gly
  85                      90                      95

```

```

Thr Leu His Glu Gly Asp Trp Glu Val Arg Pro Ala Gly Gly Leu Phe
  100                      105                      110

```

```

Phe Gly Val Val Val Val Glu Tyr Gly Val Leu Phe Phe Gly Gly Gln
  115                      120                      125

```

```

Gly Gly Gln Glu Ser Leu Gly Ser Phe Arg Gly Val Gly Asp Gly Phe
  130                      135                      140

```

```

Gly Gly Gly Ala
145

```

<210> 1263

<211> 1899

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1876)

<223> RXN02693

<400> 1263

cagaccaagt gttatttttg ttgaaaaaat cacattgttaa atcgagcaaaa accaacctat 60

gccctgcaga attgtgcattg ctctgccaaag atgactcaat atg gtt tcg ctc ccc 115
 Met Val Ser Leu Pro
 1 5

aga cta gcg tct ctg ctc acc act cgc ctg gca acg ctt aaa ccc gca 163
 Arg Leu Ala Ser Leu Leu Thr Thr Arg Leu Ala Thr Leu Lys Pro Ala
 10 15 20

cta aaa cct gcc acc cac ctc gcc tcc ctc ggc gcg cag gtc att gca 211
 Leu Lys Pro Ala Thr His Leu Ala Ser Leu Gly Ala Gln Val Ile Ala
 25 30 35

gag cta gtt ccg ggg atc cga atg tcg cca aac cgc agg cga atc ctc 259
 Glu Leu Val Pro Gly Ile Arg Met Ser Pro Asn Arg Arg Arg Ile Leu
 40 45 50

cct gca aat atg ggc gct ggc ttt atc gga gcg gaa atc gca atg tgg 307
 Pro Ala Asn Met Gly Ala Gly Phe Ile Gly Ala Glu Ile Ala Met Trp
 55 60 65

tgg gct ctc tcg ccg tca ttg ttg ccg aaa ccg tgg tgg gtt acg gct 355
 Trp Ala Leu Ser Pro Ser Leu Leu Pro Lys Pro Trp Trp Val Thr Ala
 70 75 80 85

gct aac ctg gct gtt tta caa gcg gtg ggg cat gcg gca gcg acg gga 403
 Ala Asn Leu Ala Val Leu Gln Ala Val Gly His Ala Ala Ala Thr Gly
 90 95 100

atc cac tcg atc ctc ccc aga acc aac cgg cgg gta tcc agg aaa att 451
 Ile His Ser Ile Leu Pro Arg Thr Asn Arg Arg Val Ser Arg Lys Ile
 105 110 115

tac aac gcc acc cac atc gca act ggt gcc atc acg ttg acc acc acg 499
 Tyr Asn Ala Thr His Ile Ala Thr Gly Ala Ile Thr Leu Thr Thr Thr
 120 125 130

gtt gtg gga ttg atc agg cat cgc acc caa atc cgg ctg att ggg cag 547
 Val Val Gly Leu Ile Arg His Arg Thr Gln Ile Arg Leu Ile Gly Gln
 135 140 145

aag aat ttt gga ccg aag gag acg atc gcg ggc att agt gtc ggc acc 595
 Lys Asn Phe Gly Pro Lys Glu Thr Ile Ala Gly Ile Ser Val Gly Thr
 150 155 160 165

ttg ggg tac ggc gcg ctg ctg atc acc ggc gaa tta acc cag cac agt 643
 Leu Gly Tyr Gly Ala Leu Leu Ile Thr Gly Glu Leu Thr Gln His Ser
 170 175 180

att aat gag gtc aag ctc cta att gag agg ttt tta ccg ccg tgg ata 691
 Ile Asn Glu Val Lys Leu Leu Ile Glu Arg Phe Leu Pro Pro Trp Ile
 185 190 195

agt ttc atc gca gcg gtt tcg gtc att aca ttg acc act ttg acc ttg	739
Ser Phe Ile Ala Ala Val Ser Val Ile Thr Leu Thr Thr Leu Thr Leu	
200 205 210	
gcc gat cgc gtt ttg ttg cgg cgc atc ttg cat aat tct gca att caa	787
Ala Asp Arg Val Leu Leu Arg Arg Ile Leu His Asn Ser Ala Ile Gln	
215 220 225	
gca gcg cac ctt aat cgc atg gtg ttc cca gga act gag cag ccg tgg	835
Ala Ala His Leu Asn Arg Met Val Phe Pro Gly Thr Glu Gln Pro Trp	
230 235 240 245	
gag ccg gag cgt tcg ggt agc ccg tgg tcg tat gaa aaa tgg ggt gcg	883
Glu Pro Glu Arg Ser Gly Ser Pro Trp Ser Tyr Glu Lys Trp Gly Ala	
250 255 260	
gtg ggt tcg cag ggc cgt gca gtg ttg tcg gga ggc cca cgc aaa gat	931
Val Gly Ser Gln Gly Arg Ala Val Leu Ser Gly Gly Pro Arg Lys Asp	
265 270 275	
gac atc atc acg gta acc agg ctt tct gac acg gaa aca cat gaa ccg	979
Asp Ile Ile Thr Val Thr Arg Leu Ser Asp Thr Glu Thr His Glu Pro	
280 285 290	
att cgt att ttt atc ggt atg gtt ccg gga cga tcc tta agc gat cag	1027
Ile Arg Ile Phe Ile Gly Met Val Pro Gly Arg Ser Leu Ser Asp Gln	
295 300 305	
gtg gat ctt gtc att cat gaa atg cgc cgc acg gga gcc ctg cgc cgc	1075
Val Asp Leu Val Ile His Glu Met Arg Arg Thr Gly Ala Leu Arg Arg	
310 315 320 325	
gac cac atc gtg atc aac aat tcc acg ggc acc ggc tgg atc acc gat	1123
Asp His Ile Val Ile Asn Asn Ser Thr Gly Thr Gly Trp Ile Thr Asp	
330 335 340	
tgg tcc gcc cac acc ttt gag ttc ctc acc ggc gga aac tgc gtg aca	1171
Trp Ser Ala His Thr Phe Glu Phe Leu Thr Gly Gly Asn Cys Val Thr	
345 350 355	
att tcc atg caa tat tct tat ctt ccc agt gca ctg agc tgg tac aag	1219
Ile Ser Met Gln Tyr Ser Tyr Leu Pro Ser Ala Leu Ser Trp Tyr Lys	
360 365 370	
gac aac gac ggc ccc att aat gcg gcg aga atg ctt atc gac gcc gtc	1267
Asp Asn Asp Gly Pro Ile Asn Ala Ala Arg Met Leu Ile Asp Ala Val	
375 380 385	
ctc cac gag cta gac cag ctt ccc acc ggg agt cgc cca aag ctg ttc	1315
Leu His Glu Leu Asp Gln Leu Pro Thr Gly Ser Arg Pro Lys Leu Phe	
390 395 400 405	
ctc gcg gga gag tca ctg ggg gcg tat ggg ttg gct gag gtg tgg gga	1363
Leu Ala Gly Glu Ser Leu Gly Ala Tyr Gly Leu Ala Glu Val Trp Gly	
410 415 420	
gac gtc gaa aag ctt ctt gga acc gct gac ggc gtg ctg ctc agt ggg	1411
Asp Val Glu Lys Leu Leu Gly Thr Ala Asp Gly Val Leu Leu Ser Gly	
425 430 435	
gcg ccg cgt ttt tcg gac gcc atg aat gcg ttg cgc acc ccg cgc gat	1459

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Ala Pro Arg Phe Ser Asp Ala Met Asn Ala Leu Arg Thr Arg Arg Asp
    440                      445                      450
gcg agc agc tcc gag cgg ctg ccc gtg att gat agc ggg cgg cac atc 1507
Ala Ser Ser Ser Glu Arg Leu Pro Val Ile Asp Ser Gly Arg His Ile
    455                      460                      465

cgt ttt gcg ggc gag cct gag cac ctt gat atg ccg gct acc tgg cag 1555
Arg Phe Ala Gly Glu Pro Glu His Leu Asp Met Pro Ala Thr Trp Gln
    470                      475                      480                      485

ttt ccg cgc atg atc gtg cgc cag cac gcc tct gat cca att gtg tgg 1603
Phe Pro Arg Met Ile Val Ala Gln His Ala Ser Asp Pro Ile Val Trp
    490                      495                      500

tgg aac gcg gag ctg ttt att cgg cgg ccg gaa tgg ttg aaa act ccc 1651
Trp Asn Ala Glu Leu Phe Ile Arg Arg Pro Glu Trp Leu Lys Thr Pro
    505                      510                      515

aag caa gac cac caa gat gtc ttt ccc cgc ttg cga tgg atg ccg ttt 1699
Lys Gln Asp His Gln Asp Val Phe Pro Arg Leu Arg Trp Met Pro Phe
    520                      525                      530

gta acc ggc tgg cag gtg gct ttg gat ttg ttc act tca acc tcc gtt 1747
Val Thr Gly Trp Gln Val Ala Leu Asp Leu Phe Thr Ser Thr Ser Val
    535                      540                      545

ccc ggc ggg cac ggg cac aat tat cac gag gag ttt att gat tat tgg 1795
Pro Gly Gly His Gly His Asn Tyr His Glu Glu Phe Ile Asp Tyr Trp
    550                      555                      560                      565

gca gct ctt ttg gac cgc gaa gtc acc ccc gag ctg cgc cac agc att 1843
Ala Ala Leu Leu Asp Arg Glu Val Thr Pro Glu Leu Arg His Ser Ile
    570                      575                      580

gct tat tgg atc cgc gcg aac cac atc aaa cgc tagagtgatt ccattgacgca 1896
Ala Tyr Trp Ile Arg Ala Asn His Ile Lys Arg
    585                      590

tgc 1899

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<210> 1264

<211> 592

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1264

```

Met Val Ser Leu Pro Arg Leu Ala Ser Leu Leu Thr Thr Arg Leu Ala
  1                      5                      10                      15

Thr Leu Lys Pro Ala Leu Lys Pro Ala Thr His Leu Ala Ser Leu Gly
  20                      25                      30

Ala Gln Val Ile Ala Glu Leu Val Pro Gly Ile Arg Met Ser Pro Asn
  35                      40                      45

Arg Arg Arg Ile Leu Pro Ala Asn Met Gly Ala Gly Phe Ile Gly Ala
  50                      55                      60

Glu Ile Ala Met Trp Trp Ala Leu Ser Pro Ser Leu Leu Pro Lys Pro

```

65	70					75					80				
Trp Trp Val Thr	Ala 85	Ala	Asn	Leu	Ala	Val 90	Leu	Gln	Ala	Val	Gly 95	His			
Ala Ala Ala Thr	Gly 100	Ile	His	Ser	Ile 105	Leu	Pro	Arg	Thr	Asn 110	Arg	Arg			
Val Ser Arg Lys	Ile 115	Tyr	Asn	Ala 120	Thr	His	Ile	Ala 125	Thr	Gly	Ala	Ile			
Thr Leu Thr Thr	Thr 130	Val	Val 135	Gly	Leu	Ile	Arg	His 140	Arg	Thr	Gln	Ile			
Arg Leu Ile Gly	Gln 145	Lys	Asn 150	Phe	Gly	Pro	Lys 155	Glu	Thr	Ile	Ala	Gly 160			
Ile Ser Val Gly	Thr 165	Leu	Gly	Tyr	Gly 170	Ala	Leu	Leu	Ile	Thr	Gly 175	Glu			
Leu Thr Gln His	Ser 180	Ile	Asn	Glu	Val 185	Lys	Leu	Leu	Ile	Glu	Arg	Phe			
Leu Pro Pro Trp	Ile 195	Ser	Phe	Ile 200	Ala	Val	Ser	Val 205	Ile	Thr	Leu				
Thr Thr Leu Thr	Leu 210	Ala	Asp 215	Arg	Val	Leu	Leu	Arg 220	Arg	Ile	Leu	His			
Asn Ser Ala Ile	Gln 225	Ala	Ala 230	His	Leu	Asn	Arg 235	Met	Val	Phe	Pro	Gly 240			
Thr Glu Gln Pro	Trp 245	Glu	Pro	Glu	Arg	Ser	Gly 250	Ser	Pro	Trp	Ser	Tyr 255			
Glu Lys Trp Gly	Ala 260	Val	Gly	Ser	Gln 265	Gly	Arg	Ala	Val	Leu	Ser	Gly 270			
Gly Pro Arg Lys	Asp 275	Asp	Ile	Ile 280	Thr	Val	Thr	Arg	Leu	Ser	Asp	Thr 285			
Glu Thr His Glu	Pro 290	Ile	Arg 295	Ile	Phe	Ile	Gly	Met 300	Val	Pro	Gly	Arg			
Ser Leu Ser Asp	Gln 305	Val	Asp 310	Leu	Val	Ile	His 315	Glu	Met	Arg	Arg	Thr 320			
Gly Ala Leu Arg	Arg 325	Asp	His	Ile	Val	Ile	Asn 330	Asn	Ser	Thr	Gly	Thr 335			
Gly Trp Ile Thr	Asp 340	Trp	Ser	Ala	His 345	Thr	Phe	Glu	Phe	Leu	Thr	Gly 350			
Gly Asn Cys Val	Thr 355	Ile	Ser	Met 360	Gln	Tyr	Ser	Tyr	Leu	Pro	Ser	Ala 365			
Leu Ser Trp Tyr	Lys 370	Asp	Asn	Asp 375	Gly	Pro	Ile	Asn	Ala	Ala	Arg	Met 380			
Leu Ile Asp Ala	Val 385	Leu	His	Glu	Leu	Asp	Gln 390	Leu	Pro	Thr	Gly	Ser 400			

Arg Pro Lys Leu Phe Leu Ala Gly Glu Ser Leu Gly Ala Tyr Gly Leu
 405 410 415
 Ala Glu Val Trp Gly Asp Val Glu Lys Leu Leu Gly Thr Ala Asp Gly
 420 425 430
 Val Leu Leu Ser Gly Ala Pro Arg Phe Ser Asp Ala Met Asn Ala Leu
 435 440 445
 Arg Thr Arg Arg Asp Ala Ser Ser Ser Glu Arg Leu Pro Val Ile Asp
 450 455 460
 Ser Gly Arg His Ile Arg Phe Ala Gly Glu Pro Glu His Leu Asp Met
 465 470 475 480
 Pro Ala Thr Trp Gln Phe Pro Arg Met Ile Val Ala Gln His Ala Ser
 485 490 495
 Asp Pro Ile Val Trp Trp Asn Ala Glu Leu Phe Ile Arg Arg Pro Glu
 500 505 510
 Trp Leu Lys Thr Pro Lys Gln Asp His Gln Asp Val Phe Pro Arg Leu
 515 520 525
 Arg Trp Met Pro Phe Val Thr Gly Trp Gln Val Ala Leu Asp Leu Phe
 530 535 540
 Thr Ser Thr Ser Val Pro Gly Gly His Gly His Asn Tyr His Glu Glu
 545 550 555 560
 Phe Ile Asp Tyr Trp Ala Ala Leu Leu Asp Arg Glu Val Thr Pro Glu
 565 570 575
 Leu Arg His Ser Ile Ala Tyr Trp Ile Arg Ala Asn His Ile Lys Arg
 580 585 590

<210> 1265

<211> 1747

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1747)

<223> FRXA02693

<400> 1265

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gccctgcaga attgtgcatg ctctgccaaag atgactcaat atg gtt tgg ctc ccc 115
 Met Val Ser Leu Pro
 1 5

aga cta gcg tct ctg ctc acc act cgc ctg gca acg ctt aaa ccc gca 163
 Arg Leu Ala Ser Leu Leu Thr Thr Arg Leu Ala Thr Leu Lys Pro Ala
 10 15 20

cta aaa cct gcc acc cac ctc gcc tcc ctc ggc gcg cag gtc att gca	211
Leu Lys Pro Ala Thr His Leu Ala Ser Leu Gly Ala Gln Val Ile Ala	
25 30 35	
gag cta gtt ccg ggg atc cga atg tcg cca aac cgc agg cga atc ctc	259
Glu Leu Val Pro Gly Ile Arg Met Ser Pro Asn Arg Arg Ile Leu	
40 45 50	
cct gca aat atg ggc gct ggc ttt atc gga gcg gaa atc gca atg tgg	307
Pro Ala Asn Met Gly Ala Gly Phe Ile Gly Ala Gln Ile Ala Met Trp	
55 60 65	
tgg gct ctc tcg ccg tca ttg ttg ccg aaa ccg tgg tgg gtt acg gct	355
Trp Ala Leu Ser Pro Ser Leu Leu Pro Lys Pro Trp Trp Val Thr Ala	
70 75 80 85	
gct aac ctg gct gtt tta caa gcg gtg ggg cat gcg gca gcg acg gga	403
Ala Asn Leu Ala Val Leu Gln Ala Val Gly His Ala Ala Ala Thr Gly	
90 95 100	
atc cac tcg atc ctc ccc aga acc aac ccg ccg gta tcc agg aaa att	451
Ile His Ser Ile Leu Pro Arg Thr Asn Arg Arg Val Ser Arg Lys Ile	
105 110 115	
tac aac gcc acc cac atc gca act ggt gcc atc acg ttg acc acc acg	499
Tyr Asn Ala Thr His Ile Ala Thr Gly Ala Ile Thr Leu Thr Thr Thr	
120 125 130	
gtt gtg gga ttg atc agg cat gcg acc caa atc ccg ctg att ggg cag	547
Val Val Gly Leu Ile Arg His Arg Thr Gln Ile Arg Leu Ile Gly Gln	
135 140 145	
aag aat ttt gga ccg aag gag acg atc gcg gcc att agt gtc gcc acc	595
Lys Asn Phe Gly Pro Lys Glu Thr Ile Ala Gly Ile Ser Val Gly Thr	
150 155 160 165	
ttg ggg tac ggc gcg ctg ctg atc acc gcc gaa tta acc cag cac agt	643
Leu Gly Tyr Gly Ala Leu Leu Ile Thr Gly Glu Leu Thr Gln His Ser	
170 175 180	
att aat gag gtc aag ctc cta att gag agg ttt tta ccg ccg tgg ata	691
Ile Asn Glu Val Lys Leu Leu Ile Glu Arg Phe Leu Pro Pro Trp Ile	
185 190 195	
agt ttc atc gca gcg gtt tcg gtc att aca ttg acc act ttg acc ttg	739
Ser Phe Ile Ala Ala Val Ser Val Ile Thr Leu Thr Thr Leu Leu	
200 205 210	
gcc gat cgc gtt ttg ttg ccg gcg atc ttg cat aat tct gca att caa	787
Ala Asp Arg Val Leu Leu Arg Arg Ile Leu His Asn Ser Ala Ile Gln	
215 220 225	
gca gcg cac ctt aat cgc atg gtg ttc cca gga act gag cag ccg tgg	835
Ala Ala His Leu Asn Arg Met Val Phe Pro Gly Thr Glu Gln Pro Trp	
230 235 240 245	
gag ccg gag cgt tcg ggt agc ccg tgg tcg tat gaa aaa tgg ggt gcg	883
Glu Pro Glu Arg Ser Gly Ser Pro Trp Ser Tyr Glu Lys Trp Gly Ala	
250 255 260	

gtg ggt tgc cag ggc cgt gca gtg ttg tgc gga ggc cca cgc aaa gat	931
Val Gly Ser Gln Gly Arg Ala Val Leu Ser Gly Gly Pro Arg Lys Asp	
265 270 275	
gac atc atc acg gta acc agg ctt tct gac acg gaa aca cat gaa ccg	979
Asp Ile Ile Thr Val Thr Arg Leu Ser Asp Thr Glu Thr His Glu Pro	
280 285 290	
att cgt att ttt atc ggt atg gtt ccg gga cga tcc tta agc gat cag	1027
Ile Arg Ile Phe Ile Gly Met Val Pro Gly Arg Ser Leu Ser Asp Gln	
295 300 305	
gtg gat ctt gtc att cat gaa atg cgc cgc acg gga gcc ctg cgc cgc	1075
Val Asp Leu Val Ile His Glu Met Arg Arg Thr Gly Ala Leu Arg Arg	
310 315 320 325	
gac cac atc gtg atc aac aat tcc acg ggc acc ggc tgg atc acc gat	1123
Asp His Ile Val Ile Asn Asn Ser Thr Gly Thr Gly Trp Ile Thr Asp	
330 335 340	
tgg tcc gcc cac acc ttt gag ttc ctc acc ggc gga aac tgc gtg aca	1171
Trp Ser Ala His Thr Phe Glu Phe Leu Thr Gly Gly Asn Cys Val Thr	
345 350 355	
att tcc atg caa tat tct tat ctt ccc agt gca ctg agc tgg tac aag	1219
Ile Ser Met Gln Tyr Ser Tyr Leu Pro Ser Ala Leu Ser Trp Tyr Lys	
360 365 370	
gac aac gac ggc ccc att aat gcg gcg aga atg ctt atc gac gcc gtc	1267
Asp Asn Asp Gly Pro Ile Asn Ala Ala Arg Met Leu Ile Asp Ala Val	
375 380 385	
ctc cac gag cta gac cag ctt ccc acc ggg agt cgc cca aag ctg ttc	1315
Leu His Glu Leu Asp Gln Leu Pro Thr Gly Ser Arg Pro Lys Leu Phe	
390 395 400 405	
ctc gcg gga gag tca ctg ggg gcg tat ggg ttg gct gag gtg tgg gga	1363
Leu Ala Gly Glu Ser Leu Gly Ala Tyr Gly Leu Ala Glu Val Trp Gly	
410 415 420	
gac gtc gaa aag ctt ctt gga acc gct gac ggc gtg ctg ctc agt ggg	1411
Asp Val Glu Lys Leu Leu Gly Thr Ala Asp Gly Val Leu Leu Ser Gly	
425 430 435	
gcg ccg cgt ttt tgc gac gcc atg aat gcg ttg cgc acc cgg cgc gat	1459
Ala Pro Arg Phe Ser Asp Ala Met Asn Ala Leu Arg Thr Arg Arg Asp	
440 445 450	
gcg agc agc tcc gag cgg ctg ccc gtg att gat agc ggg cgg cac atc	1507
Ala Ser Ser Ser Glu Arg Leu Pro Val Ile Asp Ser Gly Arg His Ile	
455 460 465	
cgt ttt gcg ggc gag cct gag cac ctt gat atg ccg gct acc tgg cag	1555
Arg Phe Ala Gly Glu Pro Glu His Leu Asp Met Pro Ala Thr Trp Gln	
470 475 480 485	
ttt ccg cgc atg atc gtg gcg cag cac gcc tct gat cca att gtg tgg	1603
Phe Pro Arg Met Ile Val Ala Gln His Ala Ser Asp Pro Ile Val Trp	
490 495 500	
tgg aac gcg gag ctg ttt att cgg cgg ccg gaa tgg ttg aaa act ccc	1651

Trp Asn Ala Glu Leu Phe Ile Arg Arg Pro Glu Trp Leu Lys Thr Pro
 505 510 515
 aag caa gac cac caa gat gtc ttt aac cgc ttg cga tgg atg ccg ttt 1699
 Lys Gln Asp His Gln Asp Val Phe Asn Arg Leu Arg Trp Met Pro Phe
 520 525 530
 gtt gcc ggc tgg cag gtg gct ttg gat ttg ttc act tca acc tcc gtt 1747
 Val Ala Gly Trp Gln Val Ala Leu Asp Leu Phe Thr Ser Thr Ser Val
 535 540 545
 <210> 1266
 <211> 549
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 1266
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 1 5 10 15
 Thr Leu Lys Pro Ala Leu Lys Pro Ala Thr His Leu Ala Ser Leu Gly
 20 25 30
 Ala Gln Val Ile Ala Glu Leu Val Pro Gly Ile Arg Met Ser Pro Asn
 35 40 45
 Arg Arg Arg Ile Leu Pro Ala Asn Met Gly Ala Gly Phe Ile Gly Ala
 50 55 60
 Glu Ile Ala Met Trp Trp Ala Leu Ser Pro Ser Leu Leu Pro Lys Pro
 65 70 75 80
 Trp Trp Val Thr Ala Ala Asn Leu Ala Val Leu Gln Ala Val Gly His
 85 90 95
 Ala Ala Ala Thr Gly Ile His Ser Ile Leu Pro Arg Thr Asn Arg Arg
 100 105 110
 Val Ser Arg Lys Ile Tyr Asn Ala Thr His Ile Ala Thr Gly Ala Ile
 115 120 125
 Thr Leu Thr Thr Thr Val Val Gly Leu Ile Arg His Arg Thr Gln Ile
 130 135 140
 Arg Leu Ile Gly Gln Lys Asn Phe Gly Pro Lys Glu Thr Ile Ala Gly
 145 150 155 160
 Ile Ser Val Gly Thr Leu Gly Tyr Gly Ala Leu Leu Ile Thr Gly Glu
 165 170 175
 Leu Thr Gln His Ser Ile Asn Glu Val Lys Leu Leu Ile Glu Arg Phe
 180 185 190
 Leu Pro Pro Trp Ile Ser Phe Ile Ala Ala Val Ser Val Ile Thr Leu
 195 200 205
 Thr Thr Leu Thr Leu Ala Asp Arg Val Leu Leu Arg Arg Ile Leu His
 210 215 220
 Asn Ser Ala Ile Gln Ala Ala His Leu Asn Arg Met Val Phe Pro Gly

225		230		235		240
Thr Glu Gln Pro Trp	Glu Pro Glu Arg Ser Gly Ser Pro Trp Ser Tyr					
	245			250		255
Glu Lys Trp Gly Ala Val Gly Ser Gln Gly Arg Ala Val Leu Ser Gly						
	260			265		270
Gly Pro Arg Lys Asp Asp Ile Ile Thr Val Thr Arg Leu Ser Asp Thr						
	275			280		285
Glu Thr His Glu Pro Ile Arg Ile Phe Ile Gly Met Val Pro Gly Arg						
	290			295		300
Ser Leu Ser Asp Gln Val Asp Leu Val Ile His Glu Met Arg Arg Thr						
	305			310		315
Gly Ala Leu Arg Arg Asp His Ile Val Ile Asn Asn Ser Thr Gly Thr						
	325			330		335
Gly Trp Ile Thr Asp Trp Ser Ala His Thr Phe Glu Phe Leu Thr Gly						
	340			345		350
Gly Asn Cys Val Thr Ile Ser Met Gln Tyr Ser Tyr Leu Pro Ser Ala						
	355			360		365
Leu Ser Trp Tyr Lys Asp Asn Asp Gly Pro Ile Asn Ala Ala Arg Met						
	370			375		380
Leu Ile Asp Ala Val Leu His Glu Leu Asp Gln Leu Pro Thr Gly Ser						
	385			390		395
Arg Pro Lys Leu Phe Leu Ala Gly Glu Ser Leu Gly Ala Tyr Gly Leu						
	405			410		415
Ala Glu Val Trp Gly Asp Val Glu Lys Leu Leu Gly Thr Ala Asp Gly						
	420			425		430
Val Leu Leu Ser Gly Ala Pro Arg Phe Ser Asp Ala Met Asn Ala Leu						
	435			440		445
Arg Thr Arg Arg Asp Ala Ser Ser Ser Glu Arg Leu Pro Val Ile Asp						
	450			455		460
Ser Gly Arg His Ile Arg Phe Ala Gly Glu Pro Glu His Leu Asp Met						
	465			470		475
Pro Ala Thr Trp Gln Phe Pro Arg Met Ile Val Ala Gln His Ala Ser						
	485			490		495
Asp Pro Ile Val Trp Trp Asn Ala Glu Leu Phe Ile Arg Arg Pro Glu						
	500			505		510
Trp Leu Lys Thr Pro Lys Gln Asp His Gln Asp Val Phe Asn Arg Leu						
	515			520		525
Arg Trp Met Pro Phe Val Ala Gly Trp Gln Val Ala Leu Asp Leu Phe						
	530			535		540
Thr Ser Thr Ser Val						
545						

<210> 1267

<211> 579

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(556)

<223> RXN02696

<400> 1267

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cacatgaaat	ttaagacatt	ccagggtgaag	ggaaactgcc	atg	tcc	atg	ctc	aag	115
				Met	Ser	Met	Leu	Lys	
				1				5	

aag	act	aaa	gaa	ttc	ttc	gga	ctc	gct	cca	tac	gaa	gcg	gag	cac	gag	163
Lys	Thr	Lys	Glu	Phe	Phe	Gly	Leu	Ala	Pro	Tyr	Glu	Ala	Glu	His	Glu	
			10						15				20			

gat	gct	tac	tat	gca	gat	gaa	cca	cgt	tac	gag	ggc	acc	gct	gcg	tac	211
Asp	Ala	Tyr	Tyr	Ala	Asp	Glu	Pro	Arg	Tyr	Glu	Gly	Thr	Ala	Ala	Tyr	
			25					30				35				

gca	cct	gaa	tac	cgt	gag	cgt	gac	tac	ggc	tat	gca	cca	gag	gca	cca	259
Ala	Pro	Glu	Tyr	Arg	Glu	Arg	Asp	Tyr	Gly	Tyr	Ala	Pro	Glu	Ala	Pro	
		40					45					50				

gcc	cct	gtt	gct	cca	tcg	cca	gca	cct	cgc	tct	tac	cag	tcc	acc	atc	307
Ala	Pro	Val	Ala	Pro	Ser	Pro	Ala	Pro	Arg	Ser	Tyr	Gln	Ser	Thr	Ile	
		55				60					65					

gtt	cca	gta	gag	ctt	cat	tcc	ttt	gaa	gac	gct	cag	gtt	att	ggt	gga	355
Val	Pro	Val	Glu	Leu	His	Ser	Phe	Glu	Asp	Ala	Gln	Val	Ile	Gly	Gly	
		70			75					80				85		

gca	ttt	cgc	gac	ggc	gac	gca	gtt	gtt	ttc	gac	atg	agc	ttg	ctt	tcc	403
Ala	Phe	Arg	Asp	Gly	Asp	Ala	Val	Val	Phe	Asp	Met	Ser	Leu	Leu	Ser	
			90					95					100			

cgt	gag	gaa	gca	cgc	cgc	att	gtg	gac	ttc	gct	gca	ggc	ctg	tgc	ttc	451
Arg	Glu	Glu	Ala	Arg	Arg	Ile	Val	Asp	Phe	Ala	Ala	Gly	Leu	Cys	Phe	
			105				110						115			

gca	ttg	cgt	ggc	aag	atg	cag	aag	att	gac	agc	gtc	acc	ttc	gct	gtc	499
Ala	Leu	Arg	Gly	Lys	Met	Gln	Lys	Ile	Asp	Ser	Val	Thr	Phe	Ala	Val	
		120					125					130				

gtt	cca	gag	ctg	tcc	aac	atc	agc	act	tcc	gag	ctc	gag	cgc	gcc	gca	547
Val	Pro	Glu	Leu	Ser	Asn	Ile	Ser	Thr	Ser	Glu	Leu	Glu	Arg	Ala	Ala	
		135				140					145					

cgc	atc	cgc	taa	acacacc	ctc	gtg	gtgt	gga	579
Arg	Ile	Arg							
150									

<210> 1268

<211> 152

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1268

Met Ser Met Leu Lys Lys Thr Lys Glu Phe Phe Gly Leu Ala Pro Tyr
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Glu Ala Glu His Glu Asp Ala Tyr Tyr Ala Asp Glu Pro Arg Tyr Glu
 20 25 30

Gly Thr Ala Ala Tyr Ala Pro Glu Tyr Arg Glu Arg Asp Tyr Gly Tyr
 35 40 45

Ala Pro Glu Ala Pro Ala Pro Val Ala Pro Ser Pro Ala Pro Arg Ser
 50 55 60

Tyr Gln Ser Thr Ile Val Pro Val Glu Leu His Ser Phe Glu Asp Ala
 65 70 75 80

Gln Val Ile Gly Gly Ala Phe Arg Asp Gly Asp Ala Val Val Phe Asp
 85 90 95

Met Ser Leu Leu Ser Arg Glu Glu Ala Arg Arg Ile Val Asp Phe Ala
 100 105 110

Ala Gly Leu Cys Phe Ala Leu Arg Gly Lys Met Gln Lys Ile Asp Ser
 115 120 125

Val Thr Phe Ala Val Val Pro Glu Leu Ser Asn Ile Ser Thr Ser Glu
 130 135 140

Leu Glu Arg Ala Ala Arg Ile Arg
 145 150

<210> 1269

<211> 578

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (100)..(555)

<223> FRXA02696

<400> 1269

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gctgtacatn taagtcattn ctggttnagg tganctgacctg tcc atg ctc aag aag 117
 Met Ser Met Leu Lys Lys
 1 5

act aaa gaa ttc ttc gga ctc gct cca tac gaa gcg gag cac gag gat 165
 Thr Lys Glu Phe Phe Gly Leu Ala Pro Tyr Glu Ala Glu His Glu Asp
 10 15 20

gct tac tat gca gat gaa cca cgt tac gag ggc acc gct gcg tac gca 213
 Ala Tyr Tyr Ala Asp Glu Pro Arg Tyr Glu Gly Thr Ala Ala Tyr Ala
 25 30 35

cct gaa tac cgt gag cgt gac tac ggc tat gca cca gag gca cca gcc 261
Pro Glu Tyr Arg Glu Arg Asp Tyr Gly Tyr Ala Pro Glu Ala Pro Ala
40 45 50

cct gtt gct cca tcg cca gca cct cgc tct tac cag tcc acc atc gtt 309
Pro Val Ala Pro Ser Pro Ala Pro Arg Ser Tyr Gln Ser Thr Ile Val
55 60 65 70

cca gta gag ctt cat tcc ttt gaa gac gct cag gtt att ggt gga gca 357
Pro Val Glu Leu His Ser Phe Glu Asp Ala Gln Val Ile Gly Gly Ala
75 80 85

t t t c g c g a c g g c g a c g c a g t t g t t t t c g a c a t g a g c t t g c t t t c c g t 405
Phe Arg Asp Gly Asp Ala Val Val Phe Asp Met Ser Leu Leu Ser Arg
90 95 100

gag gaa gca cgc cgc att gtg gac ttc gct gca ggc ctg tgc ttc gca 453
Glu Glu Ala Arg Arg Ile Val Asp Phe Ala Ala Gly Leu Cys Phe Ala
105 110 115

ttg cgt ggc aag atg cag aag att gac agc gtc acc ttc gct gtc gtt 501
Leu Arg Gly Lys Met Gln Lys Ile Asp Ser Val Thr Phe Ala Val Val
120 125 130

cca gag ctg tcc aac atc agc act tcc gag ctc gag cgc gcc gca cgc 549
Pro Glu Leu Ser Asn Ile Ser Thr Ser Glu Leu Glu Arg Ala Ala Arg
135 140 145 150

atc cgc taaacacacc ctcgtggtgt gga 578
Ile Arg

<210> 1270

<211> 152

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1270

Met Ser Met Leu Lys Lys Thr Lys Glu Phe Phe Gly Leu Ala Pro Tyr
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20 25 30

Gly Thr Ala Ala Tyr Ala Pro Glu Tyr Arg Glu Arg Asp Tyr Gly Tyr
35 40 45

Ala Pro Glu Ala Pro Ala Pro Val Ala Pro Ser Pro Ala Pro Arg Ser
50 55 60

Tyr Gln Ser Thr Ile Val Pro Val Glu Leu His Ser Phe Glu Asp Ala
65 70 75 80

Gln Val Ile Gly Gly Ala Phe Arg Asp Gly Asp Ala Val Val Phe Asp
85 90 95

Met Ser Leu Leu Ser Arg Glu Glu Ala Arg Arg Ile Val Asp Phe Ala
100 105 110

Ala Gly Leu Cys Phe Ala Leu Arg Gly Lys Met Gln Lys Ile Asp Ser

115	120	125	
Val Thr Phe Ala Val Val Pro Glu Leu Ser Asn Ile Ser Thr Ser Glu			
130	135	140	
Leu Glu Arg Ala Ala Arg Ile Arg			
145	150		

<210> 1271
 <211> 1650
 <212> DNA
 <213> *Corynebacterium glutamicum*
 <220>
 <221> CDS
 <222> (101)..(1627)
 <223> RXN02697
 <400> 1271
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 ggctatccgc tcaaccgaac gtcggatgta gtagacgcgt atg aca ctt ttt caa 115
 Met Thr Leu Phe Gln
 1 5
 cgt tta acc aac cct gta gtg ctc ggc ggc cta gca ggt gtt ttg ctt 163
 Arg Leu Thr Asn Pro Val Val Leu Gly Gly Leu Ala Gly Val Leu Leu
 10 15 20
 ctg ctc ggc tct ttc ggt ggc ggt gcc att cgg tac cgt ggc gga gtg 211
 Leu Leu Gly Ser Phe Gly Gly Gly Ala Ile Arg Tyr Arg Gly Gly Val
 25 30 35
 ctc gat gcg ttg ggg ctt aac ttc ctt gct ttt ggc cac gcg cag ggt 259
 Leu Asp Ala Leu Gly Leu Asn Phe Leu Ala Phe Gly His Ala Gln Gly
 40 45 50
 att tcc aat acc gtg ttg tgg gtt ggg cag ctg ctg ctg att ggc gcg 307
 Ile Ser Asn Thr Val Leu Trp Val Gly Gln Leu Leu Ile Gly Ala
 55 60 65
 tgg gtt cac ctt gga cgt cgg ttg ttc aag aaa aaa gtc gct gat gac 355
 Trp Val His Leu Gly Arg Arg Leu Phe Lys Lys Lys Val Ala Asp Asp
 70 75 80 85
 acc gca gac gct gct gac tta ggt ctt gta aag cgc acg ttg tat gcc 403
 Thr Ala Asp Ala Ala Asp Leu Gly Leu Val Lys Arg Thr Leu Tyr Ala
 90 95 100
 atg gtg gtg ccc ctc att ttt gcg gca cca atg atg tcg cgt gat gtt 451
 Met Val Val Pro Leu Ile Phe Ala Ala Pro Met Met Ser Arg Asp Val
 105 110 115
 tat tcc tat ctc atg cag ggc gcg atg ctg cgt gat ggc ttc gat ccc 499
 Tyr Ser Tyr Leu Met Gln Gly Ala Met Leu Arg Asp Gly Phe Asp Pro
 120 125 130
 tac act gag ggc gct gcg gta aac cct ggc ccc atg ttg ctt gag gtc 547
 Tyr Thr Glu Gly Ala Ala Val Asn Pro Gly Pro Met Leu Leu Glu Val
 135 140 145

tct cat gat tgg cgc aac acc acg acg ccg tat ggt cca cta cac ctg	595
Ser His Asp Trp Arg Asn Thr Thr Thr Pro Tyr Gly Pro Leu His Leu	
150 155 160 165	
tgg att gga gac atg acc acg gtt gtg ggc gat aat gtc acc ttg	643
Trp Ile Gly Asp Met Ile Thr Thr Val Val Gly Asp Asn Val Thr Leu	
170 175 180	
ggc gtc gtc gct tac aag atc ttg tcg atc att ggc ctt gct gtg aca	691
Gly Val Val Ala Tyr Lys Ile Leu Ser Ile Ile Gly Leu Ala Val Thr	
185 190 195	
ggc tgg agc att gtc cgc att gca caa cat ttt gga gcc aac cca gca	739
Gly Trp Ser Ile Val Arg Ile Ala Gln His Phe Gly Ala Asn Pro Ala	
200 205 210	
att gca ttg tgg att ggt gtg gcc aat cct gtg atg atc atc cac atg	787
Ile Ala Leu Trp Ile Gly Val Ala Asn Pro Val Met Ile Ile His Met	
215 220 225	
atc ggc ggc atg cac aat gaa tcc ctc atg gtg gga ttg gtc agc gtc	835
Ile Gly Gly Met His Asn Glu Ser Leu Met Val Gly Leu Val Ser Val	
230 235 240 245	
ggc ttg ttg cta gca ctg aag aag cgt ttc gtg gca ggt gtg gca ctc	883
Gly Leu Leu Leu Ala Leu Lys Lys Arg Phe Val Ala Gly Val Ala Leu	
250 255 260	
att gca gtg gct gtg tcg ctg aaa gct aca gcg gcg att gca ctt cct	931
Ile Ala Val Ala Val Ser Leu Lys Ala Thr Ala Ala Ile Ala Leu Pro	
265 270 275	
ttt gtg gtg tgg atc ggc atg cat cat ttc gca gga ttc tta gcc acc	979
Phe Val Val Trp Ile Gly Met His His Phe Ala Gly Phe Leu Ala Thr	
280 285 290	
aaa aag ggc aaa gac tcc cct acc ctt aag caa cag gtc ccc gcg ttc	1027
Lys Lys Gly Lys Asp Ser Pro Thr Leu Lys Gln Gln Val Pro Ala Phe	
295 300 305	
ttt gcc act gga gct gca ggt gtt gct gtc act ggt gtt gtt gtc agt	1075
Phe Ala Thr Gly Ala Ala Gly Val Ala Val Thr Gly Val Val Val Ser	
310 315 320 325	
gcg atc act tgg gcg tct ggc gct tcg tgg ggc tgg atc agt gag atc	1123
Ala Ile Thr Trp Ala Ser Gly Ala Ser Trp Gly Trp Ile Ser Glu Ile	
330 335 340	
agt ggc aac agc aag gta atc aac ccg ctg gct ttc cct tct ttg gtg	1171
Ser Gly Asn Ser Lys Val Ile Asn Pro Leu Ala Phe Pro Ser Leu Val	
345 350 355	
gcc agt gtg atc acc atg gtg gct gaa gtg ttc gtt gac gat ttc gac	1219
Ala Ser Val Ile Thr Met Val Ala Glu Val Phe Val Asp Asp Phe Asp	
360 365 370	
tac aac gca gtg gtt aat gtt gtg cgc tca atc tcc atg ctg atc atg	1267
Tyr Asn Ala Val Val Asn Val Val Arg Ser Ile Ser Met Leu Ile Met	
375 380 385	

ctt ggc ggg ttg gtc gta tgt tgg tgg ctg ttc cgc cag aac gaa cgc 1315
 Leu Gly Gly Leu Val Val Cys Trp Trp Leu Phe Arg Gln Asn Glu Arg
 390 395 400 405

agg gcg gtc act ggt aca gca gcg gct tat gcc gtg gct ttt gtg ttc 1363
 Arg Ala Val Thr Gly Thr Ala Ala Ala Tyr Ala Val Ala Phe Val Phe
 410 415 420

aat tct gtg acc ttg ccg tgg tac tac gcc agc ttg atc tct ttg ctc 1411
 Asn Ser Val Thr Leu Pro Trp Tyr Tyr Ala Ser Leu Ile Ser Leu Leu
 425 430 435

ggc aca ttt aaa cca ccg atg tgg ttg att cgc ttc gca gcg ggt gct 1459
 Gly Thr Phe Lys Pro Pro Met Trp Leu Ile Arg Phe Ala Ala Gly Ala
 440 445 450

tgc gtg ttt atc gcg ctg ttt acc gga agt gga aac cac cag ctg 1507
 Ser Val Phe Ile Ala Leu Met Phe Thr Gly Ser Gly Asn His Gln Leu
 455 460 465

tac aac atc gtt acg gtg atc atc gca gca att atc gcg tgg ctt gcc 1555
 Tyr Asn Ile Val Thr Val Ile Ile Ala Ala Ile Ile Ala Trp Leu Ala
 470 475 480 485

acc gtg gtg atc ttt gat gac act gac cct gca aca acg gcc acg gag 1603
 Thr Val Val Ile Phe Asp Asp Thr Asp Pro Ala Thr Thr Ala Thr Glu
 490 495 500

aaa ccc tcc ccg cat acc gtt tcc tagttgcata aggtaaaccg cca 1650
 Lys Pro Ser Pro His Thr Val Ser
 505

<210> 1272

<211> 509

<212> PRT

<213> Corynebacterium glutamicum

<400> 1272

Met Thr Leu Phe Gln Arg Leu Thr Asn Pro Val Val Leu Gly Gly Leu
 1 5 10 15

Ala Gly Val Leu Leu Leu Leu Gly Ser Phe Gly Gly Gly Ala Ile Arg
 20 25 30

Tyr Arg Gly Gly Val Leu Asp Ala Leu Gly Leu Asn Phe Leu Ala Phe
 35 40 45

Gly His Ala Gln Gly Ile Ser Asn Thr Val Leu Trp Val Gly Gln Leu
 50 55 60

Leu Leu Ile Gly Ala Trp Val His Leu Gly Arg Arg Leu Phe Lys Lys
 65 70 75 80

Lys Val Ala Asp Asp Thr Ala Asp Ala Ala Asp Leu Gly Leu Val Lys
 85 90 95

Arg Thr Leu Tyr Ala Met Val Val Pro Leu Ile Phe Ala Ala Pro Met
 100 105 110

Met Ser Arg Asp Val Tyr Ser Tyr Leu Met Gln Gly Ala Met Leu Arg

115										120										125										
Asp	Gly	Phe	Asp	Pro	Tyr	Thr	Glu	Gly	Ala	Ala	Val	Asn	Pro	Gly	Pro															
130						135						140																		
Met	Leu	Leu	Glu	Val	Ser	His	Asp	Trp	Arg	Asn	Thr	Thr	Thr	Pro	Tyr															
145						150						155						160												
Gly	Pro	Leu	His	Leu	Trp	Ile	Gly	Asp	Met	Ile	Thr	Thr	Val	Val	Gly															
						165						170						175												
Asp	Asn	Val	Thr	Leu	Gly	Val	Val	Ala	Tyr	Lys	Ile	Leu	Ser	Ile	Ile															
						180						185						190												
Gly	Leu	Ala	Val	Thr	Gly	Trp	Ser	Ile	Val	Arg	Ile	Ala	Gln	His	Phe															
						195						200						205												
Gly	Ala	Asn	Pro	Ala	Ile	Ala	Leu	Trp	Ile	Gly	Val	Ala	Asn	Pro	Val															
						210						215						220												
Met	Ile	Ile	His	Met	Ile	Gly	Gly	Met	His	Asn	Glu	Ser	Leu	Met	Val															
						225						230						235												
Gly	Leu	Val	Ser	Val	Gly	Leu	Leu	Leu	Ala	Leu	Lys	Lys	Arg	Phe	Val															
						245						250						255												
Ala	Gly	Val	Ala	Leu	Ile	Ala	Val	Ala	Val	Ser	Leu	Lys	Ala	Thr	Ala															
						260						265						270												
Ala	Ile	Ala	Leu	Pro	Phe	Val	Val	Trp	Ile	Gly	Met	His	His	Phe	Ala															
						275						280						285												
Gly	Phe	Leu	Ala	Thr	Lys	Lys	Gly	Lys	Asp	Ser	Pro	Thr	Leu	Lys	Gln															
						290						295						300												
Gln	Val	Pro	Ala	Phe	Phe	Ala	Thr	Gly	Ala	Ala	Gly	Val	Ala	Val	Thr															
						305						310						315												
Gly	Val	Val	Val	Ser	Ala	Ile	Thr	Trp	Ala	Ser	Gly	Ala	Ser	Trp	Gly															
						325						330						335												
Trp	Ile	Ser	Glu	Ile	Ser	Gly	Asn	Ser	Lys	Val	Ile	Asn	Pro	Leu	Ala															
						340						345						350												
Phe	Pro	Ser	Leu	Val	Ala	Ser	Val	Ile	Thr	Met	Val	Ala	Glu	Val	Phe															
						355						360						365												
Val	Asp	Asp	Phe	Asp	Tyr	Asn	Ala	Val	Val	Asn	Val	Val	Arg	Ser	Ile															
						370						375						380												
Ser	Met	Leu	Ile	Met	Leu	Gly	Gly	Leu	Val	Val	Cys	Trp	Trp	Leu	Phe															
						385						390						395												
Arg	Gln	Asn	Glu	Arg	Arg	Ala	Val	Thr	Gly	Thr	Ala	Ala	Ala	Tyr	Ala															
						405						410						415												
Val	Ala	Phe	Val	Phe	Asn	Ser	Val	Thr	Leu	Pro	Trp	Tyr	Tyr	Ala	Ser															
						420						425						430												
Leu	Ile	Ser	Leu	Leu	Gly	Thr	Phe	Lys	Pro	Pro	Met	Trp	Leu	Ile	Arg															
						435						440						445												

Phe Ala Ala Gly Ala Ser Val Phe Ile Ala Leu Met Phe Thr Gly Ser
450 455 460

Gly Asn His Gln Leu Tyr Asn Ile Val Thr Val Ile Ile Ala Ala Ile
465 470 475 480

Ile Ala Trp Leu Ala Thr Val Val Ile Phe Asp Asp Thr Asp Pro Ala
485 490 495

Thr Thr Ala Thr Glu Lys Pro Ser Pro His Thr Val Ser
500 505

<210> 1273

<211> 722

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(699)

<223> PRXA02697

<400> 1273

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Pro Phe Val Val Trp Ile Gly Met His His Phe Ala Gly Phe Leu Ala
1 5 10 15

acc aaa aag ggc aaa gac tcc cct acc ctt aag caa cag gtc ccc gcg 96
Thr Lys Lys Gly Lys Asp Ser Pro Thr Leu Lys Gln Gln Val Pro Ala
20 25 30

ttc ttt gcc act gga gct gca ggt gtt gct gtc act ggt gtt gtt gtc 144
Phe Phe Ala Thr Gly Ala Ala Gly Val Ala Val Thr Gly Val Val Val
35 40 45

agt gcg atc act tgg gcg tct ggc gct tcg tgg ggc tgg atc agt gag 192
Ser Ala Ile Thr Trp Ala Ser Gly Ala Ser Trp Gly Trp Ile Ser Glu
50 55 60

atc agt ggc aac agc aag gta atc aac ccg ctg gct ttc cct tct ttg 240
Ile Ser Gly Asn Ser Lys Val Ile Asn Pro Leu Ala Phe Pro Ser Leu
65 70 75 80

gtg gcc agt gtg atc acc atg gtg gct gaa gtg ttc gtt gac gat ttc 288
Val Ala Ser Val Ile Thr Met Val Ala Glu Val Phe Val Asp Phe
85 90 95

gac tac aac gca gtg gtt aat gtt gtg cgc tca atc tcc atg ctg atc 336
Asp Tyr Asn Ala Val Val Asn Val Val Arg Ser Ile Ser Met Leu Ile
100 105 110

atg ctt ggc ggg ttg gtc gta tgt tgg tgg ctg ttc cgc cag aac gaa 384
Met Leu Gly Gly Leu Val Val Cys Trp Trp Leu Phe Arg Gln Asn Glu
115 120 125

cgc agg gcg gtc act ggt aca gcg gcg gct tat gcc gtg gct ttt gtg 432
Arg Arg Ala Val Thr Gly Thr Ala Ala Ala Tyr Ala Val Ala Phe Val
130 135 140

ttc aat tct gtg acc ttg ccg tgg tac tac gcc agc ttg atc tct ttg 480
 Phe Asn Ser Val Thr Leu Pro Trp Tyr Tyr Ala Ser Leu Ile Ser Leu
 145 150 155 160

ctc ggc aca ttt aaa cca ccg atg tgg ttg att cgc ttc gca gcg ggt 528
 Leu Gly Thr Phe Lys Pro Pro Met Trp Leu Ile Arg Phe Ala Ala Gly
 165 170 175

gct tcg gtg ttt atc gcg ctg atg ttt acc gga agt gga aac cac cag 576
 Ala Ser Val Phe Ile Ala Leu Met Phe Thr Gly Ser Gly Asn His Gln
 180 185 190

ctg tac aac atc gtt acg gtg atc atc gca gca att atc gcg tgg ctt 624
 Leu Tyr Asn Ile Val Thr Val Ile Ile Ala Ala Ile Ile Ala Trp Leu
 195 200 205

gcc acc gtg gtg atc ttt gat gac act gac cct gca aca acg gcc acg 672
 Ala Thr Val Val Ile Phe Asp Asp Thr Asp Pro Ala Thr Ala Thr
 210 215 220

gag aaa ccc tcc ccg cat acc gtt tcc tagttgcata aggtaaacccg 719
 Glu Lys Pro Ser Pro His Thr Val Ser
 225 230

cca 722

<210> 1274
 <211> 233
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 1274
 Pro Phe Val Val Trp Ile Gly Met His His Phe Ala Gly Phe Leu Ala
 1 5 10 15

Thr Lys Lys Gly Lys Asp Ser Pro Thr Leu Lys Gln Gln Val Pro Ala
 20 25 30

Phe Phe Ala Thr Gly Ala Ala Gly Val Ala Val Thr Gly Val Val Val
 35 40 45

Ser Ala Ile Thr Trp Ala Ser Gly Ala Ser Trp Gly Trp Ile Ser Glu
 50 55 60

Ile Ser Gly Asn Ser Lys Val Ile Asn Pro Leu Ala Phe Pro Ser Leu
 65 70 75 80

Val Ala Ser Val Ile Thr Met Val Ala Glu Val Phe Val Asp Asp Phe
 85 90 95

Asp Tyr Asn Ala Val Val Asn Val Val Arg Ser Ile Ser Met Leu Ile
 100 105 110

Met Leu Gly Gly Leu Val Val Cys Trp Trp Leu Phe Arg Gln Asn Glu
 115 120 125

Arg Arg Ala Val Thr Gly Thr Ala Ala Ala Tyr Ala Val Ala Phe Val
 130 135 140

Phe Asn Ser Val Thr Leu Pro Trp Tyr Tyr Ala Ser Leu Ile Ser Leu

145	150	155	160
Leu Gly Thr Phe Lys Pro Pro Met Trp	Leu Ile Arg Phe Ala Ala Gly		
	165	170	175
Ala Ser Val Phe Ile Ala Leu Met Phe Thr Gly Ser Gly Asn His Gln			
	180	185	190
Leu Tyr Asn Ile Val Thr Val Ile Ile Ala Ala Ile Ile Ala Trp Leu			
	195	200	205
Ala Thr Val Val Ile Phe Asp Asp Thr Asp Pro Ala Thr Thr Ala Thr			
	210	215	220
Glu Lys Pro Ser Pro His Thr Val Ser			
225	230		

<210> 1275

<211> 748

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(748)

<223> FRXA02719

<400> 1275

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ggctatccgc tcaaccgaac gtccgatgta gtagacgcgt	atg aca ctt ttt caa	115
	Met Thr Leu Phe Gln	
	1	5

cgt tta acc aac cct gta gtg ctc ggc ggc cta gca ggt gtt ttg ctt	163
Arg Leu Thr Asn Pro Val Val Leu Gly Gly Leu Ala Gly Val Leu Leu	
	10
	15
	20

ctg ctc ggc tct ttc ggt ggc ggt gcc att cgg tac cgt ggc gga gtg	211
Leu Leu Gly Ser Phe Gly Gly Gly Ala Ile Arg Tyr Arg Gly Gly Val	
	25
	30
	35

ctc gat gcg ttg ggg ctt aac ttc ctt gct ttt ggc cac gcg cag ggt	259
Leu Asp Ala Leu Gly Leu Asn Phe Leu Ala Phe Gly His Ala Gln Gly	
	40
	45
	50

att tcc aat acc gtg ttg tgg gtt ggg cag ctg ctg ctg att ggc gcg	307
Ile Ser Asn Thr Val Leu Trp Val Gly Gln Leu Leu Ile Gly Ala	
	55
	60
	65

tgg gtt cac ctt gga cgt cgg ttg ttc aag aaa aaa gtc gct gat gac	355
Trp Val His Leu Gly Arg Arg Leu Phe Lys Lys Lys Val Ala Asp Asp	
	70
	75
	80
	85

acc gca gac gct gct gac tta ggt ctt gta aag cgc acg ttg tat gcc	403
Thr Ala Asp Ala Ala Asp Leu Gly Leu Val Lys Arg Thr Leu Tyr Ala	
	90
	95
	100

atg gtg gtg ccc ctc att ttt gcg gca cca atg atg tgc cgt gat gtt	451
Met Val Val Pro Leu Ile Phe Ala Ala Pro Met Met Ser Arg Asp Val	

105	110	115	
tat tcc tat ctc atg cag ggc gcg atg ctg cgt gat ggc ttc gat ccc			499
Tyr Ser Tyr Leu Met Gln Gly Ala Met Leu Arg Asp Gly Phe Asp Pro			
120	125	130	
tac act gag ggc gct gcg gta aac cct ggc ccc atg ttg ctt gag gtc			547
Tyr Thr Glu Gly Ala Ala Val Asn Pro Gly Pro Met Leu Leu Glu Val			
135	140	145	
tct cat gat tgg cgc aac acc acg acg ccg tat ggt cca cta cac ctg			595
Ser His Asp Trp Arg Asn Thr Thr Thr Pro Tyr Gly Pro Leu His Leu			
150	155	160	165
tgg att gga gac atg atc acc acg gtt gtg ggc gat aat gtc acc ttg			643
Trp Ile Gly Asp Met Ile Thr Thr Val Val Gly Asp Asn Val Thr Leu			
170	175	180	
ggc gtc gtc gct tac aag atc ttg tcg atc att ggc ctt gct gtg aca			691
Gly Val Val Ala Tyr Lys Ile Leu Ser Ile Ile Gly Leu Ala Val Thr			
185	190	195	
ggc tgg agc att gtc cgc att gca caa cat ttt gga gcc aac cca gca			739
Gly Trp Ser Ile Val Arg Ile Ala Gln His Phe Gly Ala Asn Pro Ala			
200	205	210	
att gca ttg			748
Ile Ala Leu			
215			
<210> 1276			
<211> 216			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 1276			
Met Thr Leu Phe Gln Arg Leu Thr Asn Pro Val Val Leu Gly Gly Leu			
1	5	10	15
Ala Gly Val Leu Leu Leu Leu Gly Ser Phe Gly Gly Gly Ala Ile Arg			
20	25	30	
Tyr Arg Gly Gly Val Leu Asp Ala Leu Gly Leu Asn Phe Leu Ala Phe			
35	40	45	
Gly His Ala Gln Gly Ile Ser Asn Thr Val Leu Trp Val Gly Gln Leu			
50	55	60	
Leu Leu Ile Gly Ala Trp Val His Leu Gly Arg Arg Leu Phe Lys Lys			
65	70	75	80
Lys Val Ala Asp Thr Ala Asp Ala Ala Asp Leu Gly Leu Val Lys			
85	90	95	
Arg Thr Leu Tyr Ala Met Val Val Pro Leu Ile Phe Ala Ala Pro Met			
100	105	110	
Met Ser Arg Asp Val Tyr Ser Tyr Leu Met Gln Gly Ala Met Leu Arg			
115	120	125	

Asp Gly Phe Asp Pro Tyr Thr Glu Gly Ala Val Asn Pro Gly Pro
 130 135 140
 Met Leu Leu Glu Val Ser His Asp Trp Arg Asn Thr Thr Thr Pro Tyr
 145 150 155 160
 Gly Pro Leu His Leu Trp Ile Gly Asp Met Ile Thr Thr Val Val Gly
 165 170 175
 Asp Asn Val Thr Leu Gly Val Val Ala Tyr Lys Ile Leu Ser Ile Ile
 180 185 190
 Gly Leu Ala Val Thr Gly Trp Ser Ile Val Arg Ile Ala Gln His Phe
 195 200 205
 Gly Ala Asn Pro Ala Ile Ala Leu
 210 215

<210> 1277

<211> 825

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(802)

<223> RXN02720

<400> 1277

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cgccaggccg gcgtggtgtg gctgccaaaag gaggcataaa ttg gag cgc cgc gaa 115
 Leu Glu Arg Arg Glu
 1 5

gag ctg cag gta cga ctg cag cag gtg caa gcg cgt atc gac gcg acc 163
 Glu Leu Gln Val Arg Leu Gln Gln Val Gln Ala Arg Ile Asp Ala Thr
 10 15 20

ctg aac gaa cac aac cgc ccc gag gcc agt gta cgt ctg ttg ccg gtc 211
 Leu Asn Glu His Asn Arg Pro Glu Gly Ser Val Arg Leu Leu Pro Val
 25 30 35

acc aaa ttc cac ccc gtg gaa gac atc aag atc tta caa gag ttt ggt 259
 Thr Lys Phe His Pro Val Glu Asp Ile Lys Ile Leu Gln Glu Phe Gly
 40 45 50

gtc acc gca gtg gga gag aac cgc gaa caa gaa gca cgc gcc aaa gca 307
 Val Thr Ala Val Gly Glu Asn Arg Glu Gln Glu Ala Arg Ala Lys Ala
 55 60 65

ctg gaa ctt ccc gac atg gac ttt cat atg att gcc caa atc caa tca 355
 Leu Glu Leu Pro Asp Met Asp Phe His Met Ile Gly Gln Ile Gln Ser
 70 75 80 85

aag aaa gcc aac tcg atc gcc agg tgg gca gct gca gtg cac tcc gtt 403
 Lys Lys Ala Asn Ser Ile Ala Arg Trp Ala Ala Val His Ser Val
 90 95 100

gat agc gag aaa atc gcc gaa gca ttg gcc agg gga gta gcc ctt gca 451

Asp Ser Glu Lys Ile Ala Glu Ala Leu Gly Arg Gly Val Ala Leu Ala
 105 110 115
 ttg gat aga ggc gac cgc acc agt gac gag ctt ccg tgt ttt att caa 499
 Leu Asp Arg Gly Asp Arg Thr Ser Asp Glu Leu Pro Cys Phe Ile Gln
 120 125 130
 ctg agt ttg gat ggt gac ccg agc cga ggt gga act cca ttg agc cag 547
 Leu Ser Leu Asp Gly Asp Pro Ser Arg Gly Gly Thr Pro Leu Ser Gln
 135 140 145
 gtc aca caa ctt gcc gat tgc atc agt gac acc aca cat ctg cgt ttt 595
 Val Thr Gln Leu Ala Asp Cys Ile Ser Asp Thr Thr His Leu Arg Phe
 150 155 160 165
 gag ggc ctc atg tgc gtc cca ccg ctt ggt tgg ggc cct gaa aaa gct 643
 Glu Gly Leu Met Cys Val Pro Pro Leu Gly Trp Gly Pro Glu Lys Ala
 170 175 180
 ttt tcc cag gca aga gac gta ctt tca ggt tta gag gaa cac ttt gac 691
 Phe Ser Gln Ala Arg Asp Val Leu Ser Gly Leu Glu Glu His Phe Asp
 185 190 195
 agg tct ttg gaa ttt tgc gca ggt atg tct gga gac cta gtt gct gcg 739
 Arg Ser Leu Glu Phe Ser Ala Gly Met Ser Gly Asp Leu Val Ala Ala
 200 205 210
 att aaa cac ggc tca aca atc gtg cgt gtc gga act gaa att ctt ggg 787
 Ile Lys His Gly Ser Thr Ile Val Arg Val Gly Thr Glu Ile Leu Gly
 215 220 225
 aac cga ccg cta cgc tagaaaaatca agttaagggt gtg 825
 Asn Arg Pro Leu Ala
 230
 <210> 1278
 <211> 234
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 1278
 Leu Glu Arg Arg Glu Glu Leu Gln Val Arg Leu Gln Gln Val Gln Ala
 1 5 10 15
 Arg Ile Asp Ala Thr Leu Asn Glu His Asn Arg Pro Glu Gly Ser Val
 20 25 30
 Arg Leu Leu Pro Val Thr Lys Phe His Pro Val Glu Asp Ile Lys Ile
 35 40 45
 Leu Gln Glu Phe Gly Val Thr Ala Val Gly Glu Asn Arg Glu Gln Glu
 50 55 60
 Ala Arg Ala Lys Ala Leu Glu Leu Pro Asp Met Asp Phe His Met Ile
 65 70 75 80
 Gly Gln Ile Gln Ser Lys Lys Ala Asn Ser Ile Ala Arg Trp Ala Ala
 85 90 95
 Ala Val His Ser Val Asp Ser Glu Lys Ile Ala Glu Ala Leu Gly Arg

100 105 110
 Gly Val Ala Leu Ala Leu Asp Arg Gly Asp Arg Thr Ser Asp Glu Leu
 115 120 125
 Pro Cys Phe Ile Gln Leu Ser Leu Asp Gly Asp Pro Ser Arg Gly Gly
 130 135 140
 Thr Pro Leu Ser Gln Val Thr Gln Leu Ala Asp Cys Ile Ser Asp Thr
 145 150 155 160
 Thr His Leu Arg Phe Glu Gly Leu Met Cys Val Pro Pro Leu Gly Trp
 165 170 175
 Gly Pro Glu Lys Ala Phe Ser Gln Ala Arg Asp Val Leu Ser Gly Leu
 180 185 190
 Glu Glu His Phe Asp Arg Ser Leu Glu Phe Ser Ala Gly Met Ser Gly
 195 200 205
 Asp Leu Val Ala Ala Ile Lys His Gly Ser Thr Ile Val Arg Val Gly
 210 215 220
 Thr Glu Ile Leu Gly Asn Arg Pro Leu Ala
 225 230
 <210> 1279
 <211> 727
 <212> DNA
 <213> *Corynebacterium glutamicum*
 <220>
 <221> CDS
 <222> (101)..(727)
 <223> FRXA02720
 <400> 1279
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 cgccaggccg gcgtggtgtg gctgccaaag gaggcataaa ttg gag cgc cgc gaa 115
 Leu Glu Arg Arg Glu
 1 5
 gag ctg cag gta cga ctg cag cag gtg caa gcg cgt atc gac gcg acc 163
 Glu Leu Gln Val Arg Leu Gln Gln Val Gln Ala Arg Ile Asp Ala Thr
 10 15 20
 ctc aac gaa cac aac cgc ccc gag gcc agt gta cgt ctg ttg ccg gtc 211
 Leu Asn Glu His Asn Arg Pro Glu Gly Ser Val Arg Leu Leu Pro Val
 25 30 35
 acc aaa ttc cac ccc gtg gaa gac atc aag atc tta caa gag ttt ggt 259
 Thr Lys Phe His Pro Val Glu Asp Ile Lys Ile Leu Gln Glu Phe Gly
 40 45 50
 gtc acc gca gtg gga gag aac cgc gaa caa gaa gca cgc gcc aaa gca 307
 Val Thr Ala Val Gly Glu Asn Arg Glu Gln Glu Ala Arg Ala Lys Ala
 55 60 65
 ctc gaa ctt ccc gac atg gac ttt cat atg att gcc caa atc caa tca 355

Leu Glu Leu Pro Asp Met Asp Phe His Met Ile Gly Gln Ile Gln Ser
 70 75 80 85
 aag aaa gcc aac tcg atc gcc agg tgg gca gct gca gtg cac tcc gtt 403
 Lys Lys Ala Asn Ser Ile Ala Arg Trp Ala Ala Ala Val His Ser Val
 90 95 100
 gat agc gag aaa atc gcc gaa gca ttg ggc agg gga gta gcc ctt gca 451
 Asp Ser Glu Lys Ile Ala Glu Ala Leu Gly Arg Gly Val Ala Leu Ala
 105 110 115
 ttg gat aga ggc gac cgc acc agt gac gag ctt ccg tgt ttt att caa 499
 Leu Asp Arg Gly Asp Arg Thr Ser Asp Glu Leu Pro Cys Phe Ile Gln
 120 125 130
 ctg agt ttg gat ggt gac ccg agc cga ggt gga act cca ttg agc cag 547
 Leu Ser Leu Asp Gly Asp Pro Ser Arg Gly Gly Thr Pro Leu Ser Gln
 135 140 145
 gtc aca caa ctt gcc gat tgc atc agt gac acc aca cat ctg cgt ttt 595
 Val Thr Gln Leu Ala Asp Cys Ile Ser Asp Thr Thr His Leu Arg Phe
 150 155 160 165
 gag ggc ctc atg tgc gtc cca ccg ctt ggt tgg ggc cct gaa aaa gct 643
 Glu Gly Leu Met Cys Val Pro Pro Leu Gly Trp Gly Pro Glu Lys Ala
 170 175 180
 ttt tcc cag gca aga gac gta ctt tca ggt tta gag gaa cac ttt gac 691
 Phe Ser Gln Ala Arg Asp Val Leu Ser Gly Leu Glu Glu His Phe Asp
 185 190 195
 agg tct ttg gaa ttt tcg gca ggt atg tct gga gac 727
 Arg Ser Leu Glu Phe Ser Ala Gly Met Ser Gly Asp
 200 205
 <210> 1280
 <211> 209
 <212> PRT
 <213> *Corynebacterium glutamicum*
 <400> 1280
 Leu Glu Arg Arg Glu Glu Leu Gln Val Arg Leu Gln Gln Val Gln Ala
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 Arg Ile Asp Ala Thr Leu Asn Glu His Asn Arg Pro Glu Gly Ser Val
 20 25 30
 Arg Leu Leu Pro Val Thr Lys Phe His Pro Val Glu Asp Ile Lys Ile
 35 40 45
 Leu Gln Glu Phe Gly Val Thr Ala Val Gly Glu Asn Arg Glu Gln Glu
 50 55 60
 Ala Arg Ala Lys Ala Leu Glu Leu Pro Asp Met Asp Phe His Met Ile
 65 70 75 80
 Gly Gln Ile Gln Ser Lys Lys Ala Asn Ser Ile Ala Arg Trp Ala Ala
 85 90 95
 Ala Val His Ser Val Asp Ser Glu Lys Ile Ala Glu Ala Leu Gly Arg

100	105	110
Gly Val Ala Leu Ala Leu Asp Arg	Gly Asp Arg Thr Ser Asp Glu Leu	
115	120	125
Pro Cys Phe Ile Gln Leu Ser Leu Asp Gly Asp	Pro Ser Arg Gly Gly	
130	135	140
Thr Pro Leu Ser Gln Val Thr Gln Leu Ala Asp Cys Ile Ser Asp Thr		
145	150	155
Thr His Leu Arg Phe Glu Gly Leu Met Cys Val Pro Pro Leu Gly Trp		
165	170	175
Gly Pro Glu Lys Ala Phe Ser Gln Ala Arg Asp Val Leu Ser Gly Leu		
180	185	190
Glu Glu His Phe Asp Arg Ser Leu Glu Phe Ser Ala Gly Met Ser Gly		
195	200	205

Asp

<210> 1281
 <211> 927
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(904)
 <223> RXN02744

<400> 1281
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 Met Ser Lys Pro Phe
 1 5
 gaa aac tct gcg ctc cgc ggt tct tct cga ttc cca gct gga acg ttc 163
 Glu Asn Ser Ala Leu Arg Gly Ser Ser Arg Phe Pro Ala Gly Thr Phe
 10 15 20
 acc cct gct ccc aaa cga gcc acc ccg gca aaa atg ttg gct gct cag 211
 Thr Pro Ala Thr Pro Ala Lys Met Leu Ala Ala Gln
 25 30 35
 ggc aag atg gaa tcc ctg ctg ttt ctt cgc cac ggc gaa cag caa ctg 259
 Gly Lys Met Glu Ser Leu Leu Phe Leu Arg His Gly Glu Gln Gln Leu
 40 45 50
 ctc agc atc atc att ccc ttg gtc gcg ctc atc gca cta gcg aat ttt 307
 Leu Ser Ile Ile Ile Pro Leu Val Ala Leu Ile Ala Leu Ala Asn Phe
 55 60 65
 gat ttc atc cct ggt gag aac tcc ctc gac aag act ttc ccc ttc gcg 355
 Asp Phe Ile Pro Gly Glu Asn Ser Leu Asp Lys Thr Phe Pro Phe Ala
 70 75 80 85

ctg gcc aca gca gcc atg agc gct ggt ttt aca ggt caa gcc atc agc 403
 Leu Ala Thr Ala Ala Met Ser Ala Gly Phe Thr Gly Gln Ala Ile Ser
 90 95 100

cta gct ttt gac cgc cgc tat ggt gcc ctc aag cgc acc ggc gcc agc 451
 Leu Ala Phe Asp Arg Arg Tyr Gly Ala Leu Lys Arg Thr Gly Ala Ser
 105 110 115

ggt gtt ccc gcc tgg acg att att ttt ggc aaa gtc atc gca gtc att 499
 Gly Val Pro Ala Trp Thr Ile Phe Gly Lys Val Ile Ala Val Ile
 120 125 130

gca gtc acc att gtg cag atc atc ttt ctc ggt gtg act gca ctg ctg 547
 Ala Val Thr Ile Val Gln Ile Ile Phe Leu Gly Val Thr Ala Leu Leu
 135 140 145

ttg ggc tgg tcc gca cct gtc ggt ggt gtg ctc ttt ggc atc gtg acc 595
 Leu Gly Trp Ser Ala Pro Val Gly Gly Val Leu Phe Gly Ile Val Thr
 150 155 160 165

cta ttt gtg ggt gtt tcc agc ttc acc gcg ctc ggc atg ctg atg ggc 643
 Leu Phe Val Gly Val Ser Ser Phe Thr Ala Leu Gly Met Leu Met Gly
 170 175 180

gga acg ttg tcc tcc gaa ttg gta ttg gca ctg gct aac ttg att tgg 691
 Gly Thr Leu Ser Ser Glu Leu Val Leu Ala Leu Ala Asn Leu Ile Trp
 185 190 195

att gta ctg tcc ggc ctt gca gca tgg gcg gtc ttt tcc cct tcc gtc 739
 Ile Val Leu Ser Gly Leu Ala Ala Trp Ala Val Phe Ser Pro Ser Val
 200 205 210

aac gct gaa gga gtg ctg tcc atc atc cca tcc gtt gcg ctg tcc caa 787
 Asn Ala Glu Gly Val Leu Ser Ile Ile Pro Ser Val Ala Leu Ser Gln
 215 220 225

ggt atg gtt gac gca ttc aac ggc gaa ctt ccg tgg ctc cag cta gga 835
 Gly Met Val Asp Ala Phe Asn Gly Glu Leu Pro Trp Leu Gln Leu Gly
 230 235 240 245

att ttg gtg ggc tgg cta att atc acc ggc gtg gcc gca aac aag cta 883
 Ile Leu Val Gly Trp Leu Ile Ile Thr Gly Val Ala Ala Asn Lys Leu
 250 255 260

ttt aac ttc tct gcg agc cgc tagatatacc cttagtcgga aaa 927
 Phe Asn Phe Ser Ala Ser Arg
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<210> 1282

<211> 268

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1282

 Met Ser Lys Pro Phe Glu Asn Ser Ala Leu Arg Gly Ser Ser Arg Phe
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 Pro Ala Gly Thr Phe Thr Pro Ala Pro Lys Arg Ala Thr Pro Ala Lys
 20 25 30

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Met Leu Ala Ala Gln Gly Lys Met Glu Ser Leu Leu Phe Leu Arg His
   35                               40                               45

Gly Glu Gln Gln Leu Leu Ser Ile Ile Ile Pro Leu Val Ala Leu Ile
   50                               55                               60

Ala Leu Ala Asn Phe Asp Phe Ile Pro Gly Glu Asn Ser Leu Asp Lys
   65                               70                               75                               80

Thr Phe Pro Phe Ala Leu Ala Thr Ala Ala Met Ser Ala Gly Phe Thr
           85                               90                               95

Gly Gln Ala Ile Ser Leu Ala Phe Asp Arg Arg Tyr Gly Ala Leu Lys
   100                               105                               110

Arg Thr Gly Ala Ser Gly Val Pro Ala Trp Thr Ile Ile Phe Gly Lys
   115                               120                               125

Val Ile Ala Val Ile Ala Val Thr Ile Val Gln Ile Ile Phe Leu Gly
   130                               135                               140

Val Thr Ala Leu Leu Leu Gly Trp Ser Ala Pro Val Gly Gly Val Leu
   145                               150                               155                               160

Phe Gly Ile Val Thr Leu Phe Val Gly Val Ser Ser Phe Thr Ala Leu
           165                               170                               175

Gly Met Leu Met Gly Gly Thr Leu Ser Ser Glu Leu Val Leu Ala Leu
   180                               185                               190

Ala Asn Leu Ile Trp Ile Val Leu Ser Gly Leu Ala Ala Trp Ala Val
   195                               200                               205

Phe Ser Pro Ser Val Asn Ala Glu Gly Val Leu Ser Ile Ile Pro Ser
   210                               215                               220

Val Ala Leu Ser Gln Gly Met Val Asp Ala Phe Asn Gly Glu Leu Pro
   225                               230                               235                               240

Trp Leu Gln Leu Gly Ile Leu Val Gly Trp Leu Ile Ile Thr Gly Val
           245                               250                               255

Ala Ala Asn Lys Leu Phe Asn Phe Ser Ala Ser Arg
   260                               265

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<210> 1283

<211> 927

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(904)

<223> FRXA02744

<400> 1283

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tggaacatcac cggaaaagaa ctgaggagtt aacgcacacc atg tct aaa cct ttt 115
 Met Ser Lys Pro Phe

1

5

gaa aac tct gcg ctc cgc ggt tct tct cga ttc cca gct gga acg ttc	163
Glu Asn Ser Ala Leu Arg Gly Ser Ser Arg Phe Pro Ala Gly Thr Phe	
10 15 20	
acc cct gct ccc aaa cga gcc acc ccg gca aaa atg ttg gct gct cag	211
Thr Pro Ala Pro Lys Arg Ala Thr Pro Ala Lys Met Leu Ala Ala Gln	
25 30 35	
ggc aag atg gaa tcc ctg ctg ttt ctt cgc cac ggc gaa cag caa ctg	259
Gly Lys Met Glu Ser Leu Leu Phe Leu Arg His Gly Glu Gln Gln Leu	
40 45 50	
ctc agc atc atc att ccc ttg gtc gcg ctc atc gca cta gcg aat ttt	307
Leu Ser Ile Ile Ile Pro Leu Val Ala Leu Ile Ala Leu Ala Asn Phe	
55 60 65	
gat ttc atc cct ggt gag aac tcc ctc gac aag act ttc ccc ttc gcg	355
Asp Phe Ile Pro Gly Glu Asn Ser Leu Asp Lys Thr Phe Pro Phe Ala	
70 75 80 85	
ctg gcc aca gca gcc atg agc gct ggt ttt aca ggt caa gcc atc agc	403
Leu Ala Thr Ala Ala Met Ser Ala Gly Phe Thr Gly Gln Ala Ile Ser	
90 95 100	
cta gct ttt gac cgc cgc tat ggt gcc ctc aag cgc acc ggc gcc agc	451
Leu Ala Phe Asp Arg Arg Tyr Gly Ala Leu Lys Arg Thr Gly Ala Ser	
105 110 115	
ggt gtt ccc gcc tgg acg att att ttt ggc aaa gtc atc gca gtc att	499
Gly Val Pro Ala Trp Thr Ile Ile Phe Gly Lys Val Ile Ala Val Ile	
120 125 130	
gca gtc acc att gtg cag atc atc ttt ctc ggt gtg act gca ctg ctg	547
Ala Val Thr Pro Val Gln Ile Ile Phe Leu Gly Val Thr Ala Leu Leu	
135 140 145	
ttg ggc tgg tcc gca cct gtc ggt ggt gtg ctc ttt ggc atc gtg acc	595
Leu Gly Trp Ser Ala Pro Val Gly Gly Val Leu Phe Gly Ile Val Thr	
150 155 160 165	
cta ttt gtg ggt gtt tcc agc ttc acc gcg ctc ggc atg ctg atg ggc	643
Leu Phe Val Gly Val Ser Ser Phe Thr Ala Leu Gly Met Leu Met Gly	
170 175 180	
gga acg ttg tcc tcc gaa ttg gta ttg gca ctg gct aac ttg att tgg	691
Gly Thr Leu Ser Ser Glu Leu Val Leu Ala Leu Ala Asn Leu Ile Trp	
185 190 195	
att gta ctg tcc ggc ctt gca gca tgg gcg gtc ttt tcc cct tcc gtc	739
Ile Val Leu Ser Gly Leu Ala Ala Trp Ala Val Phe Ser Pro Ser Val	
200 205 210	
aac gct gaa gga gtg ctg tcc atc atc cca tcc gtt gcg ctg tcc caa	787
Asn Ala Glu Gly Val Leu Ser Ile Ile Pro Ser Val Ala Leu Ser Gln	
215 220 225	
ggt atg gtt gac gca ttc aac ggc gaa ctt ccg tgg ctc cag cta gga	835
Gly Met Val Asp Ala Phe Asn Gly Glu Leu Pro Trp Leu Gln Leu Gly	
230 235 240 245	

att ttg gtg ggc tgg cta att atc acc ggc gtg gcc gca aac aag cta 883
 Ile Leu Val Gly Trp Leu Ile Ile Thr Gly Val Ala Ala Asn Lys Leu
 250 255 260

ttt aac ttc tct gcg agc cgc tagatatacc cttagtcgga aaa 927
 Phe Asn Phe Ser Ala Ser Arg
 265

<210> 1284

<211> 268

<212> PRT

<213> Corynebacterium glutamicum

<400> 1284

Met Ser Lys Pro Phe Glu Asn Ser Ala Leu Arg Gly Ser Ser Arg Phe
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 20 25 30

Met Leu Ala Ala Gln Gly Lys Met Glu Ser Leu Leu Phe Leu Arg His
 35 40 45

Gly Glu Gln Gln Leu Leu Ser Ile Ile Ile Pro Leu Val Ala Leu Ile
 50 55 60

Ala Leu Ala Asn Phe Asp Phe Ile Pro Gly Glu Asn Ser Leu Asp Lys
 65 70 75 80

Thr Phe Pro Phe Ala Leu Ala Thr Ala Ala Met Ser Ala Gly Phe Thr
 85 90 95

Gly Gln Ala Ile Ser Leu Ala Phe Asp Arg Arg Tyr Gly Ala Leu Lys
 100 105 110

Arg Thr Gly Ala Ser Gly Val Pro Ala Trp Thr Ile Ile Phe Gly Lys
 115 120 125

Val Ile Ala Val Ile Ala Val Thr Ile Val Gln Ile Ile Phe Leu Gly
 130 135 140

Val Thr Ala Leu Leu Leu Gly Trp Ser Ala Pro Val Gly Gly Val Leu
 145 150 155 160

Phe Gly Ile Val Thr Leu Phe Val Gly Val Ser Ser Phe Thr Ala Leu
 165 170 175

Gly Met Leu Met Gly Gly Thr Leu Ser Ser Glu Leu Val Leu Ala Leu
 180 185 190

Ala Asn Leu Ile Trp Ile Val Leu Ser Gly Leu Ala Ala Trp Ala Val
 195 200 205

Phe Ser Pro Ser Val Asn Ala Glu Gly Val Leu Ser Ile Ile Pro Ser
 210 215 220

Val Ala Leu Ser Gln Gly Met Val Asp Ala Phe Asn Gly Glu Leu Pro
 225 230 235 240

Trp Leu Gln Leu Gly Ile Leu Val Gly Trp Leu Ile Ile Thr Gly Val
245 250 255

Ala Ala Asn Lys Leu Phe Asn Phe Ser Ala Ser Arg
260 265

<210> 1285

<211> 1689

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1666)

<223> RXN02770

<400> 1285

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Met Leu Val Ala Ala
1 5

tta gtg atg aca agc tgt ggt gat ggg gaa cgg gaa cca acc agc cac 163
Leu Val Met Thr Ser Cys Gly Asp Gly Glu Pro Glu Pro Thr Ser His
10 15 20

caa aca agc ctt ttc ggc tac gca gtt aac tct tcg ctg gct aca acc 211
Gln Thr Ser Leu Phe Gly Tyr Ala Val Asn Ser Ser Leu Ala Thr Thr
25 30 35

aac gcg gcg tcg ctg ttg gga gtg gct aat gat gct ggt ctt ttg gct 259
Asn Ala Ala Ser Leu Leu Gly Val Ala Asn Asp Ala Gly Leu Leu Ala
40 45 50

gcc aga gtg tat ccg ggt gtg tat gtt cag ggt cct tct ggg cag atg 307
Ala Arg Val Tyr Pro Gly Val Tyr Val Gln Gly Pro Ser Gly Gln Met
55 60 65

att ccc aac act gat ctt gct tcc acg cag gta ttg ccg ggt att aac 355
Ile Pro Asn Thr Asp Leu Ala Ser Thr Gln Val Leu Pro Gly Ile Asn
70 75 80 85

cgc cag gtg att tac act atc aat gaa gat gcc acc tac tca gat ggt 403
Arg Gln Val Ile Tyr Thr Ile Asn Glu Asp Ala Thr Tyr Ser Asp Gly
90 95 100

cag cct gtg gtg tgt gat gat ttt ctg ctc tct gcg aca gct ggg cag 451
Gln Pro Val Val Cys Asp Asp Phe Leu Leu Ser Ala Thr Ala Gly Gln
105 110 115

atg ccg gaa ctg ttc cag tcc cat gtg cca ttg acc tcg cag att gag 499
Met Pro Glu Leu Phe Gln Ser His Val Pro Leu Thr Ser Gln Ile Glu
120 125 130

cga gtg gac tgt gta tct ggt tct aaa gta gcc acc gtg gtg ttc aag 547
Arg Val Asp Cys Val Ser Gly Ser Lys Val Ala Thr Val Val Phe Lys
135 140 145

gaa gac ctc ggt gag cgt tgg cgt tat ctt ttt gag cag gcc gat ttg 595

Glu Asp Leu Gly Glu Arg Trp Arg Tyr Leu Phe Glu Gln Gly Asp Leu	
150 155 160 165	
ttg cca gcc cat gcc gtt gct tcc aaa gca ggt atg acc ttg gag gag	643
Leu Pro Ala His Ala Val Ala Ser Lys Ala Gly Met Thr Leu Glu Glu	
170 175 180	
ctt aat cag gcg ttg aag gat aag gat cct gaa gcg ttg act gaa cct	691
Leu Asn Gln Ala Leu Lys Asp Lys Asp Pro Glu Ala Leu Thr Glu Pro	
185 190 195	
gct cgt gtg tgg agc gaa ggt ttc cag ctg tcc cag ttt gat cca gag	739
Ala Arg Val Trp Ser Glu Gly Phe Gln Leu Ser Gln Phe Asp Pro Glu	
200 205 210	
ctg cag acg gct ttt gcc ccg tac aag gtg gat tct gtg ggt gaa ttc	787
Leu Gln Thr Ala Phe Gly Pro Tyr Lys Val Asp Ser Val Gly Glu Phe	
215 220 225	
ggc gaa gtc aag ctg gta cgc aat gag ttt tac agt ggc gac cag gcg	835
Gly Glu Val Lys Leu Val Arg Asn Glu Phe Tyr Ser Gly Asp Gln Ala	
230 235 240 245	
gtt gaa gca gaa atc acg atg tgg cct aaa ggc tcg gat ctc agc gcc	883
Val Glu Ala Glu Ile Thr Met Trp Pro Lys Gly Ser Asp Leu Ser Ala	
250 255 260	
att gcg gat aat gga aac ctt cag atc gca cat gtt gtg gcg tgg gag	931
Ile Ala Asp Asn Gly Asn Leu Gln Ile Ala His Val Val Ala Trp Glu	
265 270 275	
agc gag ccg tgg gta aat cgc gat gac cca ttg aat cct tat gac att	979
Ser Glu Pro Trp Val Asn Arg Asp Asp Pro Leu Asn Pro Tyr Asp Ile	
280 285 290	
aag gaa gag gtc ggt gtt ttg act gag cag ctc acc ttg gcc agt gcc	1027
Lys Glu Glu Val Gly Val Leu Thr Glu Gln Leu Thr Leu Ala Ser Ala	
295 300 305	
ggt gtg ttt tac gct gcg gag gcc ccg cag gcg ttt gcg gcc tgc gtt	1075
Gly Val Phe Tyr Ala Ala Glu Ala Arg Gln Ala Phe Ala Ala Cys Val	
310 315 320 325	
gac cag gaa gcg gtg gct gcg gcg tcg tca agc atc tct gga atc gat	1123
Asp Gln Glu Ala Val Ala Ala Ser Ser Ser Ile Ser Gly Ile Asp	
330 335 340	
gtg cct gcc gta ggt gtg cac tcg gtg cgt cac caa aat ccg gtc gtg	1171
Val Pro Ala Val Gly Val His Ser Val Arg His Gln Asn Pro Val Val	
345 350 355	
cac caa atc ggt gat ctg cca gca cag cac atg gcg gtg gat att aat	1219
His Gln Ile Gly Asp Leu Pro Ala Gln His Met Ala Val Asp Ile Asn	
360 365 370	
gcc gca tca gcg ttg gcg ggt caa tcc atc cgc att ggc tac gac gga	1267
Ala Ala Ser Ala Leu Ala Gly Gln Ser Ile Arg Ile Gly Tyr Asp Gly	
375 380 385	
ccc gat gag cgc aag gct gca atg gtg gag gcg att cgc caa agt tgt	1315
Pro Asp Glu Arg Lys Ala Ala Met Val Glu Ala Ile Arg Gln Ser Cys	

390	395	400	405	
gag cct gcc ggt atc acc gtt atc gat gcg tcg cag gag gct gtt agt				1363
Glu Pro Ala Gly Ile Thr Val Ile Asp Ala Ser Gln Glu Ala Val Ser	410	415	420	
ctt aat gat ctc agt cga acc gaa gtc agt gaa tgg ggc tat gag cag				1411
Leu Asn Asp Leu Ser Arg Thr Glu Val Ser Glu Trp Gly Tyr Glu Gln	425	430	435	
tac ttc gaa ggg aca ctt gac gct gtt ctg cgt aca gtg gat cca cat				1459
Tyr Phe Glu Gly Thr Leu Asp Ala Val Leu Arg Thr Val Asp Pro His	440	445	450	
cgg gag tat gaa aat gcc aat acc att gga act gat gcg gag tcg acg				1507
Arg Glu Tyr Glu Asn Ala Asn Thr Ile Gly Thr Asp Ala Glu Ser Thr	455	460	465	
agg cgc act gaa gaa caa ttg tgg gct gaa gtc cca tca att cca cta				1555
Arg Arg Thr Glu Glu Gln Leu Trp Ala Glu Val Pro Ser Ile Pro Leu	470	475	480	485
gca gcg caa ccc cga gtg ttt gtg ata gat gcg aca gtc ggt aac gtt				1603
Ala Ala Gln Pro Arg Val Phe Val Ile Asp Arg Thr Val Gly Asn Val	490	495	500	
gtt gtt aat aca gac cta gcc ggt atc gga tgg aac atg gac cgt tgg				1651
Val Val Asn Thr Asp Leu Ala Gly Ile Gly Trp Asn Met Asp Arg Trp	505	510	515	
tcc aga agt gag gaa taagtagtga gcgaacaagc tct				1689
Ser Arg Ser Glu Glu	520			
<210> 1286				
<211> 522				
<212> PRT				
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35 40 45				
Ala Gly Leu Leu Ala Ala Arg Val Tyr Pro Gly Val Tyr Val Gln Gly				
50 55 60				
Pro Ser Gly Gln Met Ile Pro Asn Thr Asp Leu Ala Ser Thr Gln Val				
65 70 75 80				
Leu Pro Gly Ile Asn Arg Gln Val Ile Tyr Thr Ile Asn Glu Asp Ala				
85 90 95				
Thr Tyr Ser Asp Gly Gln Pro Val Val Cys Asp Asp Phe Leu Leu Ser				
100 105 110				

Ala Thr Ala Gly Gln Met Pro Glu Leu Phe Gln Ser His Val Pro Leu
 115 120 125
 Thr Ser Gln Ile Glu Arg Val Asp Cys Val Ser Gly Ser Lys Val Ala
 130 135 140
 Thr Val Val Phe Lys Glu Asp Leu Gly Glu Arg Trp Arg Tyr Leu Phe
 145 150 155 160
 Glu Gln Gly Asp Leu Leu Pro Ala His Ala Val Ala Ser Lys Ala Gly
 165 170 175
 Met Thr Leu Glu Glu Leu Asn Gln Ala Leu Lys Asp Lys Asp Pro Glu
 180 185 190
 Ala Leu Thr Glu Pro Ala Arg Val Trp Ser Glu Gly Phe Gln Leu Ser
 195 200 205
 Gln Phe Asp Pro Glu Leu Gln Thr Ala Phe Gly Pro Tyr Lys Val Asp
 210 215 220
 Ser Val Gly Glu Phe Gly Glu Val Lys Leu Val Arg Asn Glu Phe Tyr
 225 230 235 240
 Ser Gly Asp Gln Ala Val Glu Ala Glu Ile Thr Met Trp Pro Lys Gly
 245 250 255
 Ser Asp Leu Ser Ala Ile Ala Asp Asn Gly Asn Leu Gln Ile Ala His
 260 265 270
 Val Val Ala Trp Glu Ser Glu Pro Trp Val Asn Arg Asp Asp Pro Leu
 275 280 285
 Asn Pro Tyr Asp Ile Lys Glu Glu Val Gly Val Leu Thr Glu Gln Leu
 290 295 300
 Thr Leu Ala Ser Ala Gly Val Phe Tyr Ala Ala Glu Ala Arg Gln Ala
 305 310 315 320
 Phe Ala Ala Cys Val Asp Gln Glu Ala Val Ala Ala Ala Ser Ser Ser
 325 330 335
 Ile Ser Gly Ile Asp Val Pro Ala Val Gly Val His Ser Val Arg His
 340 345 350
 Gln Asn Pro Val Val His Gln Ile Gly Asp Leu Pro Ala Gln His Met
 355 360 365
 Ala Val Asp Ile Asn Ala Ala Ser Ala Leu Ala Gly Gln Ser Ile Arg
 370 375 380
 Ile Gly Tyr Asp Gly Pro Asp Glu Arg Lys Ala Ala Met Val Glu Ala
 385 390 395 400
 Ile Arg Gln Ser Cys Glu Pro Ala Gly Ile Thr Val Ile Asp Ala Ser
 405 410 415
 Gln Glu Ala Val Ser Leu Asn Asp Leu Ser Arg Thr Glu Val Ser Glu
 420 425 430

Trp Gly Tyr Glu Gln Tyr Phe Glu Gly Thr Leu Asp Ala Val Leu Arg
 435 440 445

Thr Val Asp Pro His Arg Glu Tyr Glu Asn Ala Asn Thr Ile Gly Thr
 450 455 460

Asp Ala Glu Ser Thr Arg Arg Thr Glu Glu Gln Leu Trp Ala Glu Val
 465 470 475 480

Pro Ser Ile Pro Leu Ala Ala Gln Pro Arg Val Phe Val Ile Asp Arg
 485 490 495

Thr Val Gly Asn Val Val Val Asn Thr Asp Leu Ala Gly Ile Gly Trp
 500 505 510

Asn Met Asp Arg Trp Ser Arg Ser Glu Glu
 515 520

<210> 1287

<211> 1343

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(1320)

<223> FRXA02770

<400> 1287

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tca gat ggt cag cct gtg gtg tgt gat gat ttt ctg ctc tct gcg aca	96
Ser Asp Gly Gln Pro Val Val Cys Asp Asp Phe Leu Leu Ser Ala Thr	
20 25 30	
gct ggg cag atg ccg gaa ctg ttc cag tcc cat gtg cca ttg acc tcg	144
Ala Gly Gln Met Pro Glu Leu Phe Gln Ser His Val Pro Leu Thr Ser	
35 40 45	
cag att gag cga gtg gac tgt gta tct ggt tct aaa gta gcc acc gtg	192
Gln Ile Glu Arg Val Asp Cys Val Ser Gly Ser Lys Val Ala Thr Val	
50 55 60	
gtg ttc aag gaa gac ctc ggt gag cgt tgg cgt tat ctt ttt gag cag	240
Val Phe Lys Glu Asp Leu Gly Glu Arg Trp Arg Tyr Leu Phe Glu Gln	
65 70 75 80	
ggc gat ttg ttg cca gcc cat gcc gtt gct tcc aaa gca ggt atg acc	288
Gly Asp Leu Leu Pro Ala His Ala Val Ala Ser Lys Ala Gly Met Thr	
85 90 95	
ttg gag gag ctt aat cag gcg ttg aag gat aag gat cct gaa gcg ttg	336
Leu Glu Glu Leu Asn Gln Ala Leu Lys Asp Lys Asp Pro Glu Ala Leu	
100 105 110	
act gaa cct gct cgt gtg tgg agc gaa ggt ttc cag ctg tcc cag ttt	384
Thr Glu Pro Ala Arg Val Trp Ser Glu Gly Phe Gln Leu Ser Gln Phe	
115 120 125	

gat cca gag ctg cag acg gct ttt ggc ccg tac aag gtg gat tct gtg Asp Pro Glu Leu Gln Thr Ala Phe Gly Pro Tyr Lys Val Asp Ser Val 130 135 140	432
ggt gaa ttc ggc gaa gtc aag ctg gta cgc aat gag ttt tac agt ggc Gly Glu Phe Gly Glu Val Lys Leu Val Arg Asn Glu Phe Tyr Ser Gly 145 150 155 160	480
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ctc agc gcc att gcg gat aat gga aac ctt cag atc gca cat gtt gtg Leu Ser Ala Ile Ala Asp Asn Gly Asn Leu Gln Ile Ala His Val Val 180 185 190	576
gcg tgg gag agc gag ccg tgg gta aat cgc gat gac cca ttg aat cct Ala Trp Glu Ser Glu Pro Trp Val Asn Arg Asp Asp Pro Leu Asn Pro 195 200 205	624
tat gac att aag gaa gag gtc ggt gtt ttg act gag cag ctc acc ttg Tyr Asp Ile Lys Glu Glu Val Gly Val Leu Thr Glu Gln Leu Thr Leu 210 215 220	672
gcc agt gcc ggt gtg ttt tac gct gcg gag gcc ccg cag gcg ttt gcg Ala Ser Ala Gly Val Phe Tyr Ala Ala Glu Ala Arg Gln Ala Phe Ala 225 230 235 240	720
gcc tgc gtt gac cag gaa gcg gtg gct gcg gcg tcg tca agc atc tct Ala Cys Val Asp Gln Glu Ala Val Ala Ala Ser Ser Ser Ile Ser 245 250 255	768
gga atc gat gtg cct gcc gta ggt gtg cac tcg gtg cgt cac caa aat Gly Ile Asp Val Pro Ala Val Gly Val His Ser Val Arg His Gln Asn 260 265 270	816
ccg gtc gtg cac caa atc ggt gat ctg cca gca cag cac atg gcg gtg Pro Val Val His Gln Ile Gly Asp Leu Pro Ala Gln His Met Ala Val 275 280 285	864
gat att aat gcc gca tca gcg ttg gcg ggt caa tcc atc cgc att ggc Asp Ile Asn Ala Ala Ser Ala Leu Ala Gly Gln Ser Ile Arg Ile Gly 290 295 300	912
tac gac gga ccc gat gag cgc aag gct gca atg gtg gag gcg att cgc Tyr Asp Gly Pro Asp Glu Arg Lys Ala Ala Met Val Glu Ala Ile Arg 305 310 315 320	960
caa agt tgt gag cct gcc ggt atc acc gtt atc gat gcg tcg cag gag Gln Ser Cys Glu Pro Ala Gly Ile Thr Val Ile Asp Ala Ser Gln Glu 325 330 335	1008
gct gtt agt ctt aat gat ctc agt cga acc gaa gtc agt gaa tgg ggc Ala Val Ser Leu Asn Asp Leu Ser Arg Thr Glu Val Ser Glu Trp Gly 340 345 350	1056
tat gag cag tac ttc gaa ggg aca ctt gac gct gtt ctg cgt aca gtg Tyr Glu Gln Tyr Phe Glu Gly Thr Leu Asp Ala Val Leu Arg Thr Val 355 360 365	1104

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 Asp Pro His Arg Glu Tyr Glu Asn Ala Asn Thr Ile Gly Thr Asp Ala
 370 375 380

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 Glu Ser Thr Arg Arg Thr Glu Glu Gln Leu Trp Ala Glu Val Pro Ser
 385 390 395 400

att cca cta gca gcg caa ccc cga gtg ttt gtg ata gat cgc aca gtc 1248
 Ile Pro Leu Ala Ala Gln Pro Arg Val Phe Val Ile Asp Arg Thr Val
 405 410 415

ggt aac gtt gtt gtt aat aca gac cta gcc ggt atc gga tgg aac atg 1296
 Gly Asn Val Val Val Asn Thr Asp Leu Ala Gly Ile Gly Trp Asn Met
 420 425 430

gac cgt tgg tcc aga agt gag gaa taagtagtga gcgaacaagc tct 1343
 Asp Arg Trp Ser Arg Ser Glu Glu
 435 440

<210> 1288

<211> 440

<212> PRT

<213> Corynebacterium glutamicum

<400> 1288

Gly Ile Asn Arg Gln Val Ile Tyr Thr Ile Asn Glu Asp Ala Thr Tyr
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Ser Asp Gly Gln Pro Val Val Cys Asp Asp Phe Leu Leu Ser Ala Thr
 20 25 30

Ala Gly Gln Met Pro Glu Leu Phe Gln Ser His Val Pro Leu Thr Ser
 35 40 45

Gln Ile Glu Arg Val Asp Cys Val Ser Gly Ser Lys Val Ala Thr Val
 50 55 60

Val Phe Lys Glu Asp Leu Gly Glu Arg Trp Arg Tyr Leu Phe Glu Gln
 65 70 75 80

Gly Asp Leu Leu Pro Ala His Ala Val Ala Ser Lys Ala Gly Met Thr
 85 90 95

Leu Glu Glu Leu Asn Gln Ala Leu Lys Asp Lys Asp Pro Glu Ala Leu
 100 105 110

Thr Glu Pro Ala Arg Val Trp Ser Glu Gly Phe Gln Leu Ser Gln Phe
 115 120 125

Asp Pro Glu Leu Gln Thr Ala Phe Gly Pro Tyr Lys Val Asp Ser Val
 130 135 140

Gly Glu Phe Gly Glu Val Lys Leu Val Arg Asn Glu Phe Tyr Ser Gly
 145 150 155 160

Asp Gln Ala Val Glu Ala Glu Ile Thr Met Trp Pro Lys Gly Ser Asp
 165 170 175

Leu Ser Ala Ile Ala Asp Asn Gly Asn Leu Gln Ile Ala His Val Val

[illegible]

<211> 1314

<213> *Corynebacterium glutamicum*

<221> CDS

 $\langle 222 \rangle$ (101) .. (1291)

<223> RXN02781

<400> 1289

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 Val Val Ala Ala Leu
 1 5

gtt ttc ggt ttc ctg ctt ccc acg tgg gaa cgt ggg ttg tcc gac gcc 163
 Val Phe Gly Phe Leu Leu Pro Thr Trp Glu Arg Gly Leu Ser Asp Ala
 10 15 20

gcg ctc aaa ttc gtt ttt gag ggt ggg cct gat gcc gcc cgc gag gtg 211
 Ala Leu Lys Phe Val Phe Glu Gly Gly Pro Asp Ala Ala Arg Glu Val
 25 30 35

ctg gcc acc atc gcc gcc tcc acg atc tca gtg acc ggt ctc atc ttc 259
 Leu Gly Thr Ile Ala Ala Ser Thr Ile Ser Val Thr Gly Leu Ile Phe
 40 45 50

tcc atc act ctc gtt gtt ctg cag ctg gtg agc agc cag ttc agc ccg 307
 Ser Ile Thr Leu Val Val Leu Gln Leu Val Ser Ser Gln Phe Ser Pro
 55 60 65

cga atg ctc aac ggc ttt ctg cgc aac cgc atc gtg cag gcc acc ctg 355
 Arg Met Leu Asn Gly Phe Leu Arg Asn Arg Ile Val Gln Ala Thr Leu
 70 75 80 85

gcg atg ttc ctg ggg acg ttc gtg ttc tcc ctg acg gtc atc cgg tac 403
 Ala Met Phe Leu Gly Thr Phe Val Phe Ser Leu Thr Val Ile Arg Tyr
 90 95 100

gtg tgg agc gag gac gag gac atc acc gga ttc gtc ccc cgt gct tca 451
 Val Trp Ser Glu Asp Glu Asp Ile Thr Gly Phe Val Pro Arg Ala Ser
 105 110 115

gtg tgc gtt gcc ttc ctg ctg gtg ctc ggg tgt ctg gga ctg ttc ctg 499
 Val Ser Val Ala Phe Leu Leu Val Leu Gly Cys Leu Gly Leu Phe Leu
 120 125 130

gcg ttc atc cgg ctc atc acc ttc tgc atg cgg gtg gcc aac gcc atc 547
 Ala Phe Ile Arg Leu Ile Thr Phe Ser Met Arg Val Ala Asn Ala Ile
 135 140 145

tcc gag atc ggg gag gag acg atg gct ctg gcc gca cgt atc tat ccc 595
 Ser Glu Ile Gly Glu Glu Thr Met Ala Leu Ala Ala Arg Ile Tyr Pro
 150 155 160 165

gtg cag agc gac gac gca gcc cca gtc cag ggg ccg gcc tgg tca ccg 643
 Val Gln Ser Asp Asp Ala Gly Pro Val Gln Gly Pro Gly Trp Ser Pro
 170 175 180

cgg ccc ggt gac ccc cgg gaa gaa atc cgg gtg ggc aac cat ggt tgg 691
 Arg Pro Gly Asp Pro Arg Glu Glu Ile Arg Val Gly Asn His Gly Ser
 185 190 195

ctg gtg tgg atc gac tac cgg aag ctg gtg tcc tgg tgc acg gaa cac 739
 Leu Val Trp Ile Asp Tyr Arg Lys Leu Val Ser Trp Ser Thr Glu His
 200 205 210

cag gcg gtg atc acg gtc gac cgg ccg gtg ggg gac ttc ctc gtc gag 787
 Gln Ala Val Ile Thr Val Asp Arg Pro Val Gly Asp Phe Leu Val Glu

215

220

225

ggc cag cgc ctg ctg cgg gtc tgg tgg gac ggg gaa ctc agc gac cgg 835
 Gly Gln Pro Leu Leu Arg Val Trp Trp Asp Gly Glu Leu Ser Asp Arg 245
 230 235 240

gac cga cgc gtt ctg cac tcg gcc atc gag gtg cgg acc gag cgg gaa 883
 Asp Arg Arg Val Leu His Ser Ala Ile Glu Val Arg Thr Glu Arg Glu 260
 250 255 260

ctt cac cag gat gtg gcg ttc gga ctg cgt caa ctg gtc gac att gcc 931
 Leu His Gln Asp Val Ala Phe Gly Leu Arg Gln Leu Val Asp Ile Ala 275
 265 270

gat cgt gcg ttg tcc ccg gcc atc aat gat ccg gcc acg gcg gcc cag 979
 Asp Arg Ala Leu Ser Pro Gly Ile Asn Asp Pro Ala Thr Ala Ala Gln 290
 280 285 290

tgt gtc cag gag atc cac cgg atc ttc cgc tat ttg gtc acc gtc atc 1027
 Cys Val Gln Glu Ile His Arg Ile Phe Arg Tyr Leu Val Thr Val Ile 305
 295 300 305

gag ccc agc ccc tac atc gcc gat gac gac ggt cgg gtc cgt gtg gtg 1075
 Glu Pro Ser Pro Tyr Ile Ala Asp Asp Asp Gly Arg Val Arg Val Val 325
 310 315 320 325

cac cag ccg caa cgt atc gcg gac atg ctc tat gag gtg atc cgt gag 1123
 His Gln Pro Gln Arg Ile Ala Asp Met Leu Tyr Glu Val Ile Arg Glu 340
 330 335 340

atc cat ctc tac ggg gcg gat tct gcg atg att ccg agg ctg ctg cgc 1171
 Ile His Leu Tyr Gly Ala Asp Ser Ala Met Ile Pro Arg Leu Leu Arg 355
 345 350 355

acc atg gtc gag gac ctg gtg acg gcc gct gcc gat cat tcc ctg cct 1219
 Thr Met Val Glu Asp Leu Val Thr Ala Ala Ala Asp His Ser Leu Pro 370
 360 365 370

gcc gtc gag cgt gcc cgc gcc atc ctg gac gat gag acg gac gag gac 1267
 Ala Val Glu Arg Ala Arg Gly Ile Leu Asp Asp Glu Thr Asp Glu Asp 385
 375 380 385

cgc gac agt gac acc gcg aac gtc tgatccggga tcaggtggcg gtg 1314
 Arg Asp Ser Asp Thr Ala Asn Val 395
 390 395

<210> 1290

<211> 397

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1290

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Gly Leu Ser Asp Ala Ala Leu Lys Phe Val Phe Glu Gly Gly Pro Asp
 20 25 30

Ala Ala Arg Glu Val Leu Gly Thr Ile Ala Ala Ser Thr Ile Ser Val
 35 40 45

Thr Gly Leu Ile Phe Ser Ile Thr Leu Val Val Leu Gln Leu Val Ser
 50 55 60
 Ser Gln Phe Ser Pro Arg Met Leu Asn Gly Phe Leu Arg Asn Arg Ile
 65 70 75 80
 Val Gln Ala Thr Leu Ala Met Phe Leu Gly Thr Phe Val Phe Ser Leu
 85 90 95
 Thr Val Ile Arg Tyr Val Trp Ser Glu Asp Glu Asp Ile Thr Gly Phe
 100 105 110
 Val Pro Arg Ala Ser Val Ser Val Ala Phe Leu Leu Val Leu Gly Cys
 115 120 125
 Leu Gly Leu Phe Leu Ala Phe Ile Arg Leu Ile Thr Phe Ser Met Arg
 130 135 140
 Val Ala Asn Ala Ile Ser Glu Ile Gly Glu Glu Thr Met Ala Leu Ala
 145 150 155 160
 Ala Arg Ile Tyr Pro Val Gln Ser Asp Asp Ala Gly Pro Val Gln Gly
 165 170 175
 Pro Gly Trp Ser Pro Arg Pro Gly Asp Pro Arg Glu Glu Ile Arg Val
 180 185 190
 Gly Asn His Gly Ser Leu Val Trp Ile Asp Tyr Arg Lys Leu Val Ser
 195 200 205
 Trp Ser Thr Glu His Gln Ala Val Ile Thr Val Asp Arg Pro Val Gly
 210 215 220
 Asp Phe Leu Val Glu Gly Gln Pro Leu Leu Arg Val Trp Trp Asp Gly
 225 230 235 240
 Glu Leu Ser Asp Arg Asp Arg Arg Val Leu His Ser Ala Ile Glu Val
 245 250 255
 Arg Thr Glu Arg Glu Leu His Gln Asp Val Ala Phe Gly Leu Arg Gln
 260 265 270
 Leu Val Asp Ile Ala Asp Arg Ala Leu Ser Pro Gly Ile Asn Asp Pro
 275 280 285
 Ala Thr Ala Ala Gln Cys Val Gln Glu Ile His Arg Ile Phe Arg Tyr
 290 295 300
 Leu Val Thr Val Ile Glu Pro Ser Pro Tyr Ile Ala Asp Asp Asp Gly
 305 310 315 320
 Arg Val Arg Val Val His Gln Pro Gln Arg Ile Ala Asp Met Leu Tyr
 325 330 335
 Glu Val Ile Arg Glu Ile His Leu Tyr Gly Ala Asp Ser Ala Met Ile
 340 345 350
 Pro Arg Leu Leu Arg Thr Met Val Glu Asp Leu Val Thr Ala Ala Ala
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Asp His Ser Leu Pro Ala Val Glu Arg Ala Arg Gly Ile Leu Asp Asp
 370 375 380

Glu Thr Asp Glu Asp Arg Asp Ser Asp Thr Ala Asn Val
 385 390 395

<210> 1291

<211> 1314

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1291)

<223> FRXA02781

<400> 1291

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ccggctgtgg cggecccttct gggcgataacc ggctgccagc gtg gtc gcg gcc ctg 115
 Val Val Ala Ala Leu
 1 5

gtt ttc ggt ttc ctg ctt ccc acg tgg gaa cgt ggg ttg tcc gac gcc 163
 Val Phe Gly Phe Leu Leu Pro Thr Trp Glu Arg Gly Leu Ser Asp Ala
 10 15 20

gcg ctc aaa ttc gtt ttt gag ggt ggg cct gat gcc gcc cgc gag gtg 211
 Ala Leu Lys Phe Val Phe Glu Gly Gly Pro Asp Ala Ala Arg Glu Val
 25 30 35

ctg gcc acc atc gcc gcc tcc acg atc tca gtg acc ggt ctc atc ttc 259
 Leu Gly Thr Ile Ala Ala Ser Thr Ile Ser Val Thr Gly Leu Ile Phe
 40 45 50

tcc atc act ctc gtt gtt ctg cag ctg gtg agc agc cag ttc agc ccg 307
 Ser Ile Thr Leu Val Val Leu Gln Leu Val Ser Ser Gln Phe Ser Pro
 55 60 65

cga atg ctc aac gcc ttt ctg cgc aac cgc atc gtg cag gcc acc ctg 355
 Arg Met Leu Asn Gly Phe Leu Arg Asn Arg Ile Val Gln Ala Thr Leu
 70 75 80 85

gcg atg ttc ctg ggg acg ttc gtg ttc tcc ctg acg gtc atc cgg tac 403
 Ala Met Phe Leu Gly Thr Phe Val Phe Ser Leu Thr Val Ile Arg Tyr
 90 95 100

gtg tgg agc gag gac gag gac atc acc gga ttc gtc ccc cgt gct tca 451
 Val Trp Ser Glu Asp Glu Asp Ile Thr Gly Phe Val Pro Arg Ala Ser
 105 110 115

gtg tcg gtt gcc ttc ctg ctg gtg ctc ggg tgt ctg gga ctg ttc ctg 499
 Val Ser Val Ala Phe Leu Leu Val Leu Gly Cys Leu Gly Leu Phe Leu
 120 125 130

gcg ttc atc cgg ctc atc acc ttc tcg atg cgg gtg gcc aac gcc atc 547
 Ala Phe Ile Arg Leu Ile Thr Phe Ser Met Arg Val Ala Asn Ala Ile
 135 140 145

tcc gag atc ggg gag gag acg atg gct ctg gcc gca cgt atc tat ccc 595

390

395

<210> 1292

<211> 397

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1292

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Gly	Leu	Ser	Asp	Ala	Ala	Leu	Lys	Phe	Val	Phe	Glu	Gly	Gly	Pro	Asp
			20					25					30		

Ala	Ala	Arg	Glu	Val	Leu	Gly	Thr	Ile	Ala	Ala	Ser	Thr	Ile	Ser	Val
		35					40					45			

Thr	Gly	Leu	Ile	Phe	Ser	Ile	Thr	Leu	Val	Val	Leu	Gln	Leu	Val	Ser
	50					55					60				

Ser	Gln	Phe	Ser	Pro	Arg	Met	Leu	Asn	Gly	Phe	Leu	Arg	Asn	Arg	Ile
	65				70					75					80

Val	Gln	Ala	Thr	Leu	Ala	Met	Phe	Leu	Gly	Thr	Phe	Val	Phe	Ser	Leu
				85					90					95	

Thr	Val	Ile	Arg	Tyr	Val	Trp	Ser	Glu	Asp	Glu	Asp	Ile	Thr	Gly	Phe
			100					105					110		

Val	Pro	Arg	Ala	Ser	Val	Ser	Val	Ala	Phe	Leu	Leu	Val	Leu	Gly	Cys
			115					120					125		

Leu	Gly	Leu	Phe	Leu	Ala	Phe	Ile	Arg	Leu	Ile	Thr	Phe	Ser	Met	Arg
	130					135					140				

Val	Ala	Asn	Ala	Ile	Ser	Glu	Ile	Gly	Glu	Glu	Thr	Met	Ala	Leu	Ala
	145				150					155					160

Ala	Arg	Ile	Tyr	Pro	Val	Gln	Ser	Asp	Asp	Ala	Gly	Pro	Val	Gln	Gly
				165					170					175	

Pro	Gly	Trp	Ser	Pro	Arg	Pro	Gly	Asp	Pro	Arg	Glu	Glu	Ile	Arg	Val
			180					185					190		

Gly	Asn	His	Gly	Ser	Leu	Val	Trp	Ile	Asp	Tyr	Arg	Lys	Leu	Val	Ser
		195					200					205			

Trp	Ser	Thr	Glu	His	Gln	Ala	Val	Ile	Thr	Val	Asp	Arg	Pro	Val	Gly
		210				215					220				

Asp	Phe	Leu	Val	Glu	Gly	Gln	Pro	Leu	Leu	Arg	Val	Trp	Trp	Asp	Gly
	225				230					235				240	

Glu	Leu	Ser	Asp	Arg	Asp	Arg	Arg	Val	Leu	His	Ser	Ala	Ile	Glu	Val
			245						250					255	

Arg	Thr	Glu	Arg	Glu	Leu	His	Gln	Asp	Val	Ala	Phe	Gly	Leu	Arg	Gln
		260						265					270		

Leu	Val	Asp	Ile	Ala	Asp	Arg	Ala	Leu	Ser	Pro	Gly	Ile	Asn	Asp	Pro
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

275 280 285

Ala Thr Ala Ala Gln Cys Val Gln Glu Ile His Arg Ile Phe Arg Tyr
290 295 300

Leu Val Thr Val Ile Glu Pro Ser Pro Tyr Ile Ala Asp Asp Asp Gly
305 310 315 320

Arg Val Arg Val Val His Gln Pro Gln Arg Ile Ala Asp Met Leu Tyr
325 330 335

Glu Val Ile Arg Glu Ile His Leu Tyr Gly Ala Asp Ser Ala Met Ile
340 345 350

Pro Arg Leu Leu Arg Thr Met Val Glu Asp Leu Val Thr Ala Ala Ala
355 360 365

Asp His Ser Leu Pro Ala Val Glu Arg Ala Arg Gly Ile Leu Asp Asp
370 375 380

Glu Thr Asp Glu Asp Arg Asp Ser Asp Thr Ala Asn Val
385 390 395

<210> 1293

<211> 1422

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1399)

<223> RXN02782

<400> 1293

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caatcacaga agctagtga gcatattgta gaatataact atg cca aca ctg ctt 115
Met Pro Thr Leu Leu
1 5

att gac acc cat ccg cat ctt gca gcg caa ctt ctt gac cct ggt tta 163
Ile Asp Thr His Pro His Leu Ala Ala Gln Leu Leu Asp Pro Gly Leu
10 15 20

ggt gaa ctt ctt aca gcc ggt tcc aac aaa aaa gtg cag tgg cag tgc 211
Gly Glu Leu Leu Thr Ala Gly Ser Asn Lys Lys Val Gln Trp Gln Cys
25 30 35

cct aag cac tcc aat cac atc tgg acg gcc tcg gtt aat aac cgc acc 259
Pro Lys His Ser Asn His Ile Trp Thr Ala Ser Val Asn Asn Arg Thr
40 45 50

aat gca aag aac ccg cgc tgc ccc tat tgt gcc gga aca cga gtg ttg 307
Asn Ala Lys Asn Pro Arg Cys Pro Tyr Cys Ala Gly Thr Arg Val Leu
55 60 65

gca ggt ttt aat gat ctc gcc acc act cac ccg cat ctt gct gta cag 355
Ala Gly Phe Asn Asp Leu Ala Thr Thr His Pro His Leu Ala Val Gln
70 75 80 85

ctg gtt gac caa gat att gcc gtc acc att tcc gct ggt tct ggc aaa	403
Leu Val Asp Gln Asp Ile Ala Val Thr Ile Ser Ala Gly Ser Gly Lys	
90 95 100	
aga caa ctg tgg cag tgt gta gta aac cca aaa cac cag tgg ttg gct	451
Arg Gln Leu Trp Gln Cys Val Val Asn Pro Lys His Gln Trp Leu Ala	
105 110 115	
acg cca aat aat cgc acg agt act aaa tct gcg agt tct ggt tgc ccc	499
Thr Pro Asn Asn Arg Thr Ser Thr Lys Ser Ala Ser Ser Gly Cys Pro	
120 125 130	
tac tgt gcc aac cga gcg gta tta gtc ggt gac aat gac ttt gca aca	547
Tyr Cys Ala Asn Arg Ala Val Leu Val Gly Asp Asn Asp Phe Ala Thr	
135 140 145	
acc tac ccc gaa ctt gca gcg caa tta gta gat caa tct gca gcg aca	595
Thr Tyr Pro Glu Leu Ala Ala Gln Leu Val Asp Gln Ser Ala Ala Thr	
150 155 160 165	
acc ttt aca gcc gcc cac aac aag cct gtt gag tgg atc tgt tgc aag	643
Thr Phe Thr Ala Gln His Asn Lys Pro Val Glu Trp Ile Cys Cys Lys	
170 175 180	
cat gaa cca cca ttt atc tgg aaa acc tca cca att ttg cgt gta cga	691
His Glu Pro Pro Phe Ile Trp Lys Thr Ser Pro Ile Leu Arg Val Arg	
185 190 195	
cag aac acc cag tgc cct gtg tgc tca gag cga act gtg gcg ccg gcg	739
Gln Asn Thr Gln Cys Pro Val Cys Ser Ser Glu Arg Thr Val Ala Pro Ala	
200 205 210	
ctt aat gat ctt gca acc act cac cct aaa ctt gcc gag caa att gca	787
Leu Asn Asp Leu Ala Thr Thr His Pro Lys Leu Ala Glu Gln Ile Ala	
215 220 225	
gat cct caa cca agt ggt gtg agc gcc gcg gcc att atc ccc acc att	835
Asp Pro Gln Pro Ser Gly Val Ser Ala Ala Ala Ile Ile Pro Thr Ile	
230 235 240 245	
agc agg ggt tcc cat acg caa tta aca tgg caa tgt tct aaa aat cat	883
Ser Arg Gly Ser His Thr Gln Leu Thr Trp Gln Cys Ser Lys Asn His	
250 255 260	
gac cac caa tgg gtc gcc aca gta aag gat cgt gtt cgc gga aca gac	931
Asp His Gln Trp Val Ala Thr Val Lys Asp Arg Val Arg Gly Thr Asp	
265 270 275	
tgc ccc acc tgc gca aat aca gga act tca cgc aaa gag gct gaa ctt	979
Cys Pro Thr Cys Ala Asn Thr Gly Thr Ser Arg Lys Gln Ala Glu Leu	
280 285 290	
att gag gtc atc cgt gca tta ttc cca aac act gat gtc cag caa ggt	1027
Ile Glu Val Ile Arg Ala Leu Phe Pro Asn Thr Asp Val Gln Gln Gly	
295 300 305	
gcg ctc att aat gga cgt acc ggt aat caa ggt gca tgc ccg tca acc	1075
Ala Leu Ile Asn Gly Arg Thr Gly Asn Gln Gly Ala Ser Pro Ser Thr	
310 315 320 325	
gat gta ctc ata ccg tcc aaa aat ctc gct atc gag ttc aac ggc ctg	1123


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Asp Val Leu Ile Pro Ser Lys Asn Leu Ala Ile Glu Phe Asn Gly Leu
      330                      335                      340

tac tgg cac tct gag ctt ttc atc aaa gat aag cat tat cat gcg aac 1171
Tyr Trp His Ser Glu Leu Phe Ile Lys Asp Lys His Tyr His Ala Asn
      345                      350                      355

aaa tca gct ctc gca gaa caa gcc ggt gtg cag ctc att cat gtg tgg 1219
Lys Ser Ala Leu Ala Glu Gln Ala Gly Val Gln Leu Ile His Val Trp
      360                      365                      370

gag gac gac tgg aat ctt cgc cgc gac att gtg atc cgc atg atc gca 1267
Glu Asp Asp Trp Asn Leu Arg Arg Asp Ile Val Ile Arg Met Ile Ala
      375                      380                      385

cac aag ctt cat gca acc cat aac ctc agt gct gtt ttg cct acc gaa 1315
His Lys Leu His Ala Thr His Asn Leu Ser Ala Val Leu Pro Thr Glu
      390                      395                      400                      405

act act gac tca cgt gtg gca acc acc gct ttc gcc gta cac tca cac 1363
Thr Thr Asp Ser Arg Val Ala Thr Thr Ala Phe Ala Val His Ser His
      410                      415                      420

tgt cgg tgg tct ctg gtt cac gcg ctg ctg cat tct tgaacagcaa 1409
Cys Arg Trp Ser Leu Val His Ala Leu Leu His Ser
      425                      430

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<210> 1294
<211> 433
<212> PRT
<213> Corynebacterium glutamicum

<400> 1294
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Leu Asp Pro Gly Leu Gly Glu Leu Leu Thr Ala Gly Ser Asn Lys Lys
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Val Gln Trp Gln Cys Pro Lys His Ser Asn His Ile Trp Thr Ala Ser
      35          40          45

Val Asn Asn Arg Thr Asn Ala Lys Asn Pro Arg Cys Pro Tyr Cys Ala
      50          55          60

Gly Thr Arg Val Leu Ala Gly Phe Asn Asp Leu Ala Thr Thr His Pro
      65          70          75          80

His Leu Ala Val Gln Leu Val Asp Gln Asp Ile Ala Val Thr Ile Ser
      85          90          95

Ala Gly Ser Gly Lys Arg Gln Leu Trp Gln Cys Val Val Asn Pro Lys
      100          105          110

His Gln Trp Leu Ala Thr Pro Asn Asn Arg Thr Ser Thr Lys Ser Ala
      115          120          125

Ser Ser Gly Cys Pro Tyr Cys Ala Asn Arg Ala Val Leu Val Gly Asp

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130					135					140				
Asn	Asp	Phe	Ala	Thr	Thr	Tyr	Pro	Glu	Leu	Ala	Gln	Leu	Val	Asp
145					150					155				160
Gln	Ser	Ala	Ala	Thr	Thr	Phe	Thr	Ala	Gly	His	Asn	Lys	Pro	Val
				165					170					175
Trp	Ile	Cys	Cys	Lys	His	Glu	Pro	Pro	Phe	Ile	Trp	Lys	Thr	Ser
				180					185					190
Ile	Leu	Arg	Val	Arg	Gln	Asn	Thr	Gln	Cys	Pro	Val	Cys	Ser	Glu
				195					200					205
Thr	Val	Ala	Pro	Ala	Leu	Asn	Asp	Leu	Ala	Thr	Thr	His	Pro	Lys
				210					215					220
Ala	Glu	Gln	Ile	Ala	Asp	Pro	Gln	Pro	Ser	Gly	Val	Ser	Ala	Ala
225														240
Ile	Ile	Pro	Thr	Ile	Ser	Arg	Gly	Ser	His	Thr	Gln	Leu	Thr	Trp
				245										255
Cys	Ser	Lys	Asn	His	Asp	His	Gln	Trp	Val	Ala	Thr	Val	Lys	Asp
				260										270
Val	Arg	Gly	Thr	Asp	Cys	Pro	Thr	Cys	Ala	Asn	Thr	Gly	Thr	Ser
				275										285
Lys	Glu	Ala	Glu	Leu	Ile	Glu	Val	Ile	Arg	Ala	Leu	Phe	Pro	Asn
				290										300
Asp	Val	Gln	Gln	Gly	Ala	Leu	Ile	Asn	Gly	Arg	Thr	Gly	Asn	Gln
305														320
Ala	Ser	Pro	Ser	Thr	Asp	Val	Leu	Ile	Pro	Ser	Lys	Asn	Leu	Ala
				325										335
Glu	Phe	Asn	Gly	Leu	Tyr	Trp	His	Ser	Glu	Leu	Phe	Ile	Lys	Asp
				340										350
His	Tyr	His	Ala	Asn	Lys	Ser	Ala	Leu	Ala	Glu	Gln	Ala	Gly	Val
				355										365
Leu	Ile	His	Val	Trp	Glu	Asp	Asp	Trp	Asn	Leu	Arg	Arg	Asp	Ile
				370										380
Ile	Arg	Met	Ile	Ala	His	Lys	Leu	His	Ala	Thr	His	Asn	Leu	Ser
385														400
Val	Leu	Pro	Thr	Glu	Thr	Thr	Asp	Ser	Arg	Val	Ala	Thr	Thr	Ala
				405										415
Ala	Val	His	Ser	His	Cys	Arg	Trp	Ser	Leu	Val	His	Ala	Leu	Leu
				420										430
Ser														

<210> 1295

<211> 795

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(772)

<223> FRXA02782

<400> 1295

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 Val Ala Pro Ala Leu
 1 5

aat gat ctt gca acc act cac cct aaa ctt gcc gag caa att gca gat 163
 Asn Asp Leu Ala Thr His Pro Lys Leu Ala Glu Gln Ile Ala Asp
 10 15 20

cct caa cca agt ggt gtg agc gcc gcg gcc att atc ccc acc att agc 211
 Pro Gln Pro Ser Gly Val Ser Ala Ala Ile Ile Pro Thr Ile Ser
 25 30 35

agg ggt tcc cat acg caa tta aca tgg caa tgt tct aaa aat cat gac 259
 Arg Gly Ser His Thr Gln Leu Thr Trp Gln Cys Ser Lys Asn His Asp
 40 45 50

cac caa tgg gtc gcc aca gta aag gat cgt gtt cgc gga aca gac tgc 307
 His Gln Trp Val Ala Thr Val Lys Asp Arg Val Arg Gly Thr Asp Cys
 55 60 65

ccc acc tgc gca aat aca gga act tca cgc aaa gag gct gaa ctt att 355
 Pro Thr Cys Ala Asn Thr Gly Thr Ser Arg Lys Glu Ala Glu Leu Ile
 70 75 80 85

gag gtc atc cgt gca tta ttc cca aac act gat gtc cag caa ggt gcg 403
 Glu Val Ile Arg Ala Leu Phe Pro Asn Thr Asp Val Gln Gln Gly Ala
 90 95 100

ctc att aat gga cgt acc ggt aat caa ggt gca tcg ccg tca acc gat 451
 Leu Ile Asn Gly Arg Thr Gly Asn Gln Gly Ala Ser Pro Ser Thr Asp
 105 110 115

gta ctc ata ccg tcc aaa aat ctc gct atc gag ttc aac ggc ctg tac 499
 Val Leu Ile Pro Ser Lys Asn Leu Ala Ile Glu Phe Asn Gly Leu Tyr
 120 125 130

tgg cac tct gag ctt ttc atc aaa gat aag cat tat cat gcg aac aaa 547
 Trp His Ser Glu Leu Phe Ile Lys Asp Lys His Tyr His Ala Asn Lys
 135 140 145

tca gct ctc gca gaa caa gcc ggt gtg cag ctc att cat gtg tgg gag 595
 Ser Ala Leu Ala Glu Gln Ala Gly Val Gln Leu Ile His Val Trp Glu
 150 155 160 165

gac gac tgg aat ctt cgc cgc gac att gtg atc cgc atg atc gca cac 643
 Asp Asp Trp Asn Leu Arg Arg Asp Ile Val Ile Arg Met Ile Ala His
 170 175 180

aag ctt cat gca acc cat aac ctc agt gct gtt ttg cct acc gaa act 691

Lys Leu His Ala Thr His Asn Leu Ser Ala Val Leu Pro Thr Glu Thr
 185 190 195
 act gac tca cgt gtg gca acc acc gct ttc gcc gta cac tca cac tgt 739
 Thr Asp Ser Arg Val Ala Thr Thr Ala Phe Ala Val His Ser His Cys
 200 205 210
 cgg tgg tct ctg gtt cac gcg ctg ctg cat tct tgaacagcaa ccatattcag 792
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<213> *Corynebacterium glutamicum*

<400> 1296

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 35 40 45
 Ser Lys Asn His Asp His Gln Trp Val Ala Thr Val Lys Asp Arg Val
 50 55 60
 Arg Gly Thr Asp Cys Pro Thr Cys Ala Asn Thr Gly Thr Ser Arg Lys
 65 70 75 80
 Glu Ala Glu Leu Ile Glu Val Ile Arg Ala Leu Phe Pro Asn Thr Asp
 85 90 95
 Val Gln Gln Gly Ala Leu Ile Asn Gly Arg Thr Gly Asn Gln Gly Ala
 100 105 110
 Ser Pro Ser Thr Asp Val Leu Ile Pro Ser Lys Asn Leu Ala Ile Glu
 115 120 125
 Phe Asn Gly Leu Tyr Trp His Ser Glu Leu Phe Ile Lys Asp Lys His
 130 135 140
 Tyr His Ala Asn Lys Ser Ala Leu Ala Glu Gln Ala Gly Val Gln Leu
 145 150 155 160
 Ile His Val Trp Glu Asp Asp Trp Asn Leu Arg Arg Asp Ile Val Ile
 165 170 175
 Arg Met Ile Ala His Lys Leu His Ala Thr His Asn Leu Ser Ala Val
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 Leu Pro Thr Glu Thr Thr Asp Ser Arg Val Ala Thr Thr Ala Phe Ala
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 <223> RXN02812

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 Val Trp Ala Val Ala
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atc aac gct gga aac ggt atc tct gaa gac caa gcc cgc gcc gcc tct 163
 Ile Asn Ala Gly Asn Gly Ile Ser Glu Asp Gln Ala Arg Ala Ala Ser
 10 15 20

gat ttc agt agc ttc agc ttc gac acc ggc aac gcc gat aac tcc gcg 211
 Asp Phe Ser Ser Phe Ser Phe Asp Thr Gly Asn Ala Asp Asn Ser Ala
 25 30 35

ctt gaa agt gtt ctc acc caa gct tca agc gaa tcc gcg gca gaa act 259
 Leu Glu Ser Val Leu Thr Gln Ala Ser Ser Glu Ser Ala Ala Glu Thr
 40 45 50

act gag gcg caa cca agc gag acc cgc gtc gag ccc gcc gct gct tcc 307
 Thr Glu Ala Gln Pro Ser Glu Thr Pro Val Glu Pro Ala Ala Ala Ser
 55 60 65

cca tcc gat acc atc atc aac ctg gat acc tca tcc aac atg gat cga 355
 Pro Ser Asp Thr Ile Ile Asn Leu Asp Thr Ser Ser Asn Met Asp Arg
 70 75 80 85

gtt gtt gac ggc agc cag gaa acc tac cac acg gtt act tcc cgg act 403
 Val Val Asp Gly Ser Gln Glu Thr Tyr His Thr Val Thr Ser Arg Thr
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ctg gcc aac ctc gcc cgc gaa act ggt gca cag gcc 439
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Ala Asp Asn Ser Ala Leu Glu Ser Val Leu Thr Gln Ala Ser Ser Glu
35 40 45

Ser Ala Ala Glu Thr Thr Glu Ala Gln Pro Ser Glu Thr Pro Val Glu
50 55 60

Pro Ala Ala Ala Ser Pro Ser Asp Thr Ile Ile Asn Leu Asp Thr Ser
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Ser Asn Met Asp Arg Val Val Asp Gly Ser Gln Glu Thr Tyr His Thr
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Gly

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<212> DNA
<213> Corynebacterium glutamicum

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ccc gtt gcc act aac tcc gga gca tcc gca gcc gta gcg ctg gcg ctg 96
Pro Val Ala Thr Asn Ser Gly Ala Ser Ala Ala Val Ala Leu Ala Leu
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gct gaa acc cca gaa gct gcc gct gct gcg ctc aac cgt gac gcc gat 144
Ala Glu Thr Pro Glu Ala Ala Ala Ala Leu Asn Arg Asp Ala Asp
35 40 45

gtc acc gca act gga gct gcc gac tcc cct gcg ttt gcc acc gtt gaa 192
Val Thr Ala Thr Gly Ala Ala Asp Ser Pro Ala Phe Ala Thr Val Glu
50 55 60

gga gca gaa ctt cca gag ggc tac acc ttt gaa gca gta gac agc gca 240
Gly Ala Glu Leu Pro Glu Gly Tyr Thr Phe Glu Ala Val Asp Ser Ala
65 70 75 80

gaa gta cct gtg tgg gct gtt gcc atc aac gct gga aac ggt atc tct 288
Glu Val Pro Val Trp Ala Val Ala Ile Asn Ala Gly Asn Gly Ile Ser
85 90 95

gaa gac caa gcc cgc gcc gcc tct gat ttc agt agc ttc agc ttc gac 336
Glu Asp Gln Ala Arg Ala Ala Ser Asp Phe Ser Ser Phe Ser Phe Asp
100 105 110

acc ggc aac gcc gat aac tcc gcg ctt gaa agt gtt ctc acc caa gct 384

Thr	Gly	Asn	Ala	Asp	Asn	Ser	Ala	Leu	Glu	Ser	Val	Leu	Thr	Gln	Ala		
		115					120					125					
tca	agc	gaa	tcc	gcg	gca	gaa	act	act	gag	gcg	caa	cca	agc	gag	acc	432	
Ser	Ser	Glu	Ser	Ala	Ala	Glu	Thr	Thr	Glu	Ala	Gln	Pro	Ser	Glu	Thr		
		130				135					140						
ccg	gtc	gag	ccc	gcc	gct	gct	tcc	cca	tcc	gat	acc	atc	atc	aac	ctg	480	
Pro	Val	Glu	Pro	Ala	Ala	Ala	Ser	Pro	Ser	Asp	Thr	Ile	Ile	Asn	Leu		
					150					155				160			
gat	acc	tca	tcc	aac	atg	gat	cga	gtt	gtt	gac	ggc	agc	cag	gaa	acc	528	
Asp	Thr	Ser	Ser	Asn	Met	Asp	Arg	Val	Val	Asp	Gly	Ser	Gln	Glu	Thr		
				165				170					175				
tac	cac	acg	gtt	act	tcc	cgg	act	ctg	gcc	aac	ctc	gcc				567	
Tyr	His	Thr	Val	Thr	Ser	Arg	Thr	Leu	Ala	Asn	Leu	Ala					
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<211> 189

<212> PRT

<213> Corynebacterium glutamicum

<400> 1300

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Ala	Glu	Thr	Pro	Glu	Ala	Ala	Ala	Ala	Leu	Asn	Arg	Asp	Ala	Asp	
		35				40					45				

Val	Thr	Ala	Thr	Gly	Ala	Ala	Asp	Ser	Pro	Ala	Phe	Ala	Thr	Val	Glu
	50				55					60					

Gly	Ala	Glu	Leu	Pro	Glu	Gly	Tyr	Thr	Phe	Glu	Ala	Val	Asp	Ser	Ala
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Glu	Val	Pro	Val	Trp	Ala	Val	Ala	Ile	Asn	Ala	Gly	Asn	Gly	Ile	Ser
			85					90					95		

Glu	Asp	Gln	Ala	Arg	Ala	Ala	Ser	Asp	Phe	Ser	Ser	Phe	Ser	Phe	Asp
	100						105					110			

Thr	Gly	Asn	Ala	Asp	Asn	Ser	Ala	Leu	Glu	Ser	Val	Leu	Thr	Gln	Ala
	115						120					125			

Ser	Ser	Glu	Ser	Ala	Ala	Glu	Thr	Thr	Glu	Ala	Gln	Pro	Ser	Glu	Thr
	130					135					140				

Pro	Val	Glu	Pro	Ala	Ala	Ala	Ser	Pro	Ser	Asp	Thr	Ile	Ile	Asn	Leu
145				150					155					160	

Asp	Thr	Ser	Ser	Asn	Met	Asp	Arg	Val	Val	Asp	Gly	Ser	Gln	Glu	Thr
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Tyr	His	Thr	Val	Thr	Ser	Arg	Thr	Leu	Ala	Asn	Leu	Ala			
			180				185								

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<223> RXN02817
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<212> PRT
<213> Corynebacterium glutamicum
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ggt tat atc gcg caa att gtg gcg ttt ttc atg ctt gcc gtc tcc gcg 355
Val Tyr Ile Ala Gln Ile Val Ala Phe Phe Met Leu Ala Val Ser Ala
70 75 80 85

atg cag gct ttt ggt ttc tct ctc gcg ggc gct gcg att ccg gca acc 403
Met Gln Ala Phe Gly Phe Ser Leu Ala Gly Ala Ala Ile Pro Ala Thr
90 95 100

att gcg tca gct gcc att ggc ctt ggt gcg cag tcg att gtt gcg gac 451
Ile Ala Ser Ala Ala Ile Gly Leu Gly Ala Gln Ser Ile Val Ala Asp
105 110 115

ttc ttg gcc gga ttt ttc atc ctg acg gaa aag caa ttc gcc gtg ggt 499
Phe Leu Ala Gly Phe Phe Ile Leu Thr Glu Lys Gln Phe Gly Val Gly
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<211> 133

<212> PRT

<213> *Corynebacterium glutamicum*

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20 25 30

Phe Leu Ile Pro Arg Ile Gly Arg Leu Ala Met Arg Ile Ile Lys Arg
35 40 45

Arg Val Glu Ser Ala Ala Asp Ala Asp Thr Thr Lys Asn Gln Leu Ala
50 55 60

Phe Ala Gly Val Gly Val Tyr Ile Ala Gln Ile Val Ala Phe Phe Met
65 70 75 80

Leu Ala Val Ser Ala Met Gln Ala Phe Gly Phe Ser Leu Ala Gly Ala
85 90 95

Ala Ile Pro Ala Thr Ile Ala Ser Ala Ala Ile Gly Leu Gly Ala Gln
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Ser Ile Val Ala Asp Phe Leu Ala Gly Phe Phe Ile Leu Thr Glu Lys
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Gln Phe Gly Val Gly
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<211> 606

<212> DNA

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<223> RXN02818

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ggc gat tat aaa ggc ctt acc gat acg gcg ttc cgt aag aag ctg cag				96
Gly Asp Tyr Lys Gly Leu Thr Asp Thr Ala Phe Arg Lys Lys Leu Gln	20	25	30	
cgc gat ctt gcc tac ctg cgc aga gtt ggc gtt cgg att gag cag ttc				144
Arg Asp Leu Ala Tyr Leu Arg Arg Val Gly Val Pro Ile Glu Gln Phe	35	40	45	
acg gtc acc tca ggc ata gct gaa ggc cag cag gcg tac cgt ctg gcc				192
Thr Val Thr Ser Gly Ile Ala Glu Gly Gln Gln Ala Tyr Arg Leu Ala	50	55	60	
cag gat tct tat aag ctc gcc gag gtc gaa ttc acc cca gat gag gcc				240
Gln Asp Ser Tyr Lys Leu Pro Glu Val Glu Phe Thr Pro Asp Glu Ala	65	70	75	80
gcc gtg ctg ggc atg gca ggg gag atg ggc cat aat cag gaa ctc ggc				288
Ala Val Leu Gly Met Ala Gly Glu Met Gly His Asn Gln Glu Leu Gly	85		90	95
gcc ttc gcg cgt tgc ggg tgg acc aaa ttg gcg gcc ggc ggc gcg cag				336
Ala Phe Ala Arg Ser Gly Trp Thr Lys Leu Ala Ala Gly Gly Ala Gln	100	105	110	
cgt gat ctg tcc acg tcc aca gcc ttg acc aat gcg ggc gat tta ggt				384
Arg Asp Leu Ser Thr Ser Thr Ala Leu Thr Asn Ala Gly Asp Leu Gly	115	120	125	
tcc ttg tct gca aaa acc ctc gat gcg atc atc aaa gcc cgc caa ttg				432
Ser Leu Ser Ala Lys Thr Leu Asp Ala Ile Ile Lys Ala Arg Gln Leu	130	135	140	
ggc aag caa atc agc ttc gaa tac cgg cgc gcc ccc aaa gac gcc ccc				480
Gly Lys Gln Ile Ser Phe Glu Tyr Arg Arg Ala Pro Lys Asp Ala Pro	145	150	155	160
tcg ctt cga cac atg gat cct tgg ggt ctg gtc cct gag cgc gac cgc				528
Ser Leu Arg His Met Asp Pro Trp Gly Leu Val Pro Glu Arg Asp Arg	165	170	175	
atc tac ctg gtc gga ttc gac ctc gac cgc caa gaa gca cgc acc ttc				576
Ile Tyr Leu Val Gly Phe Asp Leu Asp Arg Gln Glu Ala Arg Thr Phe	180	185	190	
cgc atc acc cgc gtc cgc aac atc aaa ctc				606
Arg Ile Thr Arg Val Arg Asn Ile Lys Leu	195	200		
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85 90 95			
gcc ttc gcg cgt tcg ggg tgg acc aaa ttg gcg gcc ggc ggc gcg cag Ala Phe Ala Arg Ser Gly Trp Thr Lys Leu Ala Ala Gly Gly Ala Gln	336		
100 105 110			
cgt gat ctg tcc acg tcc aca gcc ttg acc aat gcg ggc gat tta ggt Arg Asp Leu Ser Thr Ser Thr Ala Leu Thr Asn Ala Gly Asp Leu Gly	384		
115 120 125			
tcc ttg tct gca aaa acc ctc gat gcg atc atc aaa gcc cgc caa ttg Ser Leu Ser Ala Lys Thr Leu Asp Ala Ile Ile Lys Ala Arg Gln Leu	432		
130 135 140			
ggc aag caa atc agc ttc gaa tac cgg cgc gcc ccc aaa gac gcc ccc Gly Lys Gln Ile Ser Phe Glu Tyr Arg Arg Ala Pro Lys Asp Ala Pro	480		
145 150 155 160			
tcg ctt cga cac atg gat cct tgg ggt ctg gtc cct gag cgc gac cgc Ser Leu Arg His Met Asp Pro Trp Gly Leu Val Pro Glu Arg Asp Arg	528		
165 170 175			
atc tac ctg gtc gga ttc gac ctc gac cgc caa gaa gca cgc acc ttc Ile Tyr Leu Val Gly Phe Asp Leu Asp Arg Gln Glu Ala Arg Thr Phe	576		
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Arg Asp Leu Ala Tyr Leu Arg Arg Val Gly Val Pro Ile Glu Gln Phe			
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Thr Val Thr Ser Gly Ile Ala Glu Gly Gln Gln Ala Tyr Arg Leu Ala			
50 55 60			
Gln Asp Ser Tyr Lys Leu Pro Glu Val Glu Phe Thr Pro Asp Glu Ala			
65 70 75 80			
Ala Val Leu Gly Met Ala Gly Glu Met Gly His Asn Gln Glu Leu Gly			

85					90					95					
Ala	Phe	Ala	Arg	Ser	Gly	Trp	Thr	Lys	Leu	Ala	Ala	Gly	Gly	Ala	Gln
			100					105					110		
Arg	Asp	Leu	Ser	Thr	Ser	Thr	Ala	Leu	Thr	Asn	Ala	Gly	Asp	Leu	Gly
		115					120					125			
Ser	Leu	Ser	Ala	Lys	Thr	Leu	Asp	Ala	Ile	Ile	Lys	Ala	Arg	Gln	Leu
		130				135					140				
Gly	Lys	Gln	Ile	Ser	Phe	Glu	Tyr	Arg	Arg	Ala	Pro	Lys	Asp	Ala	Pro
145				150					155					160	
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			165					170					175		
Ile	Tyr	Leu	Val	Gly	Phe	Asp	Leu	Asp	Arg	Gln	Glu	Ala	Arg	Thr	Phe
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<222> {101}..{1939}

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				Met	Lys	Leu	Ala	Pro	
				1				5	

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Arg	Met	Arg	Met	Arg	Ser	Pro	Lys	Thr	Phe	Ala	Ala	Leu	Ala	Ser	Leu	
			10						15				20			

gct	tta	gtc	ata	ggt	ctc	ggc	cag	gta	ccg	atc	gcc	caa	gct	caa	acc	211
Ala	Leu	Val	Ile	Gly	Leu	Gly	Gln	Val	Pro	Ile	Ala	Gln	Ala	Gln	Thr	
		25					30					35				

gag	tat	cga	acc	gcc	tcc	gac	ggt	tcc	ctg	aac	tgg	gga	ttt	agg	caa	259
Glu	Tyr	Arg	Thr	Ala	Ser	Asp	Gly	Ser	Leu	Asn	Trp	Gly	Phe	Arg	Gln	
		40				45					50					

tcg	ttc	cgc	aat	tac	atc	caa	acc	ggc	gtg	gcc	aaa	ggt	tcc	atc	acg	307
Ser	Phe	Arg	Asn	Tyr	Ile	Gln	Thr	Gly	Val	Ala	Lys	Gly	Ser	Ile	Thr	
		55				60					65					

ctt	ggc	gac	ggc	gca	tcc	gac	aac	ggt	ggc	aac	ttc	gca	ttc	acc	cca	355
Leu	Gly	Asp	Gly	Ala	Ser	Asp	Asn	Gly	Gly	Asn	Phe	Ala	Phe	Thr	Pro	
		70				75				80					85	

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 90 95 100

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 Phe Asn Gly Ser Val His Phe Leu Gly His Gln Ala Glu Asp Lys Trp
 105 110 115

atc ctg gac acc acc atg tct gac atc aaa atg gtg ttc aac gga tcc 499
 Ile Leu Asp Thr Thr Met Ser Asp Ile Lys Met Val Phe Asn Gly Ser
 120 125 130

tcc gcg cag cta gtt gtg gat ttg gtt gcc cgc gaa ttc aag ggc acc 547
 Ser Ala Gln Leu Val Val Asp Leu Val Ala Arg Glu Phe Lys Gly Thr
 135 140 145

acc tac gat gac atc ggc gaa tac atc atc tcc gac gac atc gtg ctt 595
 Thr Tyr Asp Asp Ile Gly Glu Tyr Ile Ile Ser Asp Asp Ile Val Leu
 150 155 160 165

gcc gac gtc tcc ctc aac tcc gcc gcc gac ttc tcc caa gat tcc atc 643
 Ala Asp Val Ser Leu Asn Ser Ala Ala Asp Phe Ser Gln Asp Ser Ile
 170 175 180

gac ctg tcc ggc acc acc gac ctc acc gca gct ggc gcc caa gct ttc 691
 Asp Leu Ser Gly Thr Thr Asp Leu Thr Ala Ala Gly Ala Gln Ala Phe
 185 190 195

gga gga ttc tac gaa acc ggc gaa gcc ctc gac ccg acc ggc ggc agc 739
 Gly Gly Phe Tyr Glu Thr Gly Glu Ala Leu Asp Pro Thr Gly Gly Ser
 200 205 210

ctg acc att tcc tcc acc acc acc gcg cca tcg acc agc acg acc tcc 787
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acc tct gcc tca act tcc ggt gga acc gcc gac tgt tcc tcc ggc gca 835
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 230 235 240 245

ttg ggt gtt gtc acc acc gga acc aac gac ggc atg ctg ggc acc atc 883
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 250 255 260

cag gaa gta aac aac acc ttc gcg att tgg aac aac ctc atc gtc aac 931
 Gln Glu Val Asn Asn Thr Phe Ala Ile Trp Asn Asn Leu Ile Val Asn
 265 270 275

acc gag cgc atg ttc tgc aac att gat acc ctc aag gcg cgc ttc gac 979
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 280 285 290

acg gat gat tcc agc gat tca gcg acc tct gcg act tct ggg act act 1027
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 295 300 305

gcg tcc acc ggc acc acc gct gca act acc gcg gga acc acg ggt acc 1075
 Ala Ser Thr Gly Thr Thr Ala Ala Thr Thr Ala Gly Thr Thr Gly Thr
 310 315 320 325

act gga act gcc agc acc gct tcc gga act tcc gga act tcc gga acc 1123

Thr	Gly	Thr	Ala	Ser	Thr	Ala	Ser	Gly	Thr	Ser	Gly	Thr	Ser	Gly	Thr	
				330					335						340	
tcc	ggc	acc	gca	gca	act	gtc	gct	ggc	acc	acc	cca	act	gac	aat	ggc	1171
Ser	Gly	Thr	Ala	Ala	Thr	Val	Ala	Gly	Thr	Thr	Pro	Thr	Asp	Asn	Gly	
			345					350					355			
gtt	tgc	acc	gct	tcc	gga	tct	ttg	ggc	gtg	acc	caa	gca	tct	gcg	cag	1219
Val	Cys	Thr	Ala	Ser	Gly	Ser	Leu	Gly	Val	Thr	Gln	Ala	Ser	Ala	Gln	
			360					365					370			
tgg	ggg	gtg	aag	gcg	tcc	ttc	cag	aac	tac	att	cgc	gga	tcg	atc	gcc	1267
Trp	Gly	Val	Lys	Ala	Ser	Phe	Gln	Asn	Tyr	Ile	Arg	Gly	Ser	Ile	Ala	
			375				380				385					
aac	ggg	agc	tgg	act	ctc	aac	ggc	gtt	ggg	ttt	gat	aat	cag	cag	ttc	1315
Asn	Gly	Ser	Trp	Thr	Leu	Asn	Gly	Val	Gly	Phe	Asp	Asn	Gln	Gln	Phe	
			390			395				400					405	
caa	ttc	tct	gga	aat	tcc	gga	gca	gtc	gac	gcg	gaa	aac	aag	acc	ggc	1363
Gln	Phe	Ser	Gly	Asn	Ser	Gly	Ala	Val	Asp	Ala	Glu	Asn	Lys	Thr	Gly	
				410					415					420		
agc	atc	aat	ttc	cct	ggg	tcc	atc	cac	ttc	acg	ggg	cac	ggc	gga	atc	1411
Ser	Ile	Asn	Phe	Pro	Gly	Ser	Ile	His	Phe	Thr	Gly	His	Gly	Gly	Ile	
			425					430					435			
ttg	gac	atg	cag	atc	gca	aac	att	gag	atc	agc	ttc	aac	ggc	aac	tcc	1459
Leu	Asp	Met	Gln	Ile	Ala	Asn	Ile	Glu	Ile	Ser	Phe	Asn	Gly	Asn	Ser	
			440					445					450			
ggc	gag	ctg	att	gcg	gat	gtc	gtt	tcc	tct	gac	atg	gat	gga	aat	tcc	1507
Gly	Glu	Leu	Ile	Ala	Asp	Val	Val	Ser	Ser	Asp	Met	Asp	Gly	Asn	Ser	
			455			460					465					
acc	aac	tac	ggg	cgc	act	gtc	gtg	ggc	acc	ctg	aac	ttc	tct	gcg	ttg	1555
Thr	Asn	Tyr	Gly	Arg	Thr	Val	Val	Gly	Thr	Leu	Asn	Phe	Ser	Ala	Leu	
			470			475				480					485	
aat	gtt	tct	gca	acg	gaa	gct	tcc	ggg	tcc	gct	tcg	gtg	tcc	ctg	tca	1603
Asn	Val	Ser	Ala	Thr	Glu	Ala	Ser	Gly	Ser	Ala	Ser	Val	Ser	Leu	Ser	
				490					495					500		
cag	tcg	ggg	tcg	cag	gcg	ttc	gct	gat	ttc	tac	acc	cca	ggc	acc	cag	1651
Gln	Ser	Gly	Ser	Gln	Ala	Phe	Ala	Asp	Phe	Tyr	Thr	Pro	Gly	Thr	Gln	
			505					510					515			
ttg	gat	cgg	atc	agt	ttc	agc	gca	act	ttg	ggc	ggc	gac	gcc	agc	tcg	1699
Leu	Asp	Pro	Ile	Ser	Phe	Ser	Ala	Thr	Leu	Gly	Gly	Asp	Ala	Ser	Cys	
			520				525					530				
gcc	acc	gga	tcc	acc	tcg	acc	aca	ggc	gct	gct	gcc	acc	gcg	aac	act	1747
Ala	Thr	Gly	Ser	Thr	Ser	Thr	Thr	Gly	Ala	Ala	Ala	Thr	Ala	Asn	Thr	
			535				540				545					
gac	aac	acc	gaa	ggg	gtt	gcc	ggc	gag	gaa	tcc	acc	acc	ccc	gct	aac	1795
Asp	Asn	Thr	Glu	Gly	Val	Ala	Gly	Glu	Glu	Ser	Thr	Thr	Pro	Ala	Asn	
			550			555				560					565	
caa	aac	agc	cag	ttc	caa	atc	cgc	cag	gcc	gct	gca	gat	tcc	acc	gga	1843
Gln	Asn	Ser	Gln	Phe	Gln	Ile	Arg	Gln	Ala	Ala	Ala	Asp	Ser	Thr	Gly	

Thr Ser Thr Thr Ser Thr Ser Ala Ser Thr Ser Gly Gly Thr Ala Asp
 225 230 235 240
 Cys Ser Ser Gly Ala Leu Gly Val Val Thr Thr Gly Thr Asn Asp Gly
 245 250 255
 Met Leu Gly Thr Ile Gln Glu Val Asn Asn Thr Phe Ala Ile Trp Asn
 260 265 270
 Asn Leu Ile Val Asn Thr Glu Arg Met Phe Cys Asn Ile Asp Thr Leu
 275 280 285
 Lys Ala Arg Phe Asp Thr Asp Asp Ser Ser Asp Ser Ala Thr Ser Ala
 290 295 300
 Thr Ser Gly Thr Thr Ala Ser Thr Gly Thr Thr Ala Ala Thr Thr Ala
 305 310 315 320
 Gly Thr Thr Gly Thr Thr Gly Thr Ala Ser Thr Ala Ser Gly Thr Ser
 325 330 335
 Gly Thr Ser Gly Thr Ser Gly Thr Ala Ala Thr Val Ala Gly Thr Thr
 340 345 350
 Pro Thr Asp Asn Gly Val Cys Thr Ala Ser Gly Ser Leu Gly Val Thr
 355 360 365
 Gln Ala Ser Ala Gln Trp Gly Val Lys Ala Ser Phe Gln Asn Tyr Ile
 370 375 380
 Arg Gly Ser Ile Ala Asn Gly Ser Trp Thr Leu Asn Gly Val Gly Phe
 385 390 395 400
 Asp Asn Gln Gln Phe Gln Phe Ser Gly Asn Ser Gly Ala Val Asp Ala
 405 410 415
 Glu Asn Lys Thr Gly Ser Ile Asn Phe Pro Gly Ser Ile His Phe Thr
 420 425 430
 Gly His Gly Gly Ile Leu Asp Met Gln Ile Ala Asn Ile Glu Ile Ser
 435 440 445
 Phe Asn Gly Asn Ser Gly Glu Leu Ile Ala Asp Val Val Ser Ser Asp
 450 455 460
 Met Asp Gly Asn Ser Thr Asn Tyr Gly Arg Thr Val Val Gly Thr Leu
 465 470 475 480
 Asn Phe Ser Ala Leu Asn Val Ser Ala Thr Glu Ala Ser Gly Ser Ala
 485 490 495
 Ser Val Ser Leu Ser Gln Ser Gly Ser Gln Ala Phe Ala Asp Phe Tyr
 500 505 510
 Thr Pro Gly Thr Gln Leu Asp Pro Ile Ser Phe Ser Ala Thr Leu Gly
 515 520 525
 Gly Asp Ala Ser Cys Ala Thr Gly Ser Thr Ser Thr Thr Gly Ala Ala
 530 535 540
 Ala Thr Ala Asn Thr Asp Asn Thr Glu Gly Val Ala Gly Glu Glu Ser

545					550						555				560
Thr	Thr	Pro	Ala	Asn	Gln	Asn	Ser	Gln	Phe	Gln	Ile	Arg	Gln	Ala	Ala
				565					570					575	
Ala	Asp	Ser	Thr	Gly	Leu	Asp	Thr	Thr	Thr	Thr	Met	Leu	Leu	Ile	Leu
		580						585					590		
Ala	Ala	Phe	Val	Val	Ala	Gly	Gly	Ser	Met	Thr	Arg	Phe	Thr	Val	Gly
		595					600					605			
Asn	Pro	Thr	Gly	Lys											
	610														
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<213> <i>Corynebacterium glutamicum</i>															
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<222> (101)..(538)															
<223> FRXA01322															
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caacacttga gaaaaattgc gaaaaaggac actgtgttcc atg aaa ctt gca cct 115															
Met Lys Leu Ala Pro 1 5															
cgt atg cgg atg agg agc ccc aaa act ttc gcg gcc ctc gcc tca ctt 163															
Arg Met Arg Met Arg Ser Pro Lys Thr Phe Ala Ala Leu Ala Ser Leu 10 15 20															
gct tta gtc ata ggt ctc ggc cag gta cgg atc gcc caa gct caa acc 211															
Ala Leu Val Ile Gly Leu Gly Gln Val Pro Ile Ala Gln Ala Gln Thr 25 30 35															
gag tat cga acc gcc tcc gac ggt tcc ctg aac tgg gga ttt agg caa 259															
Glu Tyr Arg Thr Ala Ser Asp Gly Ser Leu Asn Trp Gly Phe Arg Gln 40 45 50															
tcg ttc cgc aat tac atc caa acc ggc gtg gcc aaa ggt tcc atc acg 307															
Ser Phe Arg Asn Tyr Ile Gln Thr Gly Val Ala Lys Gly Ser Ile Thr 55 60 65															
ctt ggc gac gcc gca tcc gac aac ggt gcc aac ttc gca ttc acc cca 355															
Leu Gly Asp Gly Ala Ser Asp Asn Gly Gly Asn Phe Ala Phe Thr Pro 70 75 80 85															
cgc acc aac gcc acc acc gtg acc agc gat tcc caa gcc acc gtg gaa 403															
Arg Thr Asn Gly Thr Thr Val Thr Ser Asp Ser Gln Gly Thr Val Glu 90 95 100															
ttc aac gcc tcc gtg cac ttc ctc gga cac cag gca gag gac aaa tgg 451															
Phe Asn Gly Ser Val His Phe Leu Gly His Gln Ala Glu Asp Lys Trp 105 110 115															
atc ctg gac acc acc atg tct gac atc aaa atg gtg ttc aac gga tcc 490															

Ile Leu Asp Thr Thr Met Ser Asp Ile Lys Met Val Phe Asn Gly Ser
 120 125 130

tcc gcg cag cta gtt gtg gat ttg gtt gcc cgc gaa ttc 538
 Ser Ala Gln Leu Val Val Asp Leu Val Ala Arg Glu Phe
 135 140 145

<210> 1312

<211> 146

<212> PRT

<213> Corynebacterium glutamicum

<400> 1312

Met Lys Leu Ala Pro Arg Met Arg Met Arg Ser Pro Lys Thr Phe Ala
 1 5 10 15

Ala Leu Ala Ser Leu Ala Leu Val Ile Gly Leu Gly Gln Val Pro Ile
 20 25 30

Ala Gln Ala Gln Thr Glu Tyr Arg Thr Ala Ser Asp Gly Ser Leu Asn
 35 40 45

Trp Gly Phe Arg Gln Ser Phe Arg Asn Tyr Ile Gln Thr Gly Val Ala
 50 55 60

Lys Gly Ser Ile Thr Leu Gly Asp Gly Ala Ser Asp Asn Gly Gly Asn
 65 70 75 80

Phe Ala Phe Thr Pro Arg Thr Asn Gly Thr Thr Val Thr Ser Asp Ser
 85 90 95

Gln Gly Thr Val Glu Phe Asn Gly Ser Val His Phe Leu Gly His Gln
 100 105 110

Ala Glu Asp Lys Trp Ile Leu Asp Thr Thr Met Ser Asp Ile Lys Met
 115 120 125

Val Phe Asn Gly Ser Ser Ala Gln Leu Val Val Asp Leu Val Ala Arg
 130 135 140

Glu Phe
 145

<210> 1313

<211> 528

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(528)

<223> PRXA02824

<400> 1313

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 Phe Tyr Glu Thr Gly Glu Ala Leu Asp Pro Thr Gly Asp Ser Leu Thr
 1 5 10 15

att tcc tcc acc acc acc gcg cca tcg acc agc acg acc tcc acc tct 96

Ile	Ser	Ser	Thr	Thr	Ala	Pro	Ser	Thr	Ser	Thr	Thr	Ser	Thr	Ser	
			20				25					30			
gcc	tca	act	tcc	ggg	gga	acc	gcc	gac	tgt	tcc	tcc	ggc	gca	ttg	ggg
Ala	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Asp	Cys	Ser	Ser	Gly	Ala	Leu	Gly
		35					40					45			144
gtt	gtc	acc	acc	gga	acc	aac	gac	ggc	atg	ctg	ggc	acc	atc	cag	gaa
Val	Val	Thr	Thr	Gly	Thr	Asn	Asp	Gly	Met	Leu	Gly	Thr	Ile	Gln	Glu
		50					55				60				192
gta	aac	aac	acc	ttc	gcg	att	tgg	aac	aac	ctc	atc	gtc	aac	acc	gag
Val	Asn	Asn	Thr	Phe	Ala	Ile	Trp	Asn	Asn	Leu	Ile	Val	Asn	Thr	Glu
		65				70				75				80	240
cgc	atg	ttc	tgc	aac	att	gat	acc	ctc	aag	gcg	cgc	ttc	gac	acg	gat
Arg	Met	Phe	Cys	Asn	Ile	Asp	Thr	Leu	Lys	Ala	Arg	Phe	Asp	Thr	Asp
				85					90					95	288
gat	tcc	agc	gat	tca	gcg	acc	tct	gcg	act	tct	ggg	act	act	gcg	tcc
Asp	Ser	Ser	Asp	Ser	Ala	Thr	Ser	Ala	Thr	Ser	Gly	Thr	Thr	Ala	Ser
			100					105					110		336
acc	ggc	acc	acc	gct	gca	act	acc	gcg	gga	acc	acg	ggg	acc	act	gga
Thr	Gly	Thr	Thr	Ala	Ala	Thr	Thr	Ala	Gly	Thr	Thr	Gly	Thr	Thr	Gly
			115					120				125			384
act	gcc	agc	acc	gct	tcc	gga	act	tcc	gga	act	tcc	gga	acc	tcc	ggc
Thr	Ala	Ser	Thr	Ala	Ser	Gly	Thr	Ser	Gly	Thr	Ser	Gly	Thr	Ser	Gly
		130				135					140				432
acc	gca	gca	act	gtc	gct	ggc	acc	acc	cca	act	gac	aat	ggc	gtt	tgc
Thr	Ala	Ala	Thr	Val	Ala	Gly	Thr	Thr	Pro	Thr	Asp	Asn	Gly	Val	Cys
		145				150				155				160	480
acc	gct	tcc	gga	tct	ttg	ggc	gtg	acc	caa	gca	tct	gcg	cag	tgg	ggg
Thr	Ala	Ser	Gly	Ser	Leu	Gly	Val	Thr	Gln	Ala	Ser	Ala	Gln	Trp	Gly
				165					170					175	528

<210> 1314

<211> 176

<212> PRT

<213> Corynebacterium glutamicum

<400> 1314

Phe	Tyr	Glu	Thr	Gly	Glu	Ala	Leu	Asp	Pro	Thr	Gly	Asp	Ser	Leu	Thr
1				5					10					15	

Ile	Ser	Ser	Thr	Thr	Ala	Pro	Ser	Thr	Ser	Thr	Thr	Ser	Thr	Ser	Thr
			20				25					30			

Ala	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Asp	Cys	Ser	Ser	Gly	Ala	Leu	Gly
		35					40					45			

Val	Val	Thr	Thr	Gly	Thr	Asn	Asp	Gly	Met	Leu	Gly	Thr	Ile	Gln	Glu
	50					55					60				

Val	Asn	Asn	Thr	Phe	Ala	Ile	Trp	Asn	Asn	Leu	Ile	Val	Asn	Thr	Glu
	65					70				75					80

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Arg Met Phe Cys Asn Ile Asp Thr Leu Lys Ala Arg Phe Asp Thr Asp
      85                      90                      95
Asp Ser Ser Asp Ser Ala Thr Ser Ala Thr Ser Gly Thr Thr Ala Ser
      100                    105                    110
Thr Gly Thr Thr Ala Ala Thr Thr Ala Gly Thr Thr Gly Thr Thr Gly
      115                    120                    125
Thr Ala Ser Thr Ala Ser Gly Thr Ser Gly Thr Ser Gly Thr Ser Gly
      130                    135                    140
Thr Ala Ala Thr Val Ala Gly Thr Thr Pro Thr Asp Asn Gly Val Cys
      145                    150                    155                    160
Thr Ala Ser Gly Ser Leu Gly Val Thr Gln Ala Ser Ala Gln Trp Gly
      165                    170                    175

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<210> 1315
<211> 407
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (1)..(384)
<223> FRXA02825

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<400> 1315
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Asn Val Ser Ala Thr Glu Ala Ser Gly Ser Ala Ser Val Ser Leu Ser
1 5 10 15
cag tcg ggt tcg cag gcg ttc gct gat ttc tac acc cca gcc acc cag 96
Gln Ser Gly Ser Gln Ala Phe Ala Asp Phe Tyr Thr Pro Gly Thr Gln
20 25 30
ttg gat ccg atc agt ttc agc gca act ttg ggc ggc gac gcc agc tgc 144
Leu Asp Pro Ile Ser Phe Ser Ala Thr Leu Gly Gly Asp Ala Ser Cys
35 40 45
gcc acc gga tcc acc tcg acc aca ggc gct gct gcc acc gcg aac act 192
Ala Thr Gly Ser Thr Ser Thr Thr Gly Ala Ala Thr Ala Asn Thr
50 55 60
gac aac acc gaa ggt gtt gcc ggc gag gaa tcc acc acc ccc gct aac 240
Asp Asn Thr Glu Gly Val Ala Gly Glu Glu Ser Thr Thr Pro Ala Asn
65 70 75 80
caa aac agc cag ttc caa atc cgc cag gcc gct gca gat tcc acc gga 288
Gln Asn Ser Gln Phe Gln Ile Arg Gln Ala Ala Asp Ser Thr Gly
85 90 95
ctg gat acc acc acc aca atg ttg ctc atc ctc gcg gcg ttc gtt gtc 336
Leu Asp Thr Thr Thr Met Leu Leu Ile Leu Ala Ala Phe Val Val
100 105 110

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gca ggt ggc tcc atg act cgc ttc acc gtc ggc aac ccg act gga aaa 384
 Ala Gly Gly Ser Met Thr Arg Phe Thr Val Gly Asn Pro Thr Gly Lys
 115 120 125

taaggttca catgaataac gct 407

<210> 1316

<211> 128

<212> PRT

<213> Corynebacterium glutamicum

<400> 1316

Asn Val Ser Ala Thr Glu Ala Ser Gly Ser Ala Ser Val Ser Leu Ser
 1 5 10 15

Gln Ser Gly Ser Gln Ala Phe Ala Asp Phe Tyr Thr Pro Gly Thr Gln
 20 25 30

Leu Asp Pro Ile Ser Phe Ser Ala Thr Leu Gly Gly Asp Ala Ser Cys
 35 40 45

Ala Thr Gly Ser Thr Ser Thr Thr Gly Ala Ala Ala Thr Ala Asn Thr
 50 55 60

Asp Asn Thr Glu Gly Val Ala Gly Glu Glu Ser Thr Thr Pro Ala Asn
 65 70 75 80

Gln Asn Ser Gln Phe Gln Ile Arg Gln Ala Ala Ala Asp Ser Thr Gly
 85 90 95

Leu Asp Thr Thr Thr Thr Met Leu Leu Ile Leu Ala Ala Phe Val Val
 100 105 110

Ala Gly Gly Ser Met Thr Arg Phe Thr Val Gly Asn Pro Thr Gly Lys
 115 120 125

<210> 1317

<211> 528

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(528)

<223> RXN02838

<400> 1317

aac acg ggc aag ggc ggg ggc ctg acg gtg ccg ctg ggc gac ggg cag 48
 Asn Thr Gly Lys Gly Gly Gly Leu Thr Val Pro Leu Gly Asp Gly Gln
 1 5 10 15

ggg cgg tat atc gcg aag ttc ccc tcg acc gcg ttt gtg ggg gtg tcg 96
 Gly Arg Tyr Ile Ala Lys Phe Pro Ser Thr Ala Phe Val Gly Val Ser
 20 25 30

gag aac gaa ttt gcc aat ctg gct ttg gcc gag gcg atc ggg atg gag 144

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Glu Asn Glu Phe Ala Asn Leu Ala Leu Ala Glu Ala Ile Gly Met Glu
    35          40          45
gtg ccc gcg cgc gag ttg gtg ggg cgt gcg cag ttt gaa ggc gtg ccc 192
Val Pro Ala Arg Glu Leu Val Gly Arg Ala Gln Phe Glu Gly Val Pro
    50          55          60

ccc gag ttt gag gcc atg acc gac ggg ttg gtt ttg ctg gtg cgg cgg 240
Pro Glu Phe Glu Ala Met Thr Asp Gly Leu Val Leu Val Arg Arg
    65          70          75          80

ttt gat cgc gcg ggc gat ggc gtg cgc gtg cat atg gag gat ttc gca 288
Phe Asp Arg Ala Gly Asp Gly Val Arg Val His Met Glu Asp Phe Ala
    85          90          95

cag gtg ttc ggc cta tac ccc gcg cgc aag tat gat ggg gcg gcc agt 336
Gln Val Phe Gly Leu Tyr Pro Ala Arg Lys Tyr Asp Gly Ala Ala Ser
    100          105          110

cac gat att gcg gcg gtg ctg ggc agt gcg gtg tcg atc gcg gcg ggg 384
His Asp Ile Ala Ala Val Leu Gly Ser Ala Val Ser Ile Ala Ala Gly
    115          120          125

ttg gag ttc gtg cgg cgg ctg gcg ctc tcg gtt gtg atg ggc aac ggc 432
Leu Glu Phe Val Arg Arg Leu Ala Leu Ser Val Val Met Gly Asn Gly
    130          135          140

gat atg cat ttg aag aac tgg tcg ctg atc tat cgc ggg cgg ggc gat 480
Asp Met His Leu Lys Asn Trp Ser Leu Ile Tyr Arg Gly Arg Gly Asp
    145          150          155          160

gtg ccg gcg ttg gcg cct gtg tat tat atg atg tcg acc gtg acc tat 528
Val Pro Ala Leu Ala Pro Val Tyr Tyr Met Ser Thr Val Thr Tyr
    165          170          175

<210> 1318
<211> 176
<212> PRT
<213> Corynebacterium glutamicum

<400> 1318
Asn Thr Gly Lys Gly Gly Gly Leu Thr Val Pro Leu Gly Asp Gly Gln
  1          5          10          15

Gly Arg Tyr Ile Ala Lys Phe Pro Ser Thr Ala Phe Val Gly Val Ser
    20          25          30

Glu Asn Glu Phe Ala Asn Leu Ala Leu Ala Glu Ala Ile Gly Met Glu
    35          40          45

Val Pro Ala Arg Glu Leu Val Gly Arg Ala Gln Phe Glu Gly Val Pro
    50          55          60

Pro Glu Phe Glu Ala Met Thr Asp Gly Leu Val Leu Leu Val Arg Arg
    65          70          75          80

Phe Asp Arg Ala Gly Asp Gly Val Arg Val His Met Glu Asp Phe Ala
    85          90          95

Gln Val Phe Gly Leu Tyr Pro Ala Arg Lys Tyr Asp Gly Ala Ala Ser

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100	105	110
His Asp Ile Ala Ala Val Leu Gly Ser Ala Val Ser Ile Ala Ala Gly		
115	120	125
Leu Glu Phe Val Arg Arg Leu Ala Leu Ser Val Val Met Gly Asn Gly		
130	135	140
Asp Met His Leu Lys Asn Trp Ser Leu Ile Tyr Arg Gly Arg Gly Asp		
145	150	155
Val Pro Ala Leu Ala Pro Val Tyr Tyr Met Met Ser Thr Val Thr Tyr		
165	170	175

<210> 1319

<211> 462

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(462)

<223> FRXA02838

<400> 1319

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Thr Val Pro Leu Gly Asp Gly Gln Gly Arg Tyr Ile Ala Lys Ile Pro 15

1 5 10

tcg acc gcg ttt gtg ggg gtg tcg gag aac aaa ttt gcc aat ctg gct 96

Ser Thr Ala Phe Val Gly Val Ser Glu Asn Lys Phe Ala Asn Leu Ala 30

20 25

ttg gcc gag gcg atc ggg atg gag gtg ccc gcg cgc gag ttg gtg ggg 144

Leu Ala Glu Ala Ile Gly Met Glu Val Pro Ala Arg Glu Leu Val Gly 45

35 40

cgt gcg cag ttt gaa ggc gtg ccc ccc gag ttt gag gcc atg acc gac 192

Arg Ala Gln Phe Glu Gly Val Pro Pro Glu Phe Glu Ala Met Thr Asp 60

50 55

ggg ttg gtt ttg ctg gtg cgg cgg ttt gat cgc gcg ggc gat ggc gtg 240

Gly Leu Val Leu Leu Val Arg Arg Phe Asp Arg Ala Gly Asp Gly Val 80

65 70 75

cgc gtg cat atg gag gat ttc gca cag gtg ttc ggc cta tac ccc gcg 288

Arg Val His Met Glu Asp Phe Ala Gln Val Phe Gly Leu Tyr Pro Ala 95

85 90

cgc aag tat gat ggg gcg gcc agt cac gat att gcg gcg gtg ctg ggc 336

Arg Lys Tyr Asp Gly Ala Ala Ser His Asp Ile Ala Val Leu Gly 110

100 105

agt gcg gtg tcg atc gcg gcg ggg ttg gag ttc gtg cgg cgg ctg gcg 384

Ser Ala Val Ser Ile Ala Ala Gly Leu Glu Phe Val Arg Arg Leu Ala 125

115 120

ctc tct gtt gtg atg ggc aac ggc gat atg cat ttg aag aac tgg tcg 432
 Leu Ser Val Val Met Gly Asn Gly Asp Met His Leu Lys Asn Trp Ser
 130 135 140

ctg atc tat cac ggg cgg ggc gat gtg ccg 462
 Leu Ile Tyr His Gly Arg Gly Asp Val Pro
 145 150

<210> 1320

<211> 154

<212> PRT

<213> Corynebacterium glutamicum

<400> 1320

Thr Val Pro Leu Gly Asp Gly Gln Gly Arg Tyr Ile Ala Lys Ile Pro
 1 5 10 15

Ser Thr Ala Phe Val Gly Val Ser Glu Asn Lys Phe Ala Asn Leu Ala
 20 25 30

Leu Ala Glu Ala Ile Gly Met Glu Val Pro Ala Arg Glu Leu Val Gly
 35 40 45

Arg Ala Gln Phe Glu Gly Val Pro Pro Glu Phe Glu Ala Met Thr Asp
 50 55 60

Gly Leu Val Leu Leu Val Arg Arg Phe Asp Arg Ala Gly Asp Gly Val
 65 70 75 80

Arg Val His Met Glu Asp Phe Ala Gln Val Phe Gly Leu Tyr Pro Ala
 85 90 95

Arg Lys Tyr Asp Gly Ala Ala Ser His Asp Ile Ala Ala Val Leu Gly
 100 105 110

Ser Ala Val Ser Ile Ala Ala Gly Leu Glu Phe Val Arg Arg Leu Ala
 115 120 125

Leu Ser Val Val Met Gly Asn Gly Asp Met His Leu Lys Asn Trp Ser
 130 135 140

Leu Ile Tyr His Gly Arg Gly Asp Val Pro
 145 150

<210> 1321

<211> 273

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(250)

<223> RXN02840

<400> 1321

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tgaaggcgaa tacacottca gcaccgctga gccggaagag atg acg gta atc agt 115
 Met Thr Val Ile Ser

1

5

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ggc gcg ctg aat gtg tta ctg cct gac gcg acc gac tgg cag gtg tat 163
Gly Ala Leu Asn Val Leu Leu Pro Asp Ala Thr Asp Trp Gln Val Tyr
                10                15                20

gaa gcc ggt tgg gtg ttt aat gtt ccc ggt cac agt gag ttt cat ctg 211
Glu Ala Gly Ser Val Phe Asn Val Pro Gly His Ser Glu Phe His Leu
                25                30                35

caa gtt gcc gaa ccc acc tct tat ctg tgc cgc tat ctg taattcctcg 260
Gln Val Ala Glu Pro Thr Ser Tyr Leu Cys Arg Tyr Leu
                40                45                50

ccttccccctt gaa 273

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<210> 1322

<211> 50

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1322

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Met Thr Val Ile Ser Gly Ala Leu Asn Val Leu Leu Pro Asp Ala Thr
1                5                10                15

Asp Trp Gln Val Tyr Glu Ala Gly Ser Val Phe Asn Val Pro Gly His
                20                25                30

Ser Glu Phe His Leu Gln Val Ala Glu Pro Thr Ser Tyr Leu Cys Arg
                35                40                45

Tyr Leu
50

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<210> 1323

<211> 273

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(250)

<223> FRXA02840

<400> 1323

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tgaaggcgaa tacaccttca gcaccgctga gccggaagag atg acg gta atc agt 115
                Met Thr Val Ile Ser
                1                5

ggc gcg ctg aat gtg tta ctg cct gac gcg acc gac tgg cag gtg tat 163
Gly Ala Leu Asn Val Leu Leu Pro Asp Ala Thr Asp Trp Gln Val Tyr
                10                15                20

gaa gcc ggt tgg gtg ttt aat gtt ccc ggt cac agt gag ttt cat ctg 211
Glu Ala Gly Ser Val Phe Asn Val Pro Gly His Ser Glu Phe His Leu
                25                30                35

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caa gtt gcc gaa ccc acc tct tat ctg tgc cgc tat ctg taattcctcg 260
 Gln Val Ala Glu Pro Thr Ser Tyr Leu Cys Arg Tyr Leu
 40 45 50

ccttccccctt gaa 273

<210> 1324

<211> 50

<212> PRT

<213> Corynebacterium glutamicum

<400> 1324

Met Thr Val Ile Ser Gly Ala Leu Asn Val Leu Leu Pro Asp Ala Thr
 1 5 10 15

Asp Trp Gln Val Tyr Glu Ala Gly Ser Val Phe Asn Val Pro Gly His
 20 25 30

Ser Glu Phe His Leu Gln Val Ala Glu Pro Thr Ser Tyr Leu Cys Arg
 35 40 45

Tyr Leu
 50

<210> 1325

<211> 558

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(535)

<223> RXN02841

<400> 1325

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tgtgcagggg ttgtgttttc taacaagaaa agagaccacc atg ttc aca gct ttt 115
 Met Phe Thr Ala Phe
 1 5

aaa agc aat cct acg acc att aaa aag ctg gtt tct gag ctc att aat 163
 Lys Ser Asn Pro Thr Thr Ile Lys Lys Leu Val Ser Glu Leu Ile Asn
 10 15 20

ggc gac gat gca gcg ctc aac gaa cta gag cga cac gtc act aat gaa 211
 Gly Asp Asp Ala Ala Leu Asn Glu Leu Glu Arg His Val Thr Asn Glu
 25 30 35

tca gtc cgt gct cgc gaa ctc cct aat gtc cag tac aaa gcc act gcg 259
 Ser Val Arg Ala Arg Glu Leu Pro Asn Val Gln Tyr Lys Ala Thr Ala
 40 45 50

ggg cgc aac ttc gcc ata tcc aag ctg gtc caa aat ttg cgt cgc atc 307
 Gly Arg Asn Phe Ala Ile Ser Lys Leu Val Gln Asn Leu Arg Arg Ile
 55 60 65

aac aag gca caa aac aat cca cgt ggt gtg ccc act cat gcc acc gtg 355
 Asn Lys Ala Gln Asn Asn Pro Arg Gly Val Pro Thr His Ala Thr Val

70	75	80	85	
att ctg ctt aag gaa gac ggc agc tac gac ggt gaa gaa cag tgg cgc				403
Ile Leu Leu Lys Glu Asp Gly Ser Tyr Asp Gly Glu Glu Gln Trp Arg				
	90	95	100	
att cca gaa aag gcg atc act ccg ttc gac atg cta cgt tgc cct gac				451
Ile Pro Glu Lys Ala Ile Thr Pro Phe Asp Met Leu Arg Ser Pro Asp				
	105	110	115	
ttc aac cac aac agg ctg aag aac cgg ccg ctc atg gtc gag tcc caa				499
Phe Asn His Asn Arg Leu Lys Asn Arg Pro Leu Met Val Glu Ser Gln				
	120	125	130	
tac ccc tgg ggc gtc ccc gga ctc att aaa atg aac tgatcaatcc				545
Tyr Pro Trp Gly Val Pro Gly Leu Ile Lys Met Asn				
	135	140	145	
ctgacacagc cat				558

<210> 1326

<211> 145

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1326

Met Phe Thr Ala Phe Lys Ser Asn Pro Thr Thr Ile Lys Lys Leu Val
1 5 10 15

Ser Glu Leu Ile Asn Gly Asp Asp Ala Ala Leu Asn Glu Leu Glu Arg
20 25 30

His Val Thr Asn Glu Ser Val Arg Ala Arg Glu Leu Pro Asn Val Gln
35 40 45

Tyr Lys Ala Thr Ala Gly Arg Asn Phe Ala Ile Ser Lys Leu Val Gln
50 55 60

Asn Leu Arg Arg Ile Asn Lys Ala Gln Asn Asn Pro Arg Gly Val Pro
65 70 75 80

Thr His Ala Thr Val Ile Leu Leu Lys Glu Asp Gly Ser Tyr Asp Gly
85 90 95

Glu Glu Gln Trp Arg Ile Pro Glu Lys Ala Ile Thr Pro Phe Asp Met
100 105 110

Leu Arg Ser Pro Asp Phe Asn His Asn Arg Leu Lys Asn Arg Pro Leu
115 120 125

Met Val Glu Ser Gln Tyr Pro Trp Gly Val Pro Gly Leu Ile Lys Met
130 135 140

Asn

145

<210> 1327

<211> 285

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (7)..(285)

<223> FRXA02841

<400> 1327

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Met Phe Ala Ala Phe Lys Ser Asn Leu Pro Thr Ile Lys Lys Leu
1 5 10 15

gtt tat gag gtc att aat ggc gtc gat gca gcg ctc aac gaa cta gag 99

Val Tyr Glu Val Ile Asn Gly Val Asp Ala Ala Leu Asn Glu Leu Glu
20 25 30

cga cac gtc act aat gaa tca gtc cgt gct cgc gaa ctc cct aat gtc 147

Arg His Val Thr Asn Glu Ser Val Arg Ala Arg Glu Leu Pro Asn Val
35 40 45

cag tac aaa gcc act gcg ggg cgc aac ttc gcc ata tcc aag ctg gtc 195

Gln Tyr Lys Ala Thr Ala Gly Arg Asn Phe Ala Ile Ser Lys Leu Val
50 55 60

caa aat ttg cgt cgc atc aac aag gca caa aac aat cca cgt ggt gtg 243

Gln Asn Leu Arg Arg Ile Asn Lys Ala Gln Asn Asn Pro Arg Gly Val
65 70 75

ccc act cat gcc acc gtg att ctg ctt aag gga gac ggc agc 285

Pro Thr His Ala Thr Val Ile Leu Leu Lys Gly Asp Gly Ser
80 85 90

<210> 1328

<211> 93

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1328

Met Phe Ala Ala Phe Lys Ser Asn Leu Pro Thr Ile Lys Lys Leu Val

1 5 10 15

Tyr Glu Val Ile Asn Gly Val Asp Ala Ala Leu Asn Glu Leu Glu Arg

20 25 30

His Val Thr Asn Glu Ser Val Arg Ala Arg Glu Leu Pro Asn Val Gln

35 40 45

Tyr Lys Ala Thr Ala Gly Arg Asn Phe Ala Ile Ser Lys Leu Val Gln

50 55 60

Asn Leu Arg Arg Ile Asn Lys Ala Gln Asn Asn Pro Arg Gly Val Pro

65 70 75 80

Thr His Ala Thr Val Ile Leu Leu Lys Gly Asp Gly Ser

85 90

<210> 1329

<211> 873

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(850)

<223> RXN02846

<400> 1329

tacaagcgct gaacgttgag tttagtttg gtccattgag gggtaaaggc ttacctctog 60

actaggtggg gtggcgtag agcgcctatt ctgattgac gtg tta acc atc gct 115
 Val Leu Thr Ile Ala
 1 5

att gta ctt ctc gcg tca gtc ctc atc ggt gct ctt ctc caa cgc atg 163
 Ile Val Leu Leu Ala Ser Val Leu Ile Gly Ala Leu Leu Gln Arg Met
 10 15 20

aca gga ttg ggc gtc ggt cta gtt acc ggc cca gtc ctg act tct ttg 211
 Thr Gly Leu Gly Val Gly Leu Val Thr Gly Pro Val Leu Thr Ser Leu
 25 30 35

tta ggg cgg cta gca ggc gtg acc atg gtg aat ggt ctg tcc atc atc 259
 Leu Gly Pro Leu Ala Gly Val Thr Met Val Asn Gly Leu Ser Ile Ile
 40 45 50

aac gcg gtg aat aat gcg tgg tgg gtg cgc aaa cgc act gac tgg gcc 307
 Asn Ala Val Asn Asn Ala Trp Ser Val Arg Lys Arg Thr Asp Trp Ala
 55 60 65

aaa ttc cga att ctt gcc ggc gct ttg gtg ctt ggt tct gtt cct gct 355
 Lys Phe Arg Ile Leu Ala Gly Ala Leu Val Leu Gly Ser Val Pro Ala
 70 75 80 85

gtt gca gtg gtg tat ttc ctt aac gga cca tgg ctg ttg att ttc gtt 403
 Val Ala Val Val Tyr Phe Leu Asn Gly Pro Trp Leu Leu Ile Phe Val
 90 95 100

ggt gcg atg gtg ctg ctc gcg ttg ggt gtt tcc ctg ttc cca aca gag 451
 Gly Ala Met Val Leu Leu Ala Leu Gly Val Ser Leu Phe Pro Thr Glu
 105 110 115

aaa ttc gca ctc aag caa gaa gct aaa ctg cct atg gtc atc ttc ggc 499
 Lys Phe Ala Leu Lys Gln Glu Ala Lys Leu Pro Met Val Ile Phe Gly
 120 125 130

atg att ggt gga ttc atg tcc act gtt gca ggc atc gca ggg cca tcc 547
 Met Ile Gly Gly Phe Met Ser Thr Val Ala Gly Ile Ala Gly Pro Ser
 135 140 145

ctg act gtt tat gcg cgc ctg agc cgc tgg gat tac cgc gac ttt gtg 595
 Leu Thr Val Tyr Ala Arg Leu Ser Arg Trp Asp Tyr Arg Asp Phe Val
 150 155 160 165

gcc acc ttg cac cca gtt cta ctc gtg gcc aac acc gta tgg ttc ctg 643
 Ala Thr Leu His Pro Val Leu Leu Val Ala Asn Thr Val Ser Phe Leu
 170 175 180

ctc aag gtt atc ttg atc ggt gga ctc gat ttc ggt ggc gca ccc gca 691
 Leu Lys Val Ile Leu Ile Gly Gly Leu Asp Phe Gly Gly Ala Pro Ala
 185 190 195

tgg ctc tgg atc ggt gcc gta gcg atg atc ttt gtc ggt gct tgg ttg 739
 Trp Leu Trp Ile Gly Ala Val Ala Met Ile Phe Val Gly Ala Trp Leu
 200 205 210
 ggt gaa atc gtc aac gct aag gtg tcc acc cca atg gcc aag cgc atc 787
 Gly Glu Ile Val Asn Ala Lys Val Ser Thr Pro Met Ala Lys Arg Ile
 215 220 225
 gct acg ctc ctg gca gca gct ggt gcc gca gtg gtg ttg ttc cga ggc 835
 Ala Thr Leu Leu Ala Ala Gly Ala Val Val Leu Phe Arg Gly
 230 235 240 245
 atc atg gaa ttg gtt tagcgggtctt aattggtggg aag 873
 Ile Met Glu Leu Val
 250

<210> 1330

<211> 250

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1330

Val Leu Thr Ile Ala Ile Val Leu Leu Ala Ser Val Leu Ile Gly Ala
 1 5 10 15
 Leu Leu Gln Arg Met Thr Gly Leu Gly Val Gly Leu Val Thr Gly Pro
 20 25 30
 Val Leu Thr Ser Leu Leu Gly Pro Leu Ala Gly Val Thr Met Val Asn
 35 40 45
 Gly Leu Ser Ile Ile Asn Ala Val Asn Asn Ala Trp Ser Val Arg Lys
 50 55 60
 Arg Thr Asp Trp Ala Lys Phe Arg Ile Leu Ala Gly Ala Leu Val Leu
 65 70 75 80
 Gly Ser Val Pro Ala Val Ala Val Val Tyr Phe Leu Asn Gly Pro Trp
 85 90 95
 Leu Leu Ile Phe Val Gly Ala Met Val Leu Leu Ala Leu Gly Val Ser
 100 105 110
 Leu Phe Pro Thr Glu Lys Phe Ala Leu Lys Gln Glu Ala Lys Leu Pro
 115 120 125
 Met Val Ile Phe Gly Met Ile Gly Gly Phe Met Ser Thr Val Ala Gly
 130 135 140
 Ile Ala Gly Pro Ser Leu Thr Val Tyr Ala Arg Leu Ser Arg Trp Asp
 145 150 155 160
 Tyr Arg Asp Phe Val Ala Thr Leu His Pro Val Leu Leu Val Ala Asn
 165 170 175
 Thr Val Ser Phe Leu Leu Lys Val Ile Leu Ile Gly Gly Leu Asp Phe
 180 185 190
 Gly Gly Ala Pro Ala Trp Leu Trp Ile Gly Ala Val Ala Met Ile Phe

195 200 205

Val Gly Ala Trp Leu Gly Glu Ile Val Asn Ala Lys Val Ser Thr Pro
 210 215 220

Met Ala Lys Arg Ile Ala Thr Leu Leu Ala Ala Gly Ala Ala Val
 225 230 235 240

Val Leu Phe Arg Gly Ile Met Glu Leu Val
 245 250

<210> 1331
 <211> 573
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (1)..(573)
 <223> FRXA02846

<400> 1331

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Val Asn Gly Leu Ser Ile Ile Asn Ala Val Asn Asn Ala Trp Ser Val	
1 5 10 15	
cgc aaa cgc act gac tgg gcc aaa ttc cga att ctt gcc ggc gct ttg	96
Arg Lys Arg Thr Asp Trp Ala Lys Phe Arg Ile Leu Ala Gly Ala Leu	
20 25 30	
gtg ctt ggt tct gtt cct gct gtt gca gtg gtg tat ttc ctt aac gga	144
Val Leu Gly Ser Val Pro Ala Val Ala Val Val Tyr Phe Leu Asn Gly	
35 40 45	
cca tgg ctg ttg att ttc gtt ggt gcg atg gtg ctg ctc gcg ttg ggt	192
Pro Trp Leu Leu Ile Phe Val Gly Ala Met Val Leu Leu Ala Leu Gly	
50 55 60	
ggt tcc ctg ttc cca aca gag aaa ttc gca ctc aag caa gaa gct aaa	240
Val Ser Leu Phe Pro Thr Glu Lys Phe Ala Leu Lys Gln Glu Ala Lys	
65 70 75 80	
ctg cct atg gtc atc ttc ggc atg att ggt gga ttc atg tcc act gtt	288
Leu Pro Met Val Ile Phe Gly Met Ile Gly Gly Phe Met Ser Thr Val	
85 90 95	
gca ggc atc gca ggg cca tcc ctg act gtt tat gcg cgc ctg agc cgc	336
Ala Gly Ile Ala Gly Pro Ser Leu Thr Val Tyr Ala Arg Leu Ser Arg	
100 105 110	
tgg gat tac cga gac ttt gtg gcc acc ttg cac cca gtt cta ctc gtg	384
Trp Asp Tyr Arg Asp Phe Val Ala Thr Leu His Pro Val Leu Leu Val	
115 120 125	
gcc aac acc gta tgg ttc ctg ctc aag gtt atc ttg atc ggt gga ctc	432
Ala Asn Thr Val Ser Phe Leu Leu Lys Val Ile Leu Ile Gly Gly Leu	
130 135 140	
gat ttc ggt ggc gca ccc gca tgg ctc tgg atc ggt gcc gta gcg atg	480
Asp Phe Gly Gly Ala Pro Ala Trp Leu Trp Ile Gly Ala Val Ala Met	

145	150	155	160	
atc ttt gtc ggt gct tgg ttg ggt gaa atc gtc aac gct aag gtg tcc				528
Ile Phe Val Gly Ala Trp Leu Gly Glu Ile Val Asn Ala Lys Val Ser				
165	170	175		

acc cca atg gcc aag cgc atc gct acg ctc ctg gca gca gct ggt	573	
Thr Pro Met Ala Lys Arg Ile Ala Thr Leu Leu Ala Ala Ala Gly		
180	185	190

<210> 1332

<211> 191

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1332

Val Asn Gly Leu Ser Ile Ile Asn Ala Val Asn Asn Ala Trp Ser Val
1 5 10 15

Arg Lys Arg Thr Asp Trp Ala Lys Phe Arg Ile Leu Ala Gly Ala Leu
20 25 30

Val Leu Gly Ser Val Pro Ala Val Ala Val Val Tyr Phe Leu Asn Gly
35 40 45

Pro Trp Leu Leu Ile Phe Val Gly Ala Met Val Leu Leu Ala Leu Gly
50 55 60

Val Ser Leu Phe Pro Thr Glu Lys Phe Ala Leu Lys Gln Glu Ala Lys
65 70 75 80

Leu Pro Met Val Ile Phe Gly Met Ile Gly Gly Phe Met Ser Thr Val
85 90 95

Ala Gly Ile Ala Gly Pro Ser Leu Thr Val Tyr Ala Arg Leu Ser Arg
100 105 110

Trp Asp Tyr Arg Asp Phe Val Ala Thr Leu His Pro Val Leu Leu Val
115 120 125

Ala Asn Thr Val Ser Phe Leu Leu Lys Val Ile Leu Ile Gly Gly Leu
130 135 140

Asp Phe Gly Gly Ala Pro Ala Trp Leu Trp Ile Gly Ala Val Ala Met
145 150 155 160

Ile Phe Val Gly Ala Trp Leu Gly Glu Ile Val Asn Ala Lys Val Ser
165 170 175

Thr Pro Met Ala Lys Arg Ile Ala Thr Leu Leu Ala Ala Ala Gly
180 185 190

<210> 1333

<211> 1135

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (47)..(1135)

<223> RXN02847

<400> 1333

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 Leu Ala Leu Thr
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gcc aga ggc ttt ctc aat tct gaa aga agc cag aca agg tgg aaa acc 106
 Ala Arg Gly Phe Leu Asn Ser Glu Arg Ser Gln Thr Arg Trp Lys Thr
 5 10 15 20

cac ttc acc acc cag aaa gtt cca cgc tcc ggc tac aga tat gac ctc 154
 His Phe Thr Thr Gln Lys Val Pro Arg Ser Gly Tyr Arg Tyr Asp Leu
 25 30 35

gat ggg ctc cgc ggc atc gcg atc gcc ttc gta gtt ttg ttc cat gtt 202
 Asp Gly Leu Arg Gly Ile Ala Ile Ala Phe Val Val Leu Phe His Val
 40 45 50

ttc gtc gga aaa gtc tcc ggc ggt gtg gat gtc ttc ctg ctg ctg tct 250
 Phe Val Gly Lys Val Ser Gly Gly Val Asp Val Phe Leu Leu Leu Ser
 55 60 65

ggc tat ttc ttc tta ggg tcg caa ttg cgt tat gca gat cgt cca gat 298
 Gly Tyr Phe Phe Leu Gly Ser Gln Leu Arg Tyr Ala Asp Arg Pro Asp
 70 75 80

tct tcc atc aac ccc tgg tgg ccg att tgg cgc acg cta cgc aga tta 346
 Ser Ser Ile Asn Pro Trp Trp Pro Ile Trp Arg Thr Leu Arg Arg Leu
 85 90 95 100

ctt cct gcg tta gtg ctg gtg ttg ggc gtt tcc atg gtc ctc atc ttg 394
 Leu Pro Ala Leu Val Leu Val Leu Gly Val Ser Met Val Leu Ile Leu
 105 110 115

gcg tgg gtg ccc aga ctg caa cca ata gaa ata gcc aac caa gca gta 442
 Ala Trp Val Pro Arg Leu Gln Pro Ile Glu Ile Ala Asn Gln Ala Val
 120 125 130

gcc agc ctc ttc tat gtc caa aac tgg gag ctc gca tcc caa ggt gct 490
 Ala Ser Leu Phe Tyr Val Gln Asn Trp Glu Leu Ala Ser Gln Gly Ala
 135 140 145

gcc tac gga gca gcc tct gca gaa gtc agt cct ttc cag cac ttg tgg 538
 Ala Tyr Gly Ala Ala Ser Ala Glu Val Ser Pro Phe Gln His Leu Trp
 150 155 160

tcc atg gct gtg caa ggg cag ttc tac ctc ttt gcc atc ttg ttg agc 586
 Ser Met Ala Val Gln Gly Gln Phe Tyr Leu Phe Ala Ile Leu Leu Ser
 165 170 175 180

atg gcg atc atc ctg att cgt cga tac cgc ccc gaa tac tcc gca gtg 634
 Met Ala Ile Ile Leu Ile Arg Arg Tyr Arg Pro Glu Tyr Ser Ala Val
 185 190 195

cga cta gcg act cct gtg ctg gca gtg ctc aca tcc gta tca ttt ttc 682
 Arg Leu Ala Thr Pro Val Leu Ala Val Leu Thr Ser Val Ser Phe Phe
 200 205 210

agt gca atc ctg tgg cat ttc att gat caa tca gtc aac tac tat tcc 730

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Ser Ala Ile Leu Trp His Phe Ile Asp Gln Ser Val Asn Tyr Tyr Ser
215                                220
acc ttc acc agg ttc tgg gag ctc ggc ctt ggt gca cta ttg gtg ctg 778
Thr Phe Thr Arg Phe Trp Glu Leu Gly Leu Gly Ala Leu Leu Val Leu
230                                235                                240

cat gcg cct cga att ttg att tct gcg aag act aaa tca ata ctc gca 826
His Ala Pro Arg Ile Leu Ile Ser Ala Lys Thr Lys Ser Ile Leu Ala
245                                250                                255                                260

gcc gtc ggt ttg ttt atg gtg cta tcc act gga ttc ttc atg gat ggc 874
Ala Val Gly Leu Phe Met Val Leu Ser Thr Gly Phe Phe Met Asp Gly
265                                270                                275

gca gag act ttc cct gga ttc ccc gcg ctg tat ccc atc ttg ggt gct 922
Ala Glu Thr Phe Pro Gly Phe Pro Ala Leu Tyr Pro Ile Leu Gly Ala
280                                285                                290

tgc tta gtc atc ctt ggc gac ggt aaa atc tcg gtc ttt ctc tcc cga 970
Cys Leu Val Ile Leu Gly Asp Gly Lys Ile Ser Val Phe Leu Ser Arg
295                                300                                305

aaa tgg atg ctt tgg ctc ggc gat atc gcc tac ccg ctc tac ttg tgg 1018
Lys Trp Met Leu Trp Leu Gly Asp Ile Ala Tyr Pro Leu Tyr Leu Trp
310                                315                                320

cac tgg cct ctg ctg atc att ttc acc gct ttg ttc aac caa gaa gag 1066
His Trp Pro Leu Leu Ile Ile Phe Thr Ala Leu Phe Asn Gln Glu Glu
325                                330                                335                                340

cca tcc atc tgg ctg ggt atc gcc gtg att atg ctg tcc ctt ggc ttg 1114
Pro Ser Ile Trp Leu Gly Ile Ala Val Ile Met Leu Ser Leu Gly Leu
345                                350                                355

gcg cag ctg act aac aaa tac 1135
Ala Gln Leu Thr Asn Lys Tyr
360

<210> 1334
<211> 363
<212> PRT
<213> Corynebacterium glutamicum

<400> 1334
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Arg Trp Lys Thr His Phe Thr Thr Gln Lys Val Pro Arg Ser Gly Tyr
20 25 30
Arg Tyr Asp Leu Asp Gly Leu Arg Gly Ile Ala Ile Ala Phe Val Val
35 40 45
Leu Phe His Val Phe Val Gly Lys Val Ser Gly Gly Val Asp Val Phe
50 55 60
Leu Leu Leu Ser Gly Tyr Phe Phe Leu Gly Ser Gln Leu Arg Tyr Ala
65 70 75 80

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Asp Arg Pro Asp Ser Ser Ile Asn Pro Trp Trp Pro Ile Trp Arg Thr
 85 90 95
 Leu Arg Arg Leu Leu Pro Ala Leu Val Leu Val Leu Gly Val Ser Met
 100 105 110
 Val Leu Ile Leu Ala Trp Val Pro Arg Leu Gln Pro Ile Glu Ile Ala
 115 120 125
 Asn Gln Ala Val Ala Ser Leu Phe Tyr Val Gln Asn Trp Glu Leu Ala
 130 135 140
 Ser Gln Gly Ala Ala Tyr Gly Ala Ala Ser Ala Glu Val Ser Pro Phe
 145 150 155 160
 Gln His Leu Trp Ser Met Ala Val Gln Gly Gln Phe Tyr Leu Phe Ala
 165 170 175
 Ile Leu Leu Ser Met Ala Ile Ile Leu Ile Arg Arg Tyr Arg Pro Glu
 180 185 190
 Tyr Ser Ala Val Arg Leu Ala Thr Pro Val Leu Ala Val Leu Thr Ser
 195 200 205
 Val Ser Phe Phe Ser Ala Ile Leu Trp His Phe Ile Asp Gln Ser Val
 210 215 220
 Asn Tyr Tyr Ser Thr Phe Thr Arg Phe Trp Glu Leu Gly Leu Gly Ala
 225 230 235 240
 Leu Leu Val Leu His Ala Pro Arg Ile Leu Ile Ser Ala Lys Thr Lys
 245 250 255
 Ser Ile Leu Ala Ala Val Gly Leu Phe Met Val Leu Ser Thr Gly Phe
 260 265 270
 Phe Met Asp Gly Ala Glu Thr Phe Pro Gly Phe Pro Ala Leu Tyr Pro
 275 280 285
 Ile Leu Gly Ala Cys Leu Val Ile Leu Gly Asp Gly Lys Ile Ser Val
 290 295 300
 Phe Leu Ser Arg Lys Trp Met Leu Trp Leu Gly Asp Ile Ala Tyr Pro
 305 310 315 320
 Leu Tyr Leu Trp His Trp Pro Leu Leu Ile Phe Thr Ala Leu Phe
 325 330 335
 Asn Gln Glu Glu Pro Ser Ile Trp Leu Gly Ile Ala Val Ile Met Leu
 340 345 350
 Ser Leu Gly Leu Ala Gln Leu Thr Asn Lys Tyr
 355 360

<210> 1335

<211> 694

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(694)

<223> FRXA02847

<400> 1335

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agcctctgca gaagtgcagtc ctttccagca ctgtgtgtcc atg gct gtg caa ggg 115
                                     Met Ala Val Gln Gly
                                     1 5
cag ttc tac ctc ttt gcc atc ttg ttg agc atg gcg atc atc ctg att 163
Gln Phe Tyr Leu Phe Ala Ile Leu Leu Ser Met Ala Ile Ile Leu Ile
                10                15                20
cgt cga tac cgc ccc gaa tac tcc gca gtg cga cta gcg act cct gtg 211
Arg Arg Tyr Arg Pro Glu Tyr Ser Ala Val Arg Leu Ala Thr Pro Val
                25                30                35
ctg gca gtg ctc aca tcc gta tca ttt ttc agt gca atc ctg tgg cat 259
Leu Ala Val Leu Thr Ser Val Ser Phe Phe Ser Ala Ile Leu Trp His
                40                45                50
ttc att gat caa tca gtc aac tac tat tcc acc ttc acc agg ttc tgg 307
Phe Ile Asp Gln Ser Val Asn Tyr Tyr Ser Thr Phe Thr Arg Phe Trp
                55                60                65
gag ctc ggc ctt ggt gca cta ttg gtg ctg cat gcg cct cga att ttg 355
Glu Leu Gly Leu Gly Ala Leu Leu Val Leu His Ala Pro Arg Ile Leu
                70                75                80                85
att tct gcg aag act aaa tca ata ctc gca gcc gtc ggt ttg ttt atg 403
Ile Ser Ala Lys Thr Lys Ser Ile Leu Ala Ala Val Gly Leu Phe Met
                90                95                100
gtg cta tcc act gga ttc ttc atg gat ggc gca gag act ttc cct gga 451
Val Leu Ser Thr Gly Phe Phe Met Asp Gly Ala Glu Thr Phe Pro Gly
                105                110                115
ttc ccc gcg ctg tat ccc atc ttg ggt gct tgc tta gtc atc ctt ggc 499
Phe Pro Ala Leu Tyr Pro Ile Leu Gly Ala Cys Leu Val Ile Leu Gly
                120                125                130
gac ggt aaa atc tcg gtc ttt ctc tcc cga aaa tgg atg ctt tgg ctc 547
Asp Gly Lys Ile Ser Val Phe Leu Ser Arg Lys Trp Met Leu Trp Leu
                135                140                145
ggc gat atc gcc tac ccg ctc tac ttg tgg cac tgg cct ctg ctg atc 595
Gly Asp Ile Ala Tyr Pro Leu Tyr Leu Trp His Trp Pro Leu Leu Ile
                150                155                160                165
att ttc acc gct ttg ttc aac caa gaa gag cca tcc atc tgg ctg ggt 643
Ile Phe Thr Ala Leu Phe Asn Gln Glu Pro Ser Ile Trp Leu Gly
                170                175                180
atc gcc gtg att atg ctg tcc ctt ggc ttg gcg cag ctg act aac aaa 691
Ile Ala Val Ile Met Leu Ser Leu Gly Leu Ala Gln Leu Thr Asn Lys
                185                190                195
tac 694
Tyr

```

<210> 1336

<211> 198

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1336

Met Ala Val Gln Gly Gln Phe Tyr Leu Phe Ala Ile Leu Leu Ser Met
1 5 10 15Ala Ile Ile Leu Ile Arg Arg Tyr Arg Pro Glu Tyr Ser Ala Val Arg
20 25 30Leu Ala Thr Pro Val Leu Ala Val Leu Thr Ser Val Ser Phe Phe Ser
35 40 45Ala Ile Leu Trp His Phe Ile Asp Gln Ser Val Asn Tyr Tyr Ser Thr
50 55 60Phe Thr Arg Phe Trp Glu Leu Gly Leu Gly Ala Leu Leu Val Leu His
65 70 75 80Ala Pro Arg Ile Leu Ile Ser Ala Lys Thr Lys Ser Ile Leu Ala Ala
85 90 95Val Gly Leu Phe Met Val Leu Ser Thr Gly Phe Phe Met Asp Gly Ala
100 105 110Glu Thr Phe Pro Gly Phe Pro Ala Leu Tyr Pro Ile Leu Gly Ala Cys
115 120 125Leu Val Ile Leu Gly Asp Gly Lys Ile Ser Val Phe Leu Ser Arg Lys
130 135 140Trp Met Leu Trp Leu Gly Asp Ile Ala Tyr Pro Leu Tyr Leu Trp His
145 150 155 160Trp Pro Leu Leu Ile Ile Phe Thr Ala Leu Phe Asn Gln Glu Glu Pro
165 170 175Ser Ile Trp Leu Gly Ile Ala Val Ile Met Leu Ser Leu Gly Leu Ala
180 185 190Gln Leu Thr Asn Lys Tyr
195

<210> 1337

<211> 305

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(282)

<223> RXN02849

<400> 1337

tcc cca tac ccc gtc atg atc agc acc tct gcc gac gcc tca aac gtg 48

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Ser Pro Tyr Pro Val Met Ile Ser Thr Ser Ala Asp Ala Ser Asn Val
 1          5          10          15
acc gtg cgc atc atg ggt gtg gac acc acc tcc gtg gaa tcc atc aac 96
Thr Val Arg Ile Met Gly Val Asp Thr Thr Ser Val Glu Ser Ile Asn
          20          25          30

aac gga cgt tgg tcc acc acc cag ccc aac aca gtt cga gta tcg ggt 144
Asn Gly Arg Trp Ser Thr Thr Gln Pro Asn Thr Val Arg Val Ser Gly
          35          40          45

tca gat tgt gtg cca tca acc ggt gca cca gga ttt acc acc tca gac 192
Ser Asp Cys Val Pro Ser Thr Gly Ala Pro Gly Phe Thr Thr Ser Asp
          50          55          60

acc cga atc atc agc gat ctt tct ggc aac gaa atc acc aga gaa acc 240
Thr Arg Ile Ile Ser Asp Leu Ser Gly Asn Glu Ile Thr Arg Glu Thr
          65          70          75          80

gtc acc acg gtt tac gat cct tca cca aac gtg gtc tgc tcc 282
Val Thr Thr Val Tyr Asp Pro Ser Pro Asn Val Val Cys Ser
          85          90

taaaacaaaa tgccccacca gat 305

<210> 1338
<211> 94
<212> PRT
<213> Corynebacterium glutamicum

<400> 1338
Ser Pro Tyr Pro Val Met Ile Ser Thr Ser Ala Asp Ala Ser Asn Val
 1          5          10          15
Thr Val Arg Ile Met Gly Val Asp Thr Thr Ser Val Glu Ser Ile Asn
          20          25          30
Asn Gly Arg Trp Ser Thr Thr Gln Pro Asn Thr Val Arg Val Ser Gly
          35          40          45
Ser Asp Cys Val Pro Ser Thr Thr Gly Ala Pro Gly Phe Thr Thr Ser Asp
          50          55          60
Thr Arg Ile Ile Ser Asp Leu Ser Gly Asn Glu Ile Thr Arg Glu Thr
          65          70          75          80
Val Thr Thr Val Tyr Asp Pro Ser Pro Asn Val Val Cys Ser
          85          90

<210> 1339
<211> 305
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(282)
<223> FRXA02849

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<400> 1339
 tcc cca tac ccc gtc atg atc agc acc tct gcc gac gcc tca aac gtg 48
 Ser Pro Tyr Pro Val Met Ile Ser Thr Ser Ala Asp Ala Ser Asn Val
 1 5 10 15
 acc gtg cgc atc atg ggt gtg gac acc acc tcc ttg gaa tcc atc aac 96
 Thr Val Arg Ile Met Gly Val Asp Thr Thr Ser Val Glu Ser Ile Asn
 20 25 30
 aac gga cgt tgg tcc acc acc cag ccc aac aca gtt cga gta tcg ggt 144
 Asn Gly Arg Trp Ser Thr Thr Gln Pro Asn Thr Val Arg Val Ser Gly
 35 40 45
 tca gat tgt gtg cca tca acc ggt gca cca gga ttt acc acc tca gac 192
 Ser Asp Cys Val Pro Ser Thr Thr Gly Ala Pro Gly Phe Thr Thr Ser Asp
 50 55 60
 acc cga atc atc agc gat ctt tct ggc aac gaa atc acc aga gaa ccc 240
 Thr Arg Ile Ile Ser Asp Leu Ser Gly Asn Glu Ile Thr Arg Glu Pro
 65 70 75 80
 gtc acc acg gtt tac gat cct tca cca aac gtg gtc tgc tcc 282
 Val Thr Thr Val Tyr Asp Pro Ser Pro Asn Val Val Cys Ser
 85 90
 taaaacaaaa tgccccacca gat 305
 <210> 1340
 <211> 94
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 1340
 Ser Pro Tyr Pro Val Met Ile Ser Thr Ser Ala Asp Ala Ser Asn Val
 1 5 10 15
 Thr Val Arg Ile Met Gly Val Asp Thr Thr Ser Val Glu Ser Ile Asn
 20 25 30
 Asn Gly Arg Trp Ser Thr Thr Gln Pro Asn Thr Val Arg Val Ser Gly
 35 40 45
 Ser Asp Cys Val Pro Ser Thr Gly Ala Pro Gly Phe Thr Thr Ser Asp
 50 55 60
 Thr Arg Ile Ile Ser Asp Leu Ser Gly Asn Glu Ile Thr Arg Glu Pro
 65 70 75 80
 Val Thr Thr Val Tyr Asp Pro Ser Pro Asn Val Val Cys Ser
 85 90
 <210> 1341
 <211> 582
 <212> DNA
 <213> Corynebacterium glutamicum
 <220>
 <221> CDS
 <222> {101}..(559)

400> 1341	accgcataca ttaacgtggt gatcattgcc ctagtatgcg cagtagcgcc tgctctgac	60
agcaggttacc ttttccgcgg aaatccgaag ggagccaata	atg cgc act agt aaa Met Arg Thr Ser Lys	115
aaa gag atg att ctg cgc acg gcc atc gat tat atc ggc gag tac agc	1 5	163
Lys Glu Met Ile Leu Arg Thr Ala Ile Asp Tyr Ile Gly Glu Tyr Ser	10 15 20	
ctc gag acg ctg agt tac gat tcg ctc gcc gag cgc acc ggt ctg tcc		211
Leu Glu Thr Leu Ser Tyr Asp Ser Leu Ala Glu Ala Thr Gly Leu Ser	25 30 35	
aag tcg ggc ttg att tat cat ttc ccc agc cgc cat cgc ctg ctt tta		259
Lys Ser Gly Leu Ile Tyr His Phe Pro Ser Arg His Ala Leu Leu Leu	40 45 50	
ggc atg cac gag ttg ctt gcc gac gac tgg gac aag gaa ttg cgc gac		307
Gly Met His Glu Leu Leu Ala Asp Asp Trp Asp Lys Glu Leu Arg Asp	55 60 65	
ata acc cgc gac cca gag gat cca ctt gag cga ttg cgc gcc gtc gtg		355
Ile Thr Arg Asp Pro Glu Asp Pro Leu Glu Arg Leu Arg Ala Val Val	70 75 80 85	
ggt acg ctt gct gaa aac gtt tcg cgc ccc gag ctg gtt ttg ctt atg		403
Val Thr Leu Ala Glu Asn Val Ser Arg Pro Glu Leu Val Leu Leu Met	90 95 100	
gac gcc ccc tcc cac ccg gga ttt ctt aac gcc tgg cgc act gta aat		451
Asp Ala Pro Ser His Pro Gly Phe Leu Asn Ala Trp Arg Thr Val Asn	105 110 115	
cat caa tgg atc ccc gac acc gat gat ctg gaa aac gat gcc cac aaa		499
His Gln Trp Ile Pro Asp Thr Asp Asp Leu Glu Asn Asp Ala His Lys	120 125 130	
cgc gcc gtc tac tct ggt gca gct cgc agc cga tgg cct ctt cgt gca		547
Arg Ala Val Tyr Ser Gly Ala Ala Arg Ser Arg Trp Pro Leu Arg Ala	135 140 145	
cga tta cat tca tgatgatgtc ctcagcaagt cca		582
Arg Leu His Ser	150	

```

<400> 1342
Met Arg Thr Ser Lys Lys Glu Met Ile Leu Arg Thr Ala Ile Asp Tyr
  1             5             10             15
Ile Gly Glu Tyr Ser Leu Glu Thr Leu Ser Tyr Asp Ser Leu Ala Glu
      20             25             30

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Ala Thr Gly Leu Ser Lys Ser Gly Leu Ile Tyr His Phe Pro Ser Arg
    35              40              45

His Ala Leu Leu Leu Gly Met His Glu Leu Leu Ala Asp Asp Trp Asp
    50              55              60

Lys Glu Leu Arg Asp Ile Thr Arg Asp Pro Glu Asp Pro Leu Glu Arg
    65              70              75              80

Leu Arg Ala Val Val Val Thr Leu Ala Glu Asn Val Ser Arg Pro Glu
              85              90              95

Leu Val Leu Leu Met Asp Ala Pro Ser His Pro Gly Phe Leu Asn Ala
    100              105              110

Trp Arg Thr Val Asn His Gln Trp Ile Pro Asp Thr Asp Asp Leu Glu
    115              120              125

Asn Asp Ala His Lys Arg Ala Val Tyr Ser Gly Ala Ala Arg Ser Arg
    130              135              140

Trp Pro Leu Arg Ala Arg Leu His Ser
    145              150

```

<210> 1343

<211> 666

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(643)

<223> RXN02914

<400> 1343

tgtgtgatcgc agcaattgca tcccctgggc cagacctttt cagatcatca ggctaagtgc 60

```

caaaaaaccgc cgtgatggcg tactgactgc cgtaggcatc atg gtg gga aac tcc 115
              Met Val Gly Asn Ser
              1              5

```

```

atc tgg atc ata gcc agc ctc ctt ggg ctc tcg gca ctg atc tcc acg 163
Ile Trp Ile Ile Ala Ser Leu Leu Gly Leu Ser Ala Leu Ile Ser Thr
              10              15              20

```

```

tat cca gca att ttg aac ctg ttg cag ctc gtc ggt ggc ggt tat ttg 211
Tyr Pro Ala Ile Leu Asn Leu Leu Gln Leu Val Gly Gly Tyr Leu
              25              30              35

```

```

acc tgg atg ggc atc ggg gcg gtg agg tca tgg tgg acg aaa cgc tcc 259
Thr Trp Met Gly Ile Gly Ala Val Arg Ser Trp Trp Lys Arg Ser
              40              45              50

```

```

aca cag caa gct gca gcg gat tct caa gct gta gag aat acg ttg gtg 307
Thr Gln Gln Ala Ala Ala Asp Ser Gln Ala Val Glu Asn Thr Leu Val
              55              60              65

```

```

aca gcc acg gct gca tct gtc gga gtg tgg cca gct att cga tct gcc 355
Thr Ala Thr Ala Ala Ser Val Gly Val Trp Pro Ala Ile Arg Ser Gly

```

```

70              75              80              85
att gct acc aac ttg tcc aac ccc aaa gct gtg ctg ttt ttt ggt tcc 403
Ile Ala Thr Asn Leu Ser Asn Pro Lys Ala Val Leu Phe Phe Gly Ser
              90              95              100

gtt ttc gcc caa ttt gtt aga cct gac atg gga atc ggg tgg agt att 451
Val Phe Ala Gln Phe Val Arg Pro Asp Met Gly Ile Gly Trp Ser Ile
              105              110              115

ttc att gga gtc ttc ctc acc ctc act ggc ctg ctg tgg ttt gtg ggg 499
Phe Ile Gly Val Phe Leu Thr Leu Thr Gly Leu Leu Trp Phe Val Gly
              120              125              130

ttc gcc gtc ttg gtc cgc aaa cta gcc gct ggc ctc acc cga aat gga 547
Phe Ala Val Leu Val Arg Lys Leu Ala Ala Gly Leu Thr Arg Asn Gly
              135              140              145

gcc atc atc gac ctg cta acg ggg gtg att ttc atc ggg ctg gga atg 595
Ala Ile Ile Asp Leu Leu Thr Gly Val Ile Phe Ile Gly Leu Gly Met
              150              155              160

ttc atg atc ttc gag ggg gtt gta gga atc ggt ggc agg gta gtg ggt 643
Phe Met Ile Phe Glu Gly Val Val Gly Ile Gly Gly Arg Val Val Gly
              170              175              180

tagccccgcc cccaggacgt cac 666

<210> 1344
<211> 181
<212> PRT
<213> Corynebacterium glutamicum

<400> 1344
Met Val Gly Asn Ser Ile Trp Ile Ile Ala Ser Leu Leu Gly Leu Ser
  1              5              10              15
Ala Leu Ile Ser Thr Tyr Pro Ala Ile Leu Asn Leu Leu Gln Leu Val
              20              25              30
Gly Gly Gly Tyr Leu Thr Trp Met Gly Ile Gly Ala Val Arg Ser Trp
              35              40              45
Trp Thr Lys Arg Ser Thr Gln Gln Ala Ala Ala Asp Ser Gln Ala Val
              50              55              60
Glu Asn Thr Leu Val Thr Ala Thr Ala Ala Ser Val Gly Val Trp Pro
              65              70              75              80
Ala Ile Arg Ser Gly Ile Ala Thr Asn Leu Ser Asn Pro Lys Ala Val
              85              90              95
Leu Phe Phe Gly Ser Val Phe Ala Gln Phe Val Arg Pro Asp Met Gly
              100              105              110
Ile Gly Trp Ser Ile Phe Ile Gly Val Phe Leu Thr Leu Thr Gly Leu
              115              120              125
Leu Trp Phe Val Gly Phe Ala Val Leu Val Arg Lys Leu Ala Ala Gly
              130              135              140

```

Leu Thr Arg Asn Gly Ala Ile Ile Asp Leu Leu Thr Gly Val Ile Phe
145 150 155 160

Ile Gly Leu Gly Met Phe Met Ile Phe Glu Gly Val Val Gly Ile Gly
165 170 175

Gly Arg Val Val Gly
180

<210> 1345

<211> 594

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(571)

<223> RXN02921

<400> 1345

tggaactg ggaaggggtg acgttgcgga atctctccgc agcgctcggtt cggaccctaa 60

aaaaggggtga ggaaccacat gagctgtttt aaggaatttt gtg tct gca ctt gaa 115
Val Ser Ala Leu Glu
1 5

gag tcg atc cgc atc gcg acc atc gcg gcg aaa gca gcg gat gaa aag 163
Glu Ser Ile Arg Ile Ala Thr Ile Ala Ala Lys Ala Ala Asp Glu Lys
10 15 20

aag gcc gat gac atc gct gtc atc gat gtc tct gac atg atc gca atc 211
Lys Ala Asp Asp Ile Ala Val Ile Asp Val Ser Asp Met Ile Ala Ile
25 30 35

acc gat tgc ttt gtt gtt gca tct gct gac aat gag cgc cag gtg ggc 259
Thr Asp Cys Phe Val Val Ala Ser Ala Asp Asn Glu Arg Gln Val Gly
40 45 50

gcc att gtt gag gag atc gaa gat gag atg acc aag gct ggt ttc gag 307
Ala Ile Val Glu Glu Ile Glu Asp Glu Met Thr Lys Ala Gly Phe Glu
55 60 65

cct aag cgc cgt gaa ggc aac cgc gaa aac cgt tgg gtt ctc ctt gac 355
Pro Lys Arg Arg Glu Gly Asn Arg Glu Asn Arg Trp Val Leu Leu Asp
70 75 80 85

tac gga ttg gtt gtt atc cac gtt cag cga cag gca gag cgc gag ttc 403
Tyr Gly Leu Val Val Ile His Val Gln Arg Gln Ala Glu Arg Glu Phe
90 95 100

tac gga ctg gat cgt ctg tac cgc gac tgc cca ctc att gaa att gaa 451
Tyr Gly Leu Asp Arg Leu Tyr Arg Asp Cys Pro Leu Ile Glu Ile Glu
105 110 115

gga ctt gaa acc ttc aag cgt gaa tcc tcc tgg tct gat gag gcg gat 499
Gly Leu Glu Thr Phe Lys Arg Glu Ser Ser Trp Ser Asp Glu Ala Asp
120 125 130

atc cgc aac atc gac agc att gat gaa ctc cca cct ttg cca gct gaa 547

Ile Arg Asn Ile Asp Ser Ile Asp Glu Leu Pro Pro Leu Pro Ala Glu
135 140 145

tac gag cct ggc tac gag gac gat taagaggtag tcctgtgact cgt 594
Tyr Glu Pro Gly Tyr Glu Asp Asp
150 155

<210> 1346

<211> 157

<212> PRT

<213> Corynebacterium glutamicum

<400> 1346

Val Ser Ala Leu Glu Glu Ser Ile Arg Ile Ala Thr Ile Ala Ala Lys
1 5 10 15

Ala Ala Asp Glu Lys Lys Ala Asp Asp Ile Ala Val Ile Asp Val Ser
20 25 30

Asp Met Ile Ala Ile Thr Asp Cys Phe Val Val Ala Ser Ala Asp Asn
35 40 45

Glu Arg Gln Val Gly Ala Ile Val Glu Glu Ile Glu Asp Glu Met Thr
50 55 60

Lys Ala Gly Phe Glu Pro Lys Arg Arg Glu Gly Asn Arg Glu Asn Arg
65 70 75 80

Trp Val Leu Leu Asp Tyr Gly Leu Val Val Ile His Val Gln Arg Gln
85 90 95

Ala Glu Arg Glu Phe Tyr Gly Leu Asp Arg Leu Tyr Arg Asp Cys Pro
100 105 110

Leu Ile Glu Ile Glu Gly Leu Glu Thr Phe Lys Arg Glu Ser Ser Trp
115 120 125

Ser Asp Glu Ala Asp Ile Arg Asn Ile Asp Ser Ile Asp Glu Leu Pro
130 135 140

Pro Leu Pro Ala Glu Tyr Glu Pro Gly Tyr Glu Asp Asp
145 150 155

<210> 1347

<211> 672

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(649)

<223> RXN02924

<400> 1347

ctaggcaggt gtgcgatcaa accacactgt cagaatcaaa tctgctggac gctatgccag 60

cggattgttg atcacgaaaa agcatgtcac agacaccttt gtg cct tct gta gca 115
Val Pro Ser Val Ala
1 5

```

tcc atc tca gag cgc gcc acg ttt att ctc acc gcc gat cac ttt ttg 163
Ser Ile Ser Glu Arg Ala Thr Phe Ile Leu Thr Ala Asp His Phe Leu
      10      15      20

cgc agc tgc tgc aaa gta att tat gtc cgg ggc gaa aat ttc acc gcc 211
Arg Ser Cys Ser Lys Val Ile Tyr Val Arg Gly Glu Asn Phe Thr Ala
      25      30      35

aca gca acc acc agc ctg tct gta ttt ggc aca gat ctg ggt ttg atc 259
Thr Ala Thr Thr Ser Leu Ser Val Phe Gly Thr Asp Leu Gly Leu Ile
      40      45      50

aaa tta gac ggc aaa gcc ccc acc atg cca ctt cca ctt ttc gca gat 307
Lys Leu Asp Gly Lys Ala Pro Thr Met Pro Leu Pro Leu Phe Ala Asp
      55      60      65

aag cca ctt cgc gtg ggc atg aaa acc acc acg ttc gga ttc ggc ggt 355
Lys Pro Leu Arg Val Gly Met Lys Thr Thr Thr Phe Gly Phe Gly Gly
      70      75      80      85

ctg cca tca gcc acc gtt gct aaa gaa atc cac ggg cgc gtt atc tct 403
Leu Pro Ser Ala Thr Val Ala Lys Glu Ile His Gly Arg Val Ile Ser
      90      95      100

gcc atc ccc cat ggc gta tca aga aac cgc atc acc cga gtc cat cac 451
Ala Ile Pro His Gly Val Ser Arg Asn Arg Ile Thr Arg Val His His
      105      110      115

ggc gcc ttg atc ttt aac tcc cca gaa aag gca gta aag gga gac tcc 499
Gly Ala Leu Ile Phe Asn Ser Pro Glu Lys Ala Val Lys Gly Asp Ser
      120      125      130

ggc gga cct gtg ctg gtt aat gga cga gta gcc gga atc caa tca atg 547
Gly Gly Pro Val Leu Val Asn Gly Arg Val Ala Gly Ile Gln Ser Met
      135      140      145

atc tct gac ccc ggt gga ttt aac acc ggg gtc gcc act gcc gca tcc 595
Ile Ser Asp Pro Gly Gly Phe Asn Thr Gly Val Ala Thr Ala Ala Ser
      150      155      160      165

ctt atc cag cac atg cct gcc cta gct caa gcg ctt gaa ctg ctc gaa 643
Leu Ile Gln His Met Pro Ala Leu Ala Gln Ala Leu Glu Leu Leu Glu
      170      175      180

cat agc tagctcgcta ggaaccgac gcc 672
His Ser

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<210> 1348

<211> 183

<212> PRT

<213> Corynebacterium glutamicum

<400> 1348

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Val Pro Ser Val Ala Ser Ile Ser Glu Arg Ala Thr Phe Ile Leu Thr
  1          5          10          15

Ala Asp His Phe Leu Arg Ser Cys Ser Lys Val Ile Tyr Val Arg Gly
      20      25      30

```

agc gcc aca gga ctc gtc gcg gtc gag ggc gtc gac aca cat gag ttc 259
 Ser Ala Thr Gly Leu Val Ala Val Glu Gly Val Asp Thr His Glu Phe
 40 45 50

gcc gag gtc gat gta gtc ggc tac gcg tgc tgc gta ttc gag aac ctg 307
 Ala Glu Val Asp Val Val Gly Tyr Ala Cys Cys Val Phe Glu Asn Leu
 55 60 65

gtt cat ctc atc ggt gct gcc ggt gat gcg cat gtt ctt cca gaa gtc 355
 Val His Leu Ile Gly Ala Ala Gly Asp Ala His Val Leu Pro Glu Val
 70 75 80 85

atc gcg gag ggc acg gat ctt gtt gat gcc atc ctg gag gtc ttc tac 403
 Ile Ala Glu Gly Thr Asp Leu Val Asp Ala Ile Leu Glu Val Phe Tyr
 90 95 100

gtt tcg gga aac gcc aca gga gaa gta cag gat atc gcc aag ctg gcg 451
 Val Ser Gly Asn Ala Thr Gly Glu Val Gln Asp Ile Ala Lys Leu Ala
 105 110 115

gtg gta gta ctc agg tcc gtg aac gtt gtc acc gac cca ctc tgg gcg 499
 Val Val Val Leu Arg Ser Val Asn Val Val Thr Asp Pro Leu Trp Ala
 120 125 130

gtt gcc cat gag gcg gtc aat gcg agc ctg tgc acg cgc aat cgc tgc 547
 Val Ala His Glu Ala Val Asn Ala Ser Leu Cys Thr Arg Asn Arg Cys
 135 140 145

ctg tgc ttc tgg tgc atc ctc tgacagacgc tcggagccaa gca 591
 Leu Cys Phe Trp Cys Ile Leu
 150 155

<210> 1350
 <211> 156
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 1350
 Val Ala Asp Glu Gly Ser Ile Leu Ala Trp Phe Pro Cys Gly Asp Glu
 1 5 10 15
 Ala Pro Val Leu Val Val Thr Leu Cys Phe Ala Ile Phe Gly Glu Val
 20 25 30
 Val Val Ala Glu Val Ser Ala Thr Gly Leu Val Ala Val Glu Gly Val
 35 40 45
 Asp Thr His Glu Phe Ala Glu Val Asp Val Val Gly Tyr Ala Cys Cys
 50 55 60
 Val Phe Glu Asn Leu Val His Leu Ile Gly Ala Ala Gly Asp Ala His
 65 70 75 80
 Val Leu Pro Glu Val Ile Ala Glu Gly Thr Asp Leu Val Asp Ala Ile
 85 90 95
 Leu Glu Val Phe Tyr Val Ser Gly Asn Ala Thr Gly Glu Val Gln Asp
 100 105 110
 Ile Ala Lys Leu Ala Val Val Leu Arg Ser Val Asn Val Val Thr
 115 120 125
 Asp Pro Leu Trp Ala Val Ala His Glu Ala Val Asn Ala Ser Leu Cys
 130 135 140

Thr Arg Asn Arg Cys Leu Cys Phe Trp Cys Ile Leu
145 150 155

<210> 1351
<211> 816
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> {101}..(793)
<223> RXN02928

<400> 1351
ggtttgcacc gtggtaggtc caggatgctt cgctgcgca gaacagacct gggagtgcacg 60

tcatttcggt gaagtcagtc cagaggccac ccatgggtgaa gtg gca ggt cgg tgc 115
Val Ala Gly Arg Cys
1 5

aat acg cat tgg gct gga gta tgg gtc ctc gcc aat tgc ctc ttc gta 163
Asn Thr His Trp Ala Gly Val Trp Val Leu Ala Asn Cys Leu Phe Val
10 15 20

cat ggt gaa gag gtt gga gta acg ctc gcg gat ggt gtc ctg tcc gag 211
His Gly Glu Glu Val Gly Val Thr Leu Ala Asp Gly Val Leu Ser Glu
25 30 35

gcg ctc ggt ggc gtc gcg gaa gtc cag gta tgc agc gtt gtt cag agg 259
Ala Leu Gly Gly Val Ala Glu Val Gln Val Cys Ser Val Val Gln Arg
40 45 50

tcc aac acc gag acc agc att gat ctg ctg gga gat cgc acg gga agc 307
Ser Asn Thr Glu Thr Ser Ile Asp Leu Leu Gly Asp Arg Thr Gly Ser
55 60 65

aac gtc acg tgg gac gag gtt acc gaa tgc tgg gta gcg gcg ctc cag 355
Asn Val Thr Trp Asp Glu Val Thr Glu Cys Trp Val Ala Ala Leu Gln
70 75 80 85

gaa gta gtc gcg ctc atc ctc agg gat ggt gtt tgg atc gcg gtt atc 403
Glu Val Val Ala Leu Ile Leu Arg Asp Gly Val Trp Ile Ala Val Ile
90 95 100

gtt cgg ttc ctt agg gga cca gat gcg gcc gtc gtt acg cag cga ctc 451
Val Arg Phe Leu Arg Gly Pro Asp Ala Ala Val Val Thr Gln Arg Leu
105 110 115

gga cat cag aat ggt ctt gga ctg cca ggt gga gtt cac agg cag gcc 499
Gly His Gln Asn Gly Leu Gly Leu Pro Gly Gly Val His Arg Gln Ala
120 125 130

ggt tgg gtg gaa ctg gat gaa cga tgg gga cgc gaa gta tgc gcc gcc 547
Gly Trp Val Glu Leu Asp Glu Arg Trp Gly Arg Glu Val Cys Ala Gly
135 140 145

ttc gta tgc acg cat gat gcc cga gcc gtt gga gtt ctt gcc cag ggt 595
Phe Val Cys Thr His Asp Gly Arg Gly Val Gly Val Leu Gly Gln Gly
150 155 160 165

```

gga cat gtg gta cac gtt gcc gta gcc acc ggt tgc cag gat aac ggc 643
Gly His Val Val His Val Ala Val Ala Thr Gly Cys Gln Asp Asn Gly
      170                      175                      180

atg gcc ggt gtg tgc ggt gag ctc gcc ggt gat cag gtt gcg cat gat 691
Met Ala Gly Val Cys Gly Glu Leu Ala Gly Asp Gln Val Ala His Asp
      185                      190                      195

cag gcc ttc gca gcg ctt ttc acc gtt acg ttc ggt gac aat gac gtc 739
Gln Ala Phe Ala Ala Leu Phe Thr Val Thr Phe Gly Asp Asn Asp Val
      200                      205                      210

aac cat ttc gtt atg ggt gaa gat ttc tac gga gcc gag gtg gat ctg 787
Asn His Phe Val Met Gly Glu Asp Phe Tyr Gly Ala Glu Val Asp Leu
      215                      220                      225

gcg ctg tagtgcggat gcggtggaga act 816
Ala Leu
230

```

```

<210> 1352
<211> 231
<212> PRT
<213> Corynebacterium glutamicum

<400> 1352
Val Ala Gly Arg Cys Asn Thr His Trp Ala Gly Val Trp Val Leu Ala
  1              5              10              15

Asn Cys Leu Phe Val His Gly Glu Glu Val Gly Val Thr Leu Ala Asp
  20              25              30

Gly Val Leu Ser Glu Ala Leu Gly Gly Val Ala Glu Val Gln Val Cys
  35              40              45

Ser Val Val Gln Arg Ser Asn Thr Glu Thr Ser Ile Asp Leu Leu Gly
  50              55              60

Asp Arg Thr Gly Ser Asn Val Thr Trp Asp Glu Val Thr Glu Cys Trp
  65              70              75              80

Val Ala Ala Leu Gln Glu Val Val Ala Leu Ile Leu Arg Asp Gly Val
  85              90              95

Trp Ile Ala Val Ile Val Arg Phe Leu Arg Gly Pro Asp Ala Ala Val
  100             105             110

Val Thr Gln Arg Leu Gly His Gln Asn Gly Leu Gly Leu Pro Gly Gly
  115             120             125

Val His Arg Gln Ala Gly Trp Val Glu Leu Asp Glu Arg Trp Gly Arg
  130             135             140

Glu Val Cys Ala Gly Phe Val Cys Thr His Asp Gly Arg Gly Val Gly
  145             150             155             160

Val Leu Gly Gln Gly Gly His Val Val His Val Ala Val Ala Thr Gly
  165             170             175

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Cys Gln Asp Asn Gly Met Ala Gly Val Cys Gly Glu Leu Ala Gly Asp
 180 185 190

Gln Val Ala His Asp Gln Ala Phe Ala Ala Leu Phe Thr Val Thr Phe
 195 200 205

Gly Asp Asn Asp Val Asn His Phe Val Met Gly Glu Asp Phe Tyr Gly
 210 215 220

Ala Glu Val Asp Leu Ala Leu
 225 230

<210> 1353
 <211> 348
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(325)
 <223> RXN02931

<400> 1353
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ctagtgcggt gtaagagcac tagactgttc aactatgagc atg caa cca tac ccc 115
 Met Gln Pro Tyr Pro
 1 5

cgc aac cca atc gaa aaa cgt aag caa gaa gta cgc aag aac tcc cgc 163
 Arg Asn Pro Ile Glu Lys Arg Lys Gln Glu Val Arg Lys Asn Ser Arg
 10 15 20

aac gca gtt gtc agt gtt ggc ggt ggc atc gta ggc ggt gcg gct ctg 211
 Asn Ala Val Val Ser Val Gly Gly Gly Ile Val Gly Gly Ala Ala Leu
 25 30 35

tgg cta gtg ttc ggc tct gca ttc ttt atg gga ctt gga ttg atc atc 259
 Trp Leu Val Phe Gly Ser Ala Phe Phe Met Gly Leu Gly Leu Ile Ile
 40 45 50

gcc gtg gtc ggc ggt ttt tat tac tac aac aag gtc caa aag atc att 307
 Ala Val Val Gly Gly Phe Tyr Tyr Asn Lys Val Gln Lys Ile Ile
 55 60 65

aac gaa aaa gac cgt tac tagttagaaa tctatgtcag aca 348
 Asn Glu Lys Asp Arg Tyr
 70 75

<210> 1354
 <211> 75
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1354
 Met Gln Pro Tyr Pro Arg Asn Pro Ile Glu Lys Arg Lys Gln Glu Val
 1 5 10 15

Arg Lys Asn Ser Arg Asn Ala Val Val Ser Val Gly Gly Gly Ile Val

20 25 30

Gly Gly Ala Ala Leu Trp Leu Val Phe Gly Ser Ala Phe Met Gly
35 40 45

Leu Gly Leu Ile Ile Ala Val Val Gly Gly Phe Tyr Tyr Asn Lys
50 55 60

Val Gln Lys Ile Ile Asn Glu Lys Asp Arg Tyr
65 70 75

<210> 1355
<211> 1095
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1072)
<223> RXN02932

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agcacgacca ttccagtttt aactttcttg gagttttcta gtg tcc aaa aca gaa 115
Val Ser Lys Thr Glu
1 5

gaa ggc cgt tca gcg gcc ata att att tac gcg ttt cca act ttc att 163
Glu Gly Arg Ser Ala Ala Ile Ile Ile Tyr Ala Phe Pro Thr Phe Ile
10 15 20

ctg ctg ggc gcg atc att gcg ttt atc ttc ccg gaa cca ttc att ccg 211
Leu Leu Gly Ala Ile Ile Ala Phe Ile Phe Pro Glu Pro Phe Ile Pro
25 30 35

ctg aca aac tac att aat atc ttc ctc acg atc atc atg ttc acc atg 259
Leu Thr Asn Tyr Ile Asn Ile Phe Leu Thr Ile Ile Met Phe Thr Met
40 45 50

ggt ttg acc ttg acg gtg ccc gat ttt cag atg gtg ctt aaa cgt cca 307
Gly Leu Thr Leu Thr Val Pro Asp Phe Gln Met Val Leu Lys Arg Pro
55 60 65

ctg cct atc ttg atc ggt gta gta gcg cag ttt gtc atc atg cca ttc 355
Leu Pro Ile Leu Ile Gly Val Val Ala Gln Phe Val Ile Met Pro Phe
70 75 80 85

ctg gcg atc gtg gtt gcg aaa atg ttc aac ctc aac cca gca ctc gcc 403
Leu Ala Ile Val Val Ala Lys Met Phe Asn Leu Asn Pro Ala Leu Ala
90 95 100

gtt ggc ctt ctc atg ctg gga tcc gtt ccg ggt ggc acc tcc tcc aat 451
Val Gly Leu Leu Met Leu Gly Ser Val Pro Gly Gly Thr Ser Ser Asn
105 110 115

gtg att gcg ttt ctc gcc cga gga gat gtc gcg cta tgg gtc acc atg 499
Val Ile Ala Phe Leu Ala Arg Gly Asp Val Ala Leu Ser Val Thr Met
120 125 130

acc tct gtg tcc acc att gtt tcc cca atc atg acg cct ttc ctc atg 547
 Thr Ser Val Ser Thr Ile Val Ser Pro Ile Met Thr Pro Phe Leu Met
 135 140 145

ctc atg ctg gca ggt act gaa acc gcc gtc gat ggt gga ggc atg gcg 595
 Leu Met Leu Ala Gly Thr Glu Thr Ala Val Asp Gly Gly Gly Met Ala
 150 155 160 165

tgg act ttg gta caa aca gtg ctg ctg cct gtg atc atc ggc cta gtt 643
 Trp Thr Leu Val Gln Thr Val Leu Leu Pro Val Ile Ile Gly Leu Val
 170 175 180

ctg cgt gtc ttc ttg aac aag tgg atc gac aag att ttg cag atc ctt 691
 Leu Arg Val Phe Leu Asn Lys Trp Ile Asp Lys Ile Leu Pro Ile Leu
 185 190 195

cct tat ctc tcc atc ctc ggt atc ggt gcc gtg gtg ttc ggc gca gtc 739
 Pro Tyr Leu Ser Ile Leu Gly Ile Gly Gly Val Phe Gly Ala Val
 200 205 210

gca gcc aac gcg gaa cga ctc gtg tct gtc gga ctc atc gtg ttc gtt 787
 Ala Ala Asn Ala Glu Arg Leu Val Ser Val Gly Leu Ile Val Phe Val
 215 220 225

gca gtt atc gtg cac aac gta ctt gga tac gtt gtg gga tac ctc acc 835
 Ala Val Ile Val His Asn Val Leu Gly Tyr Val Val Gly Tyr Leu Thr
 230 235 240 245

ggc cgt gta ttc aaa ttc cca gaa gca gca aac cgc acc atg gcg att 883
 Gly Arg Val Phe Lys Phe Pro Glu Ala Ala Asn Arg Thr Met Ala Ile
 250 255 260

gaa atc gga acc caa tcc gca ggc ctc gca tcg gga atg gca gga cga 931
 Glu Ile Gly Thr Gln Ser Ala Gly Leu Ala Ser Gly Met Ala Gly Arg
 265 270 275

ttc ttc acc cca gaa gca gcc ctt cca ggt gct gtc gct gcc ttg gtc 979
 Phe Phe Thr Pro Glu Ala Ala Leu Pro Gly Ala Val Ala Ala Leu Val
 280 285 290

cac aac atc acc ggc gca gtt tat gtt ggg ctg gta cga aac agg cct 1027
 His Asn Ile Thr Gly Ala Val Tyr Val Gly Leu Val Arg Asn Arg Pro
 295 300 305

ttg act aag gca tca agg aag aag gaa tcc gtc gcg gtt tcc agc 1072
 Leu Thr Lys Ala Ser Arg Lys Lys Glu Ser Val Ala Val Ser Ser
 310 315 320

taacttattt gctgccggtt aga 1095

<210> 1356

<211> 324

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1356

Val Ser Lys Thr Glu Glu Gly Arg Ser Ala Ala Ile Ile Ile Tyr Ala
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Phe Pro Thr Phe Ile Leu Leu Gly Ala Ile Ile Ala Phe Ile Phe Pro

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<211> 429
 <212> DNA
 <213> *Corynebacterium glutamicum*

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 <221> CDS
 <222> (101)..(406)
 <223> RXN02934

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tgagtggctg gccgtagtag atttctacaa ctccgccggc gtg ggt gca gac gaa 115
 Val Gly Ala Asp Glu
 1 5

ttc gat ttc atc ttt gag att gat gcg cca gaa gcc gga ttc gcg ctg 163
 Phe Asp Phe Ile Phe Glu Ile Asp Ala Pro Glu Ala Gly Phe Ala Leu
 10 15 20

gtc gac gcc ggt ggg gtt tcc ttc ttc gtc gag ttt cca cat gcg gga 211
 Val Asp Ala Gly Val Ser Phe Phe Val Glu Phe Pro His Ala Gly
 25 30 35

ttc gaa gga gag gta gtt ttc acc gtc gtg ggc gaa ggt gat ttg ctg 259
 Phe Glu Gly Glu Val Val Phe Thr Val Val Gly Glu Gly Asp Leu Leu
 40 45 50

gcc gaa tgc gta ttg tcc gtc ttc tgc ggt gtc ggc ttg gcc ttc gcc 307
 Ala Glu Cys Val Leu Ser Val Phe Cys Gly Val Gly Leu Ala Phe Ala
 55 60 65

gcg cca gac gcc gac gag agg gag gag cgc gag gag tcc gtc gtg gag 355
 Ala Pro Asp Ala Asp Glu Arg Glu Glu Arg Glu Glu Ser Val Val Glu
 70 75 80 85

gtt ggg gcc ttc gcg gag gtt agc ggt gtc gtc agg gat agg aag gtc 403
 Val Gly Ala Phe Ala Glu Val Ser Gly Val Val Arg Asp Arg Lys Val
 90 95 100

acc taggcctggg atgttgcggt gag 429
 Thr

<210> 1358
 <211> 102
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 1358
 Val Gly Ala Asp Glu Phe Asp Phe Ile Phe Glu Ile Asp Ala Pro Glu
 1 5 10 15
 Ala Gly Phe Ala Leu Val Asp Ala Gly Gly Val Ser Phe Phe Val Glu
 20 25 30
 Phe Pro His Ala Gly Phe Glu Gly Glu Val Val Phe Thr Val Val Gly
 35 40 45
 Glu Gly Asp Leu Leu Ala Glu Cys Val Leu Ser Val Phe Cys Gly Val


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      50              55              60
Gly Leu Ala Phe Ala Ala Pro Asp Ala Asp Glu Arg Glu Glu Arg Glu
65              70              75
Glu Ser Val Val Glu Val Gly Ala Phe Ala Glu Val Ser Gly Val Val
85              90              95
Arg Asp Arg Lys Val Thr
100

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<210> 1359
<211> 321
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(298)
<223> RXN02936

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<400> 1359
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agtttggcgc tggcgaagca acaagaaaacg agtgggatct gtg gtt gcg ccg ttc 115
Val Val Ala Pro Phe
1 5
cag ttg gtg ggt ttg gtt tcg gtg cag ttg agg tct tct ttc tct gag 163
Gln Leu Val Gly Leu Val Ser Val Gln Leu Arg Ser Ser Phe Ser Glu
10 15 20
ccc gca acc gaa gaa gca gaa gat aca gaa gca gaa tcc cct aca aca 211
Pro Ala Thr Glu Glu Ala Glu Asp Thr Glu Ala Glu Ser Pro Thr Thr
25 30 35
cct acc ggc tta cct gcc gct gca gca tcc atc gcc acg ttg gac aat 259
Pro Thr Gly Leu Pro Ala Ala Ala Ser Ile Ala Thr Leu Asp Asn
40 45 50
gcg tca gct cgt ttg ttt ttc tca cgc gga atc cac gta taagaaacgg 308
Ala Ser Ala Arg Leu Phe Phe Ser Arg Gly Ile His Val
55 60 65
accgatttc gga 321

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<210> 1360
<211> 66
<212> PRT
<213> Corynebacterium glutamicum

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<400> 1360
Val Val Ala Pro Phe Gln Leu Val Gly Leu Val Ser Val Gln Leu Arg
1 5 10 15
Ser Ser Phe Ser Glu Pro Ala Thr Glu Glu Ala Glu Asp Thr Glu Ala
20 25 30
Glu Ser Pro Thr Thr Pro Thr Gly Leu Pro Ala Ala Ala Ser Ile

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35

40

45

Ala Thr Leu Asp Asn Ala Ser Ala Arg Leu Phe Phe Ser Arg Gly Ile
 50 55 60

His Val
 65

<210> 1361

<211> 1725

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1702)

<223> RXN02939

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cttagacaac ttcataaacc cccctggagt gattgagata atg aat ctc cac tcc 115
 Met Asn Leu His Ser
 1 5

tta gag att cgc caa att tca tcc ggc aca att tca gaa cga aaa act 163
 Leu Glu Ile Arg Gln Ile Ser Ser Gly Thr Ile Ser Glu Arg Lys Thr
 10 15 20

tgg atc ttt ccc act gct gct cgc tca ttc aat caa aat cta gta cac 211
 Trp Ile Phe Pro Thr Ala Ala Arg Ser Phe Asn Gln Asn Leu Val His
 25 30 35

cgc caa agc att gaa atc gat gca caa acc ggc gtt att ttg gct atg 259
 Pro Gln Ser Ile Glu Ile Asp Ala Gln Thr Gly Val Ile Leu Ala Met
 40 45 50

gaa aac cga cta caa cgt acc gaa gtt gaa tca gta gag tac cca acg 307
 Glu Asn Arg Leu Gln Arg Thr Glu Val Glu Ser Val Glu Tyr Pro Thr
 55 60 65

gat ctt cct aat cct gca tgg aca ggt cca gcc att tct tgg cca cta 355
 Asp Leu Pro Asn Pro Ala Trp Thr Gly Pro Ala Ile Ser Trp Pro Leu
 70 75 80 85

aaa gac cca tca atc gat ttc cct gac cgc ctc ccc cac agc att tcc 403
 Lys Asp Pro Ser Ile Asp Phe Pro Asp Pro Leu Pro His Ser Ile Ser
 90 95 100

gaa tta cca cct caa tcc gat aat cct cgc cat ttg cga gta tcc atc 451
 Glu Leu Pro Pro Gln Ser Asp Asn Pro Arg His Leu Arg Val Ser Ile
 105 110 115

agc tta gat gca gtg gaa ggt gct ttt cgc cgc tac cgc atc gga gat 499
 Ser Leu Asp Ala Val Glu Gly Ala Phe Pro Arg Tyr Arg Ile Gly Asp
 120 125 130

tca ata cgt att cgc ctt gtc ttt gcc cgc gac acg ccc ttc atg tcc 547
 Ser Ile Arg Ile Pro Leu Val Phe Ala Arg Asp Thr Pro Phe Met Ser
 135 140 145

ggc tta gaa aca aca cgt cgc gcc tgg att gag gcg gcc acg gaa atg Gly Leu Glu Thr Thr Arg Arg Ala Trp Ile Glu Ala Ala Thr Glu Met 150 155 160 165	595
gac atc cat aac aca tgg ccc ata atc ctc acc ggt gac ggc tgg act Asp Ile His Asn Thr Trp Pro Ile Ile Leu Thr Gly Asp Gly Trp Thr 170 175 180	643
gca ctc tct cat tca gac aaa cca ata cgc cac gaa gcc gag tta aag Ala Leu Ser His Ser Asp Lys Pro Ile Arg His Glu Ala Glu Leu Lys 185 190 195	691
gga tgg ttt ttc cac agt ttg ttc ggc agt gaa atg ccc ttg act gat Gly Trp Phe Phe His Ser Leu Phe Gly Ser Glu Met Pro Leu Thr Asp 200 205 210	739
ctg aag att gaa cga atc tac gga ggc ctg ggt act ttc gac agc gga Leu Lys Ile Glu Arg Ile Tyr Gly Gly Leu Gly Thr Phe Asp Ser Gly 215 220 225	787
gcc acc cgg tgg caa gaa ctc aca gac aca gat gat gcc tac aca gaa Ala Thr Arg Trp Gln Glu Leu Thr Asp Thr Asp Asp Ala Tyr Thr Glu 230 235 240 245	835
aat ggc agc tgg ctg ttg gaa gtt atc gtc gat gcc acc ctt gac ggt Asn Gly Ser Trp Leu Leu Glu Val Ile Val Asp Ala Thr Leu Asp Gly 250 255 260	883
gca att cca cca cca ctt cag cca caa cag ttt gaa gca tcc atc act Ala Ile Pro Pro Pro Leu Gln Pro Gln Gln Phe Glu Ala Ser Ile Thr 265 270 275	931
cac atc gtc gat gag caa cta tgg gtc ctt ggg cag atg ctt cca gtt His Ile Val Asp Glu Gln Leu Trp Val Leu Gly Gln Met Leu Pro Val 280 285 290	979
cta cga tgc tgg gat ctt gaa acc gga aaa tac ctg ggg caa acc tat Leu Arg Cys Trp Asp Leu Glu Thr Gly Lys Tyr Leu Gly Gln Thr Tyr 295 300 305	1027
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ttg att cac gat tat gaa aat gcc tgg tcg ctg aat cct ggg gtg cgc Leu Ile His Asp Tyr Glu Asn Ala Trp Ser Leu Asn Pro Gly Val Arg 330 335 340	1123
atg ctt gcg gag cca cag ccg tgg ata gag cct gtc att gaa ctc gac Met Leu Ala Glu Pro Gln Pro Trp Ile Glu Pro Val Ile Glu Leu Asp 345 350 355	1171
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tcc cta act gat gga gag caa aca gca ctg ggt cga agc act cca gca Ser Leu Thr Asp Gly Glu Gln Thr Ala Leu Gly Arg Ser Thr Pro Ala 375 380 385	1267

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 Gly Gln Leu Glu Ile Cys Val Ile Ser Asn Asp Gly Ser Arg Ile Leu
 390 395 400 405

 aac gca ggc cga gta gaa gac ctg tac ttt gtg caa ttc tgg ggc atg 1363
 Asn Ala Gly Arg Val Glu Asp Leu Tyr Phe Val Gln Phe Trp Gly Met
 410 415 420

 acc gtc ttt ttg aat tcc aac ttt caa gtg caa agt gcc gaa gaa cat 1411
 Thr Val Phe Leu Asn Ser Asn Phe Gln Val Gln Ser Ala Glu Glu His
 425 430 435

 cag ctt ggt gcg aaa cgt gaa cgc tgg att aca caa gaa ggc gta gct 1459
 Gln Leu Gly Ala Lys Arg Glu Arg Trp Ile Thr Gln Glu Gly Val Ala
 440 445 450

 gcc aag ttc acc gaa gaa gat gaa atc gta ttc ctc gat cag ata tct 1507
 Ala Lys Phe Thr Glu Glu Asp Glu Ile Val Phe Leu Asp Gln Ile Ser
 455 460 465

 gaa agc gaa ata acc agg tgg aaa aca cca gaa gga tac ttc act gag 1555
 Glu Ser Glu Ile Thr Arg Trp Lys Thr Pro Glu Gly Tyr Phe Thr Glu
 470 475 480 485

 gtc aga att ctg tca cca aac cac ttc aac ata ctg gtt act ccg cct 1603
 Val Arg Ile Leu Ser Pro Asn His Phe Asn Ile Leu Val Thr Pro Pro
 490 495 500

 act ggt tct gac tat ctc aaa cca gta cct tcc tct gtc tca gtg ttt 1651
 Thr Gly Ser Asp Tyr Leu Lys Pro Val Pro Ser Ser Val Ser Val Phe
 505 510 515

 aga gac ggt caa tgg agc aac att aaa ttc gag gac gtc tct gta gaa 1699
 Arg Asp Gly Gln Trp Ser Asn Ile Lys Phe Glu Asp Val Ser Val Glu
 520 525 530

 atc tagggctttc gaecgttgag ccc 1725
 Ile

<210> 1362

<211> 534

<212> PRT

<213> Corynebacterium glutamicum

<400> 1362

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Ser Glu Arg Lys Thr Trp Ile Phe Pro Thr Ala Ala Arg Ser Phe Asn
 20 25 30

Gln Asn Leu Val His Pro Gln Ser Ile Glu Ile Asp Ala Gln Thr Gly
 35 40 45

Val Ile Leu Ala Met Glu Asn Arg Leu Gln Arg Thr Glu Val Glu Ser
 50 55 60

Val Glu Tyr Pro Thr Asp Leu Pro Asn Pro Ala Trp Thr Gly Pro Ala
 65 70 75 80

Ile	Ser	Trp	Pro	Leu	Lys	Asp	Pro	Ser	Ile	Asp	Phe	Pro	Asp	Pro	Leu
				85											
Pro	His	Ser	Ile	Ser	Glu	Leu	Pro	Pro	Gln	Ser	Asp	Asn	Pro	Arg	His
				100											
Leu	Arg	Val	Ser	Ile	Ser	Leu	Asp	Ala	Val	Glu	Gly	Ala	Phe	Pro	Arg
				115											
Tyr	Arg	Ile	Gly	Asp	Ser	Ile	Arg	Ile	Pro	Leu	Val	Phe	Ala	Arg	Asn
				130											
Thr	Pro	Phe	Met	Ser	Gly	Leu	Glu	Thr	Thr	Arg	Arg	Ala	Trp	Ile	Glu
				145											
Ala	Ala	Thr	Glu	Met	Asp	Ile	His	Asn	Thr	Trp	Pro	Ile	Ile	Leu	Thr
				165											
Gly	Asp	Gly	Trp	Thr	Ala	Leu	Ser	His	Ser	Asp	Lys	Pro	Ile	Arg	His
				180											
Glu	Ala	Glu	Leu	Lys	Gly	Trp	Phe	Phe	His	Ser	Leu	Phe	Gly	Ser	Glu
				195											
Met	Pro	Leu	Thr	Asp	Leu	Lys	Ile	Glu	Arg	Ile	Tyr	Gly	Gly	Leu	Gly
				210											
Thr	Phe	Asp	Ser	Gly	Ala	Thr	Arg	Trp	Gln	Glu	Leu	Thr	Asp	Thr	Asp
				225											
Asp	Ala	Tyr	Thr	Glu	Asn	Gly	Ser	Trp	Leu	Leu	Glu	Val	Ile	Val	Asp
				245											
Ala	Thr	Leu	Asp	Gly	Ala	Ile	Pro	Pro	Pro	Leu	Gln	Pro	Gln	Gln	Phe
				260											
Glu	Ala	Ser	Ile	Thr	His	Ile	Val	Asp	Glu	Gln	Leu	Trp	Val	Leu	Gly
				275											
Gln	Met	Leu	Pro	Val	Leu	Arg	Cys	Trp	Asp	Leu	Glu	Thr	Gly	Lys	Tyr
				290											
Leu	Gly	Gln	Thr	Tyr	Val	Pro	Ile	Ser	Val	Ser	His	Ser	Ser	Arg	Leu
				305											
Gln	Phe	Ser	Glu	Gly	Leu	Ile	His	Asp	Tyr	Glu	Asn	Ala	Trp	Ser	Leu
				325											
Asn	Pro	Gly	Val	Arg	Met	Leu	Ala	Glu	Pro	Gln	Pro	Trp	Ile	Glu	Pro
				340											
Val	Ile	Glu	Leu	Asp	Val	Pro	Ala	Pro	Trp	Glu	Leu	Gln	Glu	Ser	Phe
				355											
Pro	Asp	Gly	Leu	Tyr	Ser	Leu	Thr	Asp	Gly	Glu	Gln	Thr	Ala	Leu	Gly
				370											
Arg	Ser	Thr	Pro	Ala	Gly	Gln	Leu	Glu	Ile	Cys	Val	Ile	Ser	Asn	Asp
				385											
				390											
				395											
				400											

Gly Ser Arg Ile Leu Asn Ala Gly Arg Val Glu Asp Leu Tyr Phe Val
 405 410 415
 Gln Phe Trp Gly Met Thr Val Phe Leu Asn Ser Asn Phe Gln Val Gln
 420 425 430
 Ser Ala Glu Glu His Gln Leu Gly Ala Lys Arg Glu Arg Trp Ile Thr
 435 440 445
 Gln Glu Gly Val Ala Ala Lys Phe Thr Glu Glu Asp Glu Ile Val Phe
 450 455 460
 Leu Asp Gln Ile Ser Glu Ser Glu Ile Thr Arg Trp Lys Thr Pro Glu
 465 470 475 480
 Gly Tyr Phe Thr Glu Val Arg Ile Leu Ser Pro Asn His Phe Asn Ile
 485 490 495
 Leu Val Thr Pro Pro Thr Gly Ser Asp Tyr Leu Lys Pro Val Pro Ser
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 Ser Val Ser Val Phe Arg Asp Gly Gln Trp Ser Asn Ile Lys Phe Glu
 515 520 525
 Asp Val Ser Val Glu Ile
 530

<210> 1363
 <211> 1243
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1243)
 <223> FRXA01383

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 Met Asn Leu His Ser
 1 5
 tta gag att cgc caa att tca tcc gcc aca att tca gaa cga aaa act 163
 Leu Glu Ile Arg Gln Ile Ser Ser Gly Thr Ile Ser Glu Arg Lys Thr
 10 15 20
 tgg atc ttt ccc act gct gct cgc tca ttc aat caa aat cta gta cac 211
 Trp Ile Phe 25 Thr Ala Ala Arg Ser Phe Asn Gln Asn Leu Val His 35
 ccg caa agc att gaa atc gat gca caa acc gcc gtt att ttg gct atg 259
 Pro Gln Ser Ile Glu Ile Asp Ala Gln Thr Gly Val Ile Leu Ala Met
 40 45 50
 gaa aac cga cta caa cgt acc gaa gtt gaa tca gta gag tac cca acg 307
 Glu Asn Arg Leu Gln Arg Thr Glu Val Glu Ser Val Glu Tyr Pro Thr
 55 60 65

gat ctt cct aat cct gca tgg aca ggt cca gcc att tct tgg cca cta	355
Asp Leu Pro Asn Pro Ala Trp Thr Gly Pro Ala Ile Ser Trp Pro Leu	
70 75 80 85	
aaa gac cca tca atc gat ttc cct gac cgg ctc ccc cac agc att tcc	403
Lys Asp Pro Ser Ile Asp Phe Pro Asp Pro Leu Pro His Ser Ile Ser	
90 95 100	
gaa tta cca cct caa tcc gat aat cct cgg cat ttg cga gta tcc atc	451
Glu Leu Pro Pro Gln Ser Asp Asn Pro Arg His Leu Arg Val Ser Ile	
105 110 115	
agc tta gat gca gtg gaa ggt gct ttt cgg cgc tac cgg atc gga gat	499
Ser Leu Asp Ala Val Glu Gly Ala Phe Pro Arg Tyr Arg Ile Gly Asp	
120 125 130	
tca ata cgt att cgg ctt gtc ttt gcc cgg gac acg ccc ttc atg tcc	547
Ser Ile Arg Ile Pro Leu Val Phe Ala Arg Asp Thr Pro Phe Met Ser	
135 140 145	
ggc tta gaa aca aca cgt cgc gcc tgg att gag gcg gcc acg gaa atg	595
Gly Leu Glu Thr Thr Arg Arg Ala Trp Ile Glu Ala Ala Thr Glu Met	
150 155 160 165	
gac atc cat aac aca tgg ccc ata atc ctc acc ggt gac ggc tgg act	643
Asp Ile His Asn Thr Trp Pro Ile Ile Leu Thr Gly Asp Gly Trp Thr	
170 175 180	
gca ctc tct cat tca gac aaa cca ata cgc cac gaa gcc gag tta aag	691
Ala Leu Ser His Ser Asp Lys Pro Ile Arg His Glu Ala Glu Leu Lys	
185 190 195	
gga tgg ttt ttc cac agt ttg ttc gcc agt gaa atg ccc ttg act gat	739
Gly Trp Phe Phe His Ser Leu Phe Gly Ser Glu Met Pro Leu Thr Asp	
200 205 210	
ctg aag att gaa cga atc tac gga gcc ctg ggt act ttc gac agc gga	787
Leu Lys Ile Glu Arg Ile Tyr Gly Gly Leu Gly Thr Phe Asp Ser Gly	
215 220 225	
gcc acc cgg tgg caa gaa ctc aca gac aca gat gat gcc tac aca gaa	835
Ala Thr Arg Trp Gln Glu Leu Thr Asp Thr Asp Ala Tyr Thr Glu	
230 235 240 245	
aat ggc agc tgg ctg ttg gaa gtt atc gtc gat gcc acc ctt gac ggt	883
Asn Gly Ser Trp Leu Leu Glu Val Ile Val Asp Ala Thr Leu Asp Gly	
250 255 260	
gca att cca cca cca ctt cag cca caa cag ttt gaa gca tcc atc act	931
Ala Ile Pro Pro Pro Leu Gln Pro Gln Gln Phe Glu Ala Ser Ile Thr	
265 270 275	
cac atc gtc gat gag caa cta tgg gtc ctt ggg cag atg ctt cca gtt	979
His Ile Val Asp Glu Gln Leu Trp Val Leu Gly Gln Met Leu Pro Val	
280 285 290	
cta cga tgc tgg gat ctt gaa acc gga aaa tac ctg ggg caa acc tat	1027
Leu Arg Cys Trp Asp Leu Glu Thr Gly Lys Tyr Leu Gly Gln Thr Tyr	
295 300 305	
gta cct att tgg gtt tct cat agt tct cgg ctt cag ttt tgg gaa ggg	1075

Val Pro Ile Ser Val Ser His Ser Ser Arg Leu Gln Phe Ser Glu Gly
 310 315 320 325
 ttg att cac gat tat gaa aat gcc tgg tgc ctg aat cct ggg gtg cgc 1123
 Leu Ile His Asp Tyr Glu Asn Ala Trp Ser Leu Asn Pro Gly Val Arg
 330 335 340
 atg ctt gcg gag cca cag ccg tgg ata gag cct gtc att gaa ctc gac 1171
 Met Leu Ala Glu Pro Gln Pro Trp Ile Glu Pro Val Ile Glu Leu Asp
 345 350 355
 gtt cca gcg cca tgg gaa tta caa gaa agc ttc ccc gat ggg ctt tac 1219
 Val Pro Ala Pro Trp Glu Leu Gln Glu Ser Phe Pro Asp Gly Leu Tyr
 360 365 370
 ttc cta act gat ggc aag caa aca 1243
 Phe Leu Thr Asp Gly Lys Gln Thr
 375 380

 <210> 1364
 <211> 381
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 1364
 Met Asn Leu His Ser Leu Glu Ile Arg Gln Ile Ser Ser Gly Thr Ile
 1 5 10 15
 Ser Glu Arg Lys Thr Trp Ile Phe Pro Thr Ala Ala Arg Ser Phe Asn
 20 25 30
 Gln Asn Leu Val His Pro Gln Ser Ile Glu Ile Asp Ala Gln Thr Gly
 35 40 45
 Val Ile Leu Ala Met Glu Asn Arg Leu Gln Arg Thr Glu Val Glu Ser
 50 55 60
 Val Glu Tyr Pro Thr Asp Leu Pro Asn Pro Ala Trp Thr Gly Pro Ala
 65 70 75 80
 Ile Ser Trp Pro Leu Lys Asp Pro Ser Ile Asp Phe Pro Asp Pro Leu
 85 90 95
 Pro His Ser Ile Ser Glu Leu Pro Pro Gln Ser Asp Asn Pro Arg His
 100 105 110
 Leu Arg Val Ser Ile Ser Leu Asp Ala Val Glu Gly Ala Phe Pro Arg
 115 120 125
 Tyr Arg Ile Gly Asp Ser Ile Arg Ile Pro Leu Val Phe Ala Arg Asp
 130 135 140
 Thr Pro Phe Met Ser Gly Leu Glu Thr Thr Arg Arg Ala Trp Ile Glu
 145 150 155 160
 Ala Ala Thr Glu Met Asp Ile His Asn Thr Trp Pro Ile Ile Leu Thr
 165 170 175
 Gly Asp Gly Trp Thr Ala Leu Ser His Ser Asp Lys Pro Ile Arg His
 180 185 190

Glu Ala Glu Leu Lys Gly Trp Phe Phe His Ser Leu Phe Gly Ser Glu
 195 200 205
 Met Pro Leu Thr Asp Leu Lys Ile Glu Arg Ile Tyr Gly Gly Leu Gly
 210 215 220
 Thr Phe Asp Ser Gly Ala Thr Arg Trp Gln Glu Leu Thr Asp Thr Asp
 225 230 235 240
 Asp Ala Tyr Thr Glu Asn Gly Ser Trp Leu Leu Glu Val Ile Val Asp
 245 250 255
 Ala Thr Leu Asp Gly Ala Ile Pro Pro Pro Leu Gln Pro Gln Gln Phe
 260 265 270
 Glu Ala Ser Ile Thr His Ile Val Asp Glu Gln Leu Trp Val Leu Gly
 275 280 285
 Gln Met Leu Pro Val Leu Arg Cys Trp Asp Leu Glu Thr Gly Lys Tyr
 290 295 300
 Leu Gly Gln Thr Tyr Val Pro Ile Ser Val Ser His Ser Ser Arg Leu
 305 310 315 320
 Gln Phe Ser Glu Gly Leu Ile His Asp Tyr Glu Asn Ala Trp Ser Leu
 325 330 335
 Asn Pro Gly Val Arg Met Leu Ala Glu Pro Gln Pro Trp Ile Glu Pro
 340 345 350
 Val Ile Glu Leu Asp Val Pro Ala Pro Trp Glu Leu Gln Glu Ser Phe
 355 360 365
 Pro Asp Gly Leu Tyr Phe Leu Thr Asp Gly Lys Gln Thr
 370 375 380

<210> 1365

<211> 447

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(424)

<223> RXN02950

<400> 1365

tccgacctat ttcagcaatg ttttaataccg gtggaatcgt ttttattagg atgggtggat 60

 acctatcttt agtgagccgt actagcgaga aagctgcccc atg act gtt ttc aat 115
 Met Thr Val Phe Asn
 1 5

 gtt ctc cat gac gca ccc gca cca cag ccg gat aaa aac cgc ccc ggt 163
 Val Leu His Asp Ala Pro Ala Pro Gln Pro Asp Lys Asn Arg Pro Gly
 10 15 20

 gtc aaa cgt ctc ctc caa ggt gat ggc gca aac ctc atc gcc ttc act 211
 Val Lys Arg Leu Leu Gln Gly Asp Gly Ala Asn Leu Ile Ala Phe Thr

```

                25                      30                      35
ttc agc cct gga cag tca ctt ccc gac cac cgc gcc gca cat ccc atc 259
Phe Ser Pro Gly Gln Ser Leu Pro Asp His Arg Ala Ala His Pro Ile
          40                      45                      50

acc gtg acc gca ttt tct ggc cag ctc acc ttc agc tat ggc gag gaa 307
Thr Val Thr Ala Phe Ser Gly Gln Leu Thr Phe Ser Tyr Gly Glu Glu
          55                      60                      65

acc ttt gag ctc tcc ccc ggt gtg aca gtg cac ttg gaa gca gga gtt 355
Thr Phe Glu Leu Ser Pro Gly Val Thr Val His Leu Glu Ala Gly Val
          70                      75                      80                      85

acc cac cgc gtg gac tgc ccg cca gaa gca cca ggc gat gca agt aat 403
Thr His Arg Val Asp Cys Pro Pro Glu Ala Pro Gly Asp Ala Ser Asn
          90                      95                      100

gct gtt aac tat gct cac tgg tgaaaaaacac tcagtcaacc agg 447
Ala Val Asn Tyr Ala His Trp
          105

```

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<210> 1366
<211> 108
<212> PRT
<213> Corynebacterium glutamicum

<400> 1366
Met Thr Val Phe Asn Val Leu His Asp Ala Pro Ala Pro Gln Pro Asp
 1          5          10          15

Lys Asn Arg Pro Gly Val Lys Arg Leu Leu Gln Gly Asp Gly Ala Asn
          20          25          30

Leu Ile Ala Phe Thr Phe Ser Pro Gly Gln Ser Leu Pro Asp His Arg
          35          40          45

Ala Ala His Pro Ile Thr Val Thr Ala Phe Ser Gly Gln Leu Thr Phe
          50          55          60

Ser Tyr Gly Glu Glu Thr Phe Glu Leu Ser Pro Gly Val Thr Val His
          65          70          75          80

Leu Glu Ala Gly Val Thr His Arg Val Asp Cys Pro Pro Glu Ala Pro
          85          90          95

Gly Asp Ala Ser Asn Ala Val Asn Tyr Ala His Trp
          100          105

```

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<210> 1367
<211> 732
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(709)
<223> RXN02951

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<400> 1367
gataatgagt cagaaaatga aggtagcact acttgctgga ttaattttca aggttttctt 60
tcagaaatta atccatagcc gatatttaag gtgagaacac atg agc tcc acg ctc 115
Met Ser Ser Thr Leu
1 5
gca cga aaa gct tca ggc gac ggt tcc gaa aag aag aag cct ggc ttg 163
Ala Arg Lys Ala Ser Gly Asp Gly Ser Glu Lys Lys Lys Pro Gly Leu
10 15 20
ttt aga cgt gcg ctt cgt ttc ctc acc cac cca cct cac aaa cag gta 211
Phe Arg Arg Ala Leu Arg Phe Leu Thr His Pro Pro His Lys Gln Val
25 30 35
gac aac agc ctt gcg gat atc cgt gaa gga tta ggc ctc ggg gtg gac 259
Asp Asn Ser Ser Leu Ala Asp Ile Arg Glu Gly Leu Gly Val Asp
40 45 50
gat tcc cac gaa gga tcc aaa ccc agc aac gat cat tct ttg ctg cat 307
Asp Ser His Glu Gly Ser Lys Pro Ser Asn Asp His Ser Leu Leu His
55 60 65
gaa aag cct gaa att tcc gtc atg ccg acc gaa tca atg gca cgg ctg 355
Glu Lys Pro Glu Ile Ser Val Met Pro Thr Glu Ser Met Ala Arg Leu
70 75 80 85
atc ttt tat gcg cct gat atg gat ggg caa aca gac ccc ggt gaa gta 403
Ile Phe Tyr Ala Pro Asp Met Asp Gly Gln Thr Asp Pro Gly Glu Val
90 95 100
gtg tgg att tgg gca cca gcc gat ggc ccc cag caa cca ccc cgt aaa 451
Val Trp Ile Trp Ala Pro Ala Asp Gly Pro Gln Gln Pro Pro Arg Lys
105 110 115
cgt gcc atc gtt gtt gtt gga aga aac cga aac gcc att tta ggt ctg 499
Arg Ala Ile Val Val Val Gly Arg Asn Arg Asn Ala Ile Leu Gly Leu
120 125 130
ctc att tcc tgc aac ccc gag cac cgc act gat gaa gac tgg atc gac 547
Leu Ile Ser Cys Asn Pro Glu His Arg Thr Asp Glu Asp Trp Ile Asp
135 140 145
att gga tct ggc agc tgg gac cct cga ggt cgc caa agt tgg gta cga 595
Ile Gly Ser Gly Ser Trp Asp Pro Arg Gly Arg Gln Ser Trp Val Arg
150 155 160 165
ctc gac cgc gtt ctg gag gta ccc gaa ttg ggt atc cgg cgc caa gga 643
Leu Asp Arg Val Leu Glu Val Pro Glu Leu Gly Ile Arg Arg Gln Gly
170 175 180
aca gtc gtc ccc ccg ggg cgc ttt gag cgt atc gcc aac cgc ctc cgc 691
Thr Val Val Pro Pro Gly Arg Phe Glu Arg Ile Ala Asn Arg Leu Arg
185 190 195
aac gat ttc aac tgg gtc taacatttat ttggttaattg ggc 732
Asn Asp Phe Asn Trp Val
200

<210> 1368

<211> 203

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1368

Met Ser Ser Thr Leu Ala Arg Lys Ala Ser Gly Asp Gly Ser Glu Lys
 1 5 10 15

Lys Lys Pro Gly Leu Phe Arg Arg Ala Leu Arg Phe Leu Thr His Pro
 20 25 30

Pro His Lys Gln Val Asp Asn Ser Leu Ala Asp Ile Arg Glu Gly Leu
 35 40 45

Gly Leu Gly Val Asp Asp Ser His Glu Gly Ser Lys Pro Ser Asn Asp
 50 55 60

His Ser Leu Leu His Glu Lys Pro Glu Ile Ser Val Met Pro Thr Glu
 65 70 75 80

Ser Met Ala Arg Leu Ile Phe Tyr Ala Pro Asp Met Asp Gly Gln Thr
 85 90 95

Asp Pro Gly Glu Val Val Trp Ile Trp Ala Pro Ala Asp Gly Pro Gln
 100 105 110

Gln Pro Pro Arg Lys Arg Ala Ile Val Val Val Gly Arg Asn Arg Asn
 115 120 125

Ala Ile Leu Gly Leu Leu Ile Ser Cys Asn Pro Glu His Arg Thr Asp
 130 135 140

Glu Asp Trp Ile Asp Ile Gly Ser Gly Ser Trp Asp Pro Arg Gly Arg
 145 150 155 160

Gln Ser Trp Val Arg Leu Asp Arg Val Leu Glu Val Pro Glu Leu Gly
 165 170 175

Ile Arg Arg Gln Gly Thr Val Val Pro Gly Arg Phe Glu Arg Ile
 180 185 190

Ala Asn Arg Leu Arg Asn Asp Phe Asn Trp Val
 195 200

<210> 1369

<211> 414

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(391)

<223> RXN02957

<400> 1369

gcacgtctatt gcgcgtccggg tgggagattc tgtcgtccat gccgcggttg tgggtggcgca 60

atgactgcgc cccgggcacg gaatggctcc gggtcaccaa atg caa act gcc caa 115
 Met Gln Thr Ala Gln
 1 5

gga gga agg gtc tac acc tca ctg atg gac gag aag tcc ctt tcc ccg 163
 Gly Gly Arg Val Tyr Thr Ser Leu Met Asp Glu Lys Ser Leu Ser Pro
 10 15 20

ttg atc ggt ctg ccg ggt cgg gag aac atc ggc ctg gcc cga cac tgg 211
 Leu Ile Gly Leu Pro Gly Arg Glu Asn Ile Gly Leu Gly Arg His Trp
 25 30 35

cac ggt ctg tgg acg atg ttg cgg gtg ctc aac ggc atc gtc tac gtc 259
 His Gly Leu Ser Thr Met Leu Arg Val Leu Asn Gly Ile Val Tyr Val
 40 45 50

gtt ctg ctg ttc gcc acc ggg ctg tgg caa gcc att atc ccc acc tcc 307
 Val Leu Leu Phe Ala Thr Gly Leu Trp Gln Gly Ile Ile Pro Thr Ser
 55 60 65

tgg gac gtc ttc ccc gag gcg tgg gag aca ttg aag gtt tac ctg gcc 355
 Trp Asp Val Phe Pro Glu Ala Trp Glu Thr Leu Lys Val Tyr Leu Gly
 70 75 80 85

ttt cgt gcc cca gcc atc gag cac ttc acc ccc cta tgacgccttg 401
 Phe Arg Ala Pro Gly Ile Glu His Phe Thr Pro Leu
 90 95

caaatgctgg gct 414

<210> 1370

<211> 97

<212> PRT

<213> Corynebacterium glutamicum

<400> 1370

Met Gln Thr Ala Gln Gly Gly Arg Val Tyr Thr Ser Leu Met Asp Glu
 1 5 10 15

Lys Ser Leu Ser Pro Leu Ile Gly Leu Pro Gly Arg Glu Asn Ile Gly
 20 25 30

Leu Gly Arg His Trp His Gly Leu Ser Thr Met Leu Arg Val Leu Asn
 35 40 45

Gly Ile Val Tyr Val Val Leu Leu Phe Ala Thr Gly Leu Trp Gln Gly
 50 55 60

Ile Ile Pro Thr Ser Trp Asp Val Phe Pro Glu Ala Trp Glu Thr Leu
 65 70 75 80

Lys Val Tyr Leu Gly Phe Arg Ala Pro Gly Ile Glu His Phe Thr Pro
 85 90 95

Leu

<210> 1371

<211> 441

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(418)

<223> RXN02967

<400> 1371

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ttccggttga	gcgggcaatc	agtggcgcgc	cggggaggat	atg	gat	ctg	ttg	gtc	115
				Met	Asp	Leu	Leu	Val	
				1				5	

gtt	gcc	gtg	cat	gag	ggg	gga	cag	cca	cgt	cag	tcc	gat	tgc	aat	gcc	163
Val	Ala	Val	His	Glu	Gly	Gly	Gln	Pro	Arg	Gln	Ser	Asp	Cys	Asn	Ala	
			10					15						20		

ccc	ggc	tgc	gcc	cat	acc	tgg	ctt	tgt	gcc	atc	aac	ttc	cag	ttg	ggc	211
Pro	Gly	Cys	Ala	His	Thr	Trp	Leu	Cys	Ala	Ile	Asn	Phe	Gln	Leu	Gly	
			25					30					35			

gca	ggc	gtg	gtg	gag	ggc	ggc	gtc	gag	aag	cga	aat	gtc	ttt	ttc	ggg	259
Ala	Gly	Val	Val	Glu	Gly	Gly	Val	Glu	Lys	Arg	Asn	Val	Phe	Phe	Gly	
		40					45					50				

ggc	acc	ttt	ttg	ggg	ccc	gaa	tac	ggg	ggc	cgc	gcc	ctg	cgg	gcc	ggg	307
Gly	Thr	Phe	Leu	Gly	Pro	Glu	Tyr	Gly	Gly	Arg	Ala	Leu	Arg	Ala	Gly	
		55				60				65						

ggc	ggg	ggc	gtc	gac	atc	ggg	gag	cag	gat	cca	ttc	gac	ggc	ggc	tgc	355
Gly	Gly	Gly	Val	Asp	Ile	Gly	Glu	Gln	Asp	Pro	Phe	Asp	Gly	Gly	Cys	
	70				75					80					85	

ggg	gat	gtt	gag	ttc	ggc	ggg	atc	gat	gta	atc	gag	gtt	gat	gag	gtc	403
Gly	Asp	Val	Glu	Phe	Gly	Gly	Ile	Asp	Val	Ile	Glu	Val	Asp	Glu	Val	
				90					95					100		

ggc	gcc	acc	ggg	tgc	tagtgcgtag	ccctctttgt	tgc									441
Gly	Ala	Thr	Gly	Ser												
			105													

<210> 1372

<211> 106

<212> PRT

<213> Corynebacterium glutamicum

<400> 1372

Met	Asp	Leu	Leu	Val	Val	Ala	Val	His	Glu	Gly	Gly	Gln	Pro	Arg	Gln
1				5					10					15	

Ser	Asp	Cys	Asn	Ala	Pro	Gly	Cys	Ala	His	Thr	Trp	Leu	Cys	Ala	Ile
			20						25					30	

Asn	Phe	Gln	Leu	Gly	Ala	Gly	Val	Val	Glu	Gly	Gly	Val	Glu	Lys	Arg
		35					40					45			

Asn	Val	Phe	Phe	Gly	Gly	Thr	Phe	Leu	Gly	Pro	Glu	Tyr	Gly	Gly	Arg
	50					55					60				

Ala	Leu	Arg	Ala	Gly	Gly	Gly	Gly	Val	Asp	Ile	Gly	Glu	Gln	Asp	Pro
65					70					75					80

Phe Asp Gly Gly Cys Gly Asp Val Glu Phe Gly Gly Ile Asp Val Ile
 85 90 95

Glu Val Asp Glu Val Gly Ala Thr Gly Ser
 100 105

<210> 1373

<211> 435

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(412)

<223> RXN02971

<400> 1373

ttctgtccg gattttcggg gaatacacgcg agggagaaac gtggcacgcc attcaagtgg 60

gaattcaaac ttaaggttat ctaaatcgct aaccattgcg ttg att gcc atc gtc 115
 Leu Ile Ala Ile Val
 1 5

gct ctc atc gtg gca ctt gtg gtg tgg ctt ttt aac cgt tca gat gat 163
 Ala Leu Ile Val Ala Leu Val Val Trp Leu Phe Asn Arg Ser Asp Asp
 10 15 20

tct ggc tcc acc acg acc acc tca caa gag tgc atc tcc gga aac ttg 211
 Ser Gly Ser Thr Thr Thr Thr Ser Gln Glu Cys Ile Ser Gly Asn Leu
 25 30 35

agt ctg ccc gtt ggt ggc gat tcc acc gca gcc gaa gaa tta gtg aac 259
 Ser Leu Pro Val Gly Gly Asp Ser Thr Ala Ala Glu Glu Leu Val Asn
 40 45 50

aaa ttt aat gac tca tca cct gtc agc cgt gat ttc tgt gtt gag gcg 307
 Lys Phe Asn Asp Ser Ser Pro Val Ser Arg Asp Phe Cys Val Glu Ala
 55 60 65

gaa gct gtg gac ggt aac gtc ccc gct gcc acg tac ctg ttc gct ggt 355
 Glu Ala Val Asp Gly Asn Val Pro Ala Ala Thr Tyr Leu Phe Ala Gly
 70 75 80 85

tct cgt tct gat gct gcc acc gca ctt gct gaa acc ggt gcc gta gca 403
 Ser Arg Ser Asp Ala Ala Thr Ala Leu Ala Glu Thr Gly Ala Val Ala
 90 95 100

agc agc tct taaagctctt ggccctaggt tgg 435
 Ser Ser Ser

<210> 1374

<211> 104

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1374

Leu Ile Ala Ile Val Ala Leu Ile Val Ala Leu Val Val Trp Leu Phe

```

      1           5           10           15
Asn Arg Ser Asp Asp Ser Gly Ser Thr Thr Thr Ser Gln Glu Cys
      20           25           30
Ile Ser Gly Asn Leu Ser Leu Pro Val Gly Gly Asp Ser Thr Ala Ala
      35           40           45
Glu Glu Leu Val Asn Lys Phe Asn Asp Ser Ser Pro Val Ser Arg Asp
      50           55           60
Phe Cys Val Glu Ala Glu Ala Val Asp Gly Asn Val Pro Ala Ala Thr
      65           70           75           80
Tyr Leu Phe Ala Gly Ser Arg Ser Asp Ala Ala Thr Ala Leu Ala Glu
      85           90           95
Thr Gly Ala Val Ala Ser Ser Ser
      100

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<210> 1375

<211> 1632

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1609)

<223> RXN02978

<400> 1375

gcctcttaaa atcagacaat ttcagtgttg gaatagctac aagggtctac tgtaaacgaa 60

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gaacgctcga tagggctgtg tacctcaacy gaggtaaaac gtg att gat cga cct 115
                               Val Ile Asp Arg Pro
                               1           5

```

```

gta tgg ttg ttt gaa ctt tat aac acc gcg aaa gaa gta gta tat tcg 163
Val Trp Leu Phe Glu Leu Tyr Asn Thr Ala Lys Glu Val Val Tyr Ser
           10           15           20

```

```

cta ctc att gat caa gta act ggg gaa aat aca ata ctc aag aag gat 211
Leu Leu Ile Asp Gln Val Thr Gly Glu Asn Thr Ile Leu Lys Lys Asp
           25           30           35

```

```

gat ggt tgg cga gat caa ttc atg att gag tct ttc ttt gct tat gat 259
Asp Gly Trp Arg Asp Gln Phe Met Ile Glu Ser Phe Phe Ala Tyr Asp
           40           45           50

```

```

tca gaa gct gac gcg acc tcg tgg agc ggt aag aac atg aat agc tac 307
Ser Glu Ala Asp Ala Thr Ser Trp Ser Gly Lys Asn Met Asn Ser Tyr
           55           60           65

```

```

tgg ttc gtt agc gat cta atc agc aat ata tcc ttc gct gag cga tcc 355
Trp Phe Val Ser Asp Leu Ile Ser Asn Ile Ser Phe Ala Glu Arg Ser
           70           75           80           85

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ttg gaa agc ttt tct tgg gct ctt cga gat ctt gag gat ctt tct tct 403
Leu Glu Ser Phe Ser Trp Ala Leu Arg Asp Leu Glu Asp Leu Ser Ser
           90           95           100

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agt gaa act gaa ttt gaa ggg ctt gaa gag ctg aat cta aag ttt agt 451
 Ser Glu Thr Glu Phe Glu Gly Leu Glu Glu Leu Asn Leu Lys Phe Ser
 105 110 115

gag ctc caa gaa tgg tat acg aac ctg gaa ctt cct ttt cag ccg tcg 499
 Glu Leu Gln Glu Trp Tyr Thr Asn Leu Glu Leu Pro Phe Gln Pro Ser
 120 125 130

gct gct gat gtt gat gag gtg gag cag tat ctg caa gct gaa gtg aca 547
 Ala Ala Asp Val Asp Glu Val Glu Gln Tyr Leu Glu Ala Glu Val Thr
 135 140 145

agg caa cgg ggt gac tat caa tgg tct cct gag ttt tgg ata cca aag 595
 Arg Gln Arg Gly Asp Tyr Gln Trp Ser Pro Glu Phe Trp Ile Pro Lys
 150 155 160 165

ccg gat tca tac tat atc gac cat gca cta gcg gtt gtc aca gat gtt 643
 Pro Asp Ser Tyr Tyr Ile Asp His Ala Leu Ala Val Val Thr Asp Val
 170 175 180

ttg gga gct att gaa caa ggg gag ctg cgt gaa gaa gta gag gtg cag 691
 Leu Gly Ala Ile Glu Gln Gly Glu Leu Arg Glu Glu Val Glu Val Gln
 185 190 195

cag gct tta gac gag gta tct gaa aat tgg aat cct ttg gaa gat tct 739
 Gln Ala Leu Asp Glu Val Ser Glu Asn Trp Asn Pro Leu Glu Asp Ser
 200 205 210

gat tac tac tta cag gat cac cgt ggg cgc cct gta caa gat ctt tcc 787
 Asp Tyr Tyr Leu Gln Asp His Arg Gly Arg Pro Val Gln Asp Leu Ser
 215 220 225

cgg gaa atg gag gag ttg gtc aga tgt cta atg ctt gac caa gag tgg 835
 Arg Glu Met Glu Glu Leu Val Arg Cys Leu Met Leu Asp Gln Glu Trp
 230 235 240 245

tgg ggt gca gag gca agg att aga aag ctt gtt gaa tca gtt gag tgg 883
 Trp Gly Ala Glu Ala Arg Ile Arg Lys Leu Val Glu Ser Val Glu Trp
 250 255 260

gag gat act cag gcg atc agc tct tta att gaa cac gag caa tat tgg 931
 Glu Asp Thr Gln Ala Ile Ser Ser Leu Ile Glu His Glu Gln Tyr Trp
 265 270 275

gag gat ggt cgt ttt cgc cca cct cta cat aag ttt tcg gaa gga cta 979
 Glu Asp Gly Arg Phe Arg Pro Pro Leu His Lys Phe Ser Glu Gly Leu
 280 285 290

gac gag cca gag ccc ttg ccg atg acg aga aaa atg ata ctt gcg acg 1027
 Asp Glu Pro Glu Pro Leu Pro Met Thr Arg Lys Met Ile Leu Ala Thr
 295 300 305

aat cac cct gat gtt tta cgc gta aac att gct gat tat tat cag cag 1075
 Asn His Pro Asp Val Leu Arg Val Asn Ile Ala Asp Tyr Tyr Gln Gln
 310 315 320 325

cat agg cgc att gct act cag aag gtg gaa tgt tat aag gaa gtt ttg 1123
 His Arg Arg Ile Ala Thr Gln Lys Val Glu Cys Tyr Lys Glu Val Leu
 330 335 340

gca ttg tat cca gag att ctt aag aaa ttt gat gat tca tct ttc gtc 1171
 Ala Leu Tyr Pro Glu Ile Leu Lys Lys Phe Asp Asp Ser Ser Phe Val
 345 350 355

 aat cga cat tgg atc tat agg gcg ttt gat cgc gaa ggt cag ctt ttg 1219
 Asn Arg His Trp Ile Tyr Arg Ala Phe Asp Arg Glu Gly Gln Leu Leu
 360 365 370

 tat atc ggg gag aca ata aac cct ctt gta cgg ttg agg gag cat gcc 1267
 Tyr Ile Gly Glu Thr Ile Asn Pro Leu Val Arg Leu Arg Glu His Ala
 375 380 385

 ggc tta ggg tct att aac cac gca cat cat agg cta gta tgc ccg tgg 1315
 Gly Leu Gly Ser Ile Asn His Ala His His Arg Leu Val Ser Pro Trp
 390 395 400 405

 ttt tct acg atg gct aca ttt cat ctt gaa tct tgc ttt acc cag gct 1363
 Phe Ser Thr Met Ala Thr Phe His Leu Glu Ser Cys Phe Thr Gln Ala
 410 415 420

 gag gca aaa gag aag gag gct tta tat att aag ctg gaa cag cca aga 1411
 Glu Ala Lys Glu Lys Glu Ala Leu Tyr Ile Lys Leu Glu Gln Pro Arg
 425 430 435

 tat aat aag acg cat aat tct gct aga ttg gcg gtt tct gaa gaa ggg 1459
 Tyr Asn Lys Thr His Asn Ser Ala Arg Leu Ala Val Ser Glu Glu Gly
 440 445 450

 gtg ccg gtg aac gag gtg ccg tca aga aat gat ccg agg aat gtc ggt 1507
 Val Pro Val Asn Glu Val Pro Ser Arg Asn Asp Pro Arg Asn Val Gly
 455 460 465

 tgg aag ggt cat agg cac gtg cca cca atg ttg ccg att gtt gca cgt 1555
 Trp Lys Gly His Arg His Val Pro Pro Met Leu Pro Ile Val Ala Arg
 470 475 480 485

 gtt gtc gat gaa tgc aca aca cgt gag gga tat gcg ttt tac gag gac 1603
 Val Val Asp Glu Ser Thr Thr Arg Glu Gly Tyr Ala Phe Tyr Glu Asp
 490 495 500

 aac cgg tagcggttgcg atctctcggtg gaa 1632
 Asn Arg

<210> 1376

<211> 503

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1376

Val Ile Asp Arg Pro Val Trp Leu Phe Glu Leu Tyr Asn Thr Ala Lys
 1 5 10 15

Glu Val Val Tyr Ser Leu Leu Ile Asp Gln Val Thr Gly Glu Asn Thr
 20 25 30

Ile Leu Lys Lys Asp Asp Gly Trp Arg Asp Gln Phe Met Ile Glu Ser
 35 40 45

Phe Phe Ala Tyr Asp Ser Glu Ala Asp Ala Thr Ser Trp Ser Gly Lys

50										55										60																			
Asn	Met	Asn	Ser	Tyr	Trp	Phe	Val	Ser	Asp	Leu	Ile	Ser	Asn	Ile	Ser	65	70	75	80	Asn	Met	Asn	Ser	Tyr	Trp	Phe	Val	Ser	Asp	Leu	Ile	Ser	Asn	Ile	Ser	65	70	75	80
Phe	Ala	Glu	Arg	Ser	Leu	Glu	Ser	Phe	Ser	Trp	Ala	Leu	Arg	Asp	Leu	85	90	95		Phe	Ala	Glu	Arg	Ser	Leu	Glu	Ser	Phe	Ser	Trp	Ala	Leu	Arg	Asp	Leu	85	90	95	
Glu	Asp	Leu	Ser	Ser	Ser	Glu	Thr	Glu	Phe	Glu	Gly	Leu	Glu	Glu	Leu	100	105	110		Glu	Asp	Leu	Ser	Ser	Ser	Glu	Thr	Glu	Phe	Glu	Gly	Leu	Glu	Glu	Leu	100	105	110	
Asn	Leu	Lys	Phe	Ser	Glu	Leu	Gln	Glu	Trp	Tyr	Thr	Asn	Leu	Glu	Leu	115	120	125		Asn	Leu	Lys	Phe	Ser	Glu	Leu	Gln	Glu	Trp	Tyr	Thr	Asn	Leu	Glu	Leu	115	120	125	
Pro	Phe	Gln	Pro	Ser	Ala	Ala	Asp	Val	Asp	Glu	Val	Glu	Gln	Tyr	Leu	130	135	140		Pro	Phe	Gln	Pro	Ser	Ala	Ala	Asp	Val	Asp	Glu	Val	Glu	Gln	Tyr	Leu	130	135	140	
Gln	Ala	Glu	Val	Thr	Arg	Gln	Arg	Gly	Asp	Tyr	Gln	Trp	Ser	Pro	Glu	145	150	155	160	Gln	Ala	Glu	Val	Thr	Arg	Gln	Arg	Gly	Asp	Tyr	Gln	Trp	Ser	Pro	Glu	145	150	155	160
Phe	Trp	Ile	Pro	Lys	Pro	Asp	Ser	Tyr	Tyr	Ile	Asp	His	Ala	Leu	Ala	165	170	175		Phe	Trp	Ile	Pro	Lys	Pro	Asp	Ser	Tyr	Tyr	Ile	Asp	His	Ala	Leu	Ala	165	170	175	
Val	Val	Thr	Asp	Val	Leu	Gly	Ala	Ile	Glu	Gln	Gly	Glu	Leu	Arg	Glu	180	185	190		Val	Val	Thr	Asp	Val	Leu	Gly	Ala	Ile	Glu	Gln	Gly	Glu	Leu	Arg	Glu	180	185	190	
Glu	Val	Glu	Val	Gln	Gln	Ala	Leu	Asp	Glu	Val	Ser	Glu	Asn	Trp	Asn	195	200	205		Glu	Val	Glu	Val	Gln	Gln	Ala	Leu	Asp	Glu	Val	Ser	Glu	Asn	Trp	Asn	195	200	205	
Pro	Leu	Glu	Asp	Ser	Asp	Tyr	Tyr	Leu	Gln	Asp	His	Arg	Gly	Arg	Pro	210	215	220		Pro	Leu	Glu	Asp	Ser	Asp	Tyr	Tyr	Leu	Gln	Asp	His	Arg	Gly	Arg	Pro	210	215	220	
Val	Gln	Asp	Leu	Ser	Arg	Glu	Met	Glu	Glu	Leu	Val	Arg	Cys	Leu	Met	225	230	235	240	Val	Gln	Asp	Leu	Ser	Arg	Glu	Met	Glu	Glu	Leu	Val	Arg	Cys	Leu	Met	225	230	235	240
Leu	Asp	Gln	Glu	Trp	Trp	Gly	Ala	Glu	Ala	Arg	Ile	Arg	Lys	Leu	Val	245	250	255		Leu	Asp	Gln	Glu	Trp	Trp	Gly	Ala	Glu	Ala	Arg	Ile	Arg	Lys	Leu	Val	245	250	255	
Glu	Ser	Val	Glu	Trp	Glu	Asp	Thr	Gln	Ala	Ile	Ser	Ser	Leu	Ile	Glu	260	265	270		Glu	Ser	Val	Glu	Trp	Glu	Asp	Thr	Gln	Ala	Ile	Ser	Ser	Leu	Ile	Glu	260	265	270	
His	Glu	Gln	Tyr	Trp	Glu	Asp	Gly	Arg	Phe	Arg	Pro	Pro	Leu	His	Lys	275	280	285		His	Glu	Gln	Tyr	Trp	Glu	Asp	Gly	Arg	Phe	Arg	Pro	Pro	Leu	His	Lys	275	280	285	
Phe	Ser	Glu	Gly	Leu	Asp	Glu	Pro	Glu	Pro	Leu	Pro	Met	Thr	Arg	Lys	290	295	300		Phe	Ser	Glu	Gly	Leu	Asp	Glu	Pro	Glu	Pro	Leu	Pro	Met	Thr	Arg	Lys	290	295	300	
Met	Ile	Leu	Ala	Thr	Asn	His	Pro	Asp	Val	Leu	Arg	Val	Asn	Ile	Ala	305	310	315	320	Met	Ile	Leu	Ala	Thr	Asn	His	Pro	Asp	Val	Leu	Arg	Val	Asn	Ile	Ala	305	310	315	320
Asp	Tyr	Tyr	Gln	Gln	His	Arg	Arg	Ile	Ala	Thr	Gln	Lys	Val	Glu	Cys	325	330	335		Asp	Tyr	Tyr	Gln	Gln	His	Arg	Arg	Ile	Ala	Thr	Gln	Lys	Val	Glu	Cys	325	330	335	
Tyr	Lys	Glu	Val	Leu	Ala	Leu	Tyr	Pro	Glu	Ile	Leu	Lys	Lys	Phe	Asp	340	345	350		Tyr	Lys	Glu	Val	Leu	Ala	Leu	Tyr	Pro	Glu	Ile	Leu	Lys	Lys	Phe	Asp	340	345	350	
Asp	Ser	Ser	Phe	Val	Asn	Arg	His	Trp	Ile	Tyr	Arg	Ala	Phe	Asp	Arg	355	360	365		Asp	Ser	Ser	Phe	Val	Asn	Arg	His	Trp	Ile	Tyr	Arg	Ala	Phe	Asp	Arg	355	360	365	
Glu	Gly	Gln	Leu	Leu	Tyr	Ile	Gly	Glu	Thr	Ile	Asn	Pro	Leu	Val	Arg	370	375	380		Glu	Gly	Gln	Leu	Leu	Tyr	Ile	Gly	Glu	Thr	Ile	Asn	Pro	Leu	Val	Arg	370	375	380	

Leu Arg Glu His Ala Gly Leu Gly Ser Ile Asn His Ala His His Arg
385 390 395 400

Leu Val Ser Pro Trp Phe Ser Thr Met Ala Thr Phe His Leu Glu Ser
405 410 415

Cys Phe Thr Gln Ala Glu Ala Lys Glu Lys Glu Ala Leu Tyr Ile Lys
420 425 430

Leu Glu Gln Pro Arg Tyr Asn Lys Thr His Asn Ser Ala Arg Leu Ala
435 440 445

Val Ser Glu Glu Gly Val Pro Val Asn Glu Val Pro Ser Arg Asn Asp
450 455 460

Pro Arg Asn Val Gly Trp Lys Gly His Arg His Val Pro Pro Met Leu
465 470 475 480

Pro Ile Val Ala Arg Val Val Asp Glu Ser Thr Thr Arg Glu Gly Tyr
485 490 495

Ala Phe Tyr Glu Asp Asn Arg
500

<210> 1377

<211> 1689

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1666)

<223> RXN02995

<400> 1377

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tcgcgcaaca gggatacaat gagcaaccgt gacgcagcaa ttg aac cac gca aag 115
Leu Asn His Ala Lys
1 5

gta aat caa cat ccc ggt caa gcc acc ctc cca gaa acc gca gag ggg 163
Val Asn Gln His Pro Gly Gln Ala Thr Leu Pro Glu Thr Ala Glu Gly
10 15 20

cag gtt cgc acc tac gag gta aaa acc tac ggc tgt cag atg aat gtg 211
Gln Val Arg Thr Tyr Glu Val Lys Thr Tyr Gly Cys Gln Met Asn Val
25 30 35

cac gat tct gag cgc ctt tcg ggc ctg ctc gag gag gct gga tac gtt 259
His Asp Ser Glu Arg Leu Ser Gly Leu Leu Glu Glu Ala Gly Tyr Val
40 45 50

gct gct ccg gag gac acc act ccg gat ctt gtc gta ttt aat acg tgc 307
Ala Ala Pro Glu Asp Thr Thr Pro Asp Leu Val Val Phe Asn Thr Cys
55 60 65

gcc gtg cgt gaa aac gcc gat atg cgc ctc tat ggc act ttg ggc aac 355
Ala Val Arg Glu Asn Ala Asp Met Arg Leu Tyr Gly Thr Leu Gly Asn

70	75	80	85	
ctg cgc agc gtg aaa gaa aag aac cca ggc atg caa atc gct gtc ggt				403
Leu Arg Ser Val Lys 90	Glu Lys Asn Pro Gly 95	Met Gln Ile Ala Val 100	Lys Gly	
ggt tgt ttg gct caa aaa gac aaa gat acc gtg gtg aaa aaa gca ccg				451
Gly Cys Leu Ala Gln Lys Asp Lys 105	Asp Thr Val Val Lys Lys 110	Ala Pro		
tgg gtg gac gtg gtg ttt ggt acc cac aac att ggt tcc ttg cca acc				499
Trp Val Asp Val Val Phe Gly Thr 120	His Asn Ile Gly Ser Leu Pro Thr 125			
ttg ctt cag cgc gcg gag cac aat gcc caa gcg gaa gtc gaa att gtc				547
Leu Leu Gln Arg Ala Glu His Asn Ala Gln Ala Glu Val Glu Ile Val 135				
gat tcc ctc gag cag ttc ccg tca gta ctt cct gca aag cgc gag tct				595
Asp Ser Leu Glu Gln Phe 150	Pro Ser Val Leu Pro Ala Lys Arg Glu Ser 155			
gct tac gct ggt tgg gtg tcc gta tca gtc gga tgt aac aac acc tgt				643
Ala Tyr Ala Gly Trp Val Ser Val Ser Val Gly Cys Asn Asn Thr Cys 170				
act ttc tgc atc gtt ccg tgc ctg cgc ggt aaa gag cag gac cgt cga				691
Thr Phe Cys Ile Val Pro Ser Leu Arg Gly Lys Glu Gln Asp Arg Arg 185				
cca gga gac atc ctc gca gag gta caa gca ctg gtg gat cag gga gtt				739
Pro Gly Asp Ile Leu Ala Glu Val Gln Ala Leu Val Asp Gln Gly Val 200				
acc gag gta act cta ctt ggc caa aac gta aat gct tac ggc gtg aac				787
Thr Glu Val Thr Leu Leu Gly 215	Gln Asn Val Asn Ala Tyr Gly Val Asn 220			
ttt gtt gat cct gag cta gag cgc gat cgc agt gca ttt tcc aag ctg				835
Phe Val Asp Pro Glu Leu Glu Arg Asp Arg Ser Ala Phe Ser Lys Leu 230				
ctt cgt gcc tgt ggt gag atc gaa gcc ctc gag cgg gtt cgc ttc acc				883
Leu Arg Ala Cys Gly Glu Ile Glu Gly Leu Glu Arg Val Arg Phe Thr 250				
agc cct cac cct gca gaa ttc acc tct gat gtc att gac gcc atg gca				931
Ser Pro His Pro Ala Glu Phe Thr Ser Asp Val Ile Asp Ala Met Ala 265				
gag acc cca aac atc tgc ccg cag ctg cac atg cca ctg cag tcc gga				979
Glu Thr Pro Asn Ile Cys Pro Gln Leu His Met Pro Leu Gln Ser Gly 280				
tct gac aag gtg ctc aaa gag atg cgc cgt tcc tac cga tcc aag aag				1027
Ser Asp Lys Val Leu Lys 295	Glu Met Arg Arg Ser Tyr Arg Ser Lys Lys 300			
ttc ctc tcc atc ttg gat gag gtc cgt gcg aag atc cct cac gcc tct				1075
Phe Leu Ser Ile Leu Asp 310	Glu Val Arg Ala Lys 315	Ile Pro His Ala Ser 320		

atc acc acc gat att att gtc gga ttc cct ggc gaa aca gag gag gat 1123
 Ile Thr Thr Asp Ile Ile Val Gly Phe Pro Gly Glu Thr Glu Glu Asp
 330 335 340

ttc caa gca acc ctc gac gtt gtc aag aag gca cgc ttt act tct gct 1171
 Phe Gln Ala Thr Leu Asp Val Val Lys Lys Ala Arg Phe Thr Ser Ala
 345 350 355

tac acc ttc caa tac agc cca cgc cct ggc acc cct gca gcg gaa tat 1219
 Tyr Thr Phe Gln Tyr Ser Pro Arg Pro Gly Thr Pro Ala Ala Glu Tyr
 360 365 370

gaa aac cag ctt cca aaa gaa gtt gtg cag gaa cgc tac gag cgc ctc 1267
 Glu Asn Gln Leu Pro Lys Glu Val Val Gln Glu Arg Tyr Glu Arg Leu
 375 380 385

atg gtc gtt cag gaa caa gtc tgc gaa gaa gaa aac caa aag ctc atc 1315
 Met Val Val Gln Glu Gln Val Cys Glu Glu Glu Asn Gln Lys Leu Ile
 390 395 400 405

ggc acc acc gtc gaa ttg ctg gtc cag gct ggc gga ggc cgc aag aac 1363
 Gly Thr Thr Val Glu Leu Leu Val Gln Ala Gly Gly Gly Arg Lys Asn
 410 415 420

gat gcc acc aag cgc atg agt ggt cgc gca cgc gat gga cgc ctc gtg 1411
 Asp Ala Thr Lys Arg Met Ser Gly Arg Ala Arg Asp Gly Arg Leu Val
 425 430 435

cac ttt gcg cca gag ggc gac att gat ggt gag atc cgc ccc ggc gat 1459
 His Phe Ala Pro Glu Gly Asp Ile Asp Gly Glu Ile Arg Pro Gly Asp
 440 445 450

ttt gtc act gtc acg gtg act gag gcc aag cct ttc ttc ctc atc gca 1507
 Phe Val Thr Val Thr Val Thr Glu Ala Lys Pro Phe Phe Leu Ile Ala
 455 460 465

gac tcc ggt gtg cag acc cac cgc cgc acc aaa gct ggt gac aac tct 1555
 Asp Ser Gly Val Gln Thr His Arg Arg Thr Lys Ala Gly Asp Asn Ser
 470 475 480 485

gca gtt ggt caa gtt cca acc aca gca ccg atc ggt gtg ggc ttg gga 1603
 Ala Val Gly Gln Val Pro Thr Thr Ala Pro Ile Gly Val Gly Leu Gly
 490 495 500

ctg cca caa atc ggc gca cca aag gtg gct cct gcc aca gaa tct gcc 1651
 Leu Pro Gln Ile Gly Ala Pro Lys Val Ala Pro Ala Thr Glu Ser Ala
 505 510 515

tgc tgc tcc att aac taaaaattgc aggctagaat aga 1689
 Cys Cys Ser Ile Asn
 520

<210> 1378

<211> 522

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1378

Leu Asn His Ala Lys Val Asn Gln His Pro Gly Gln Ala Thr Leu Pro

1	5	10	15
Glu Thr Ala	Glu Gly Gln Val Arg	Thr Tyr Glu Val Lys	Thr Tyr Gly
	20	25	30
Cys Gln Met	Asn Val His Asp Ser	Glu Arg Leu Ser Gly	Leu Leu Glu
	35	40	45
Glu Ala Gly	Tyr Val Ala Ala	Pro Glu Asp Thr Thr	Pro Asp Leu Val
	50	55	60
Val Phe Asn	Thr Cys Ala Val Arg	Glu Asn Ala Asp	Met Arg Leu Tyr
	65	70	75
Gly Thr Leu	Gly Asn Leu Arg	Ser Val Lys Glu Lys	Asn Pro Gly Met
	85	90	95
Gln Ile Ala	Val Gly Gly Cys Leu Ala	Gln Lys Asp Lys Asp	Thr Val
	100	105	110
Val Lys Lys	Ala Pro Trp Val Asp	Val Val Phe Gly Thr	His Asn Ile
	115	120	125
Gly Ser Leu	Pro Thr Leu Leu	Gln Arg Ala Glu His	Asn Ala Gln Ala
	130	135	140
Glu Val Glu	Ile Val Asp Ser Leu Glu	Gln Phe Pro Ser Val	Leu Pro
	145	150	155
Ala Lys Arg	Glu Ser Ala Tyr Ala Gly	Trp Val Ser Val Ser	Val Gly
	165	170	175
Cys Asn Asn	Thr Cys Thr Phe Cys	Ile Val Pro Ser Leu	Arg Gly Lys
	180	185	190
Glu Gln Asp	Arg Arg Pro Gly Asp	Ile Leu Ala Glu Val	Gln Ala Leu
	195	200	205
Val Asp Gln	Gly Val Thr Glu Val Thr	Leu Leu Gly Gln	Asn Val Asn
	210	215	220
Ala Tyr Gly	Val Asn Phe Val Asp	Pro Glu Leu Glu Arg	Asp Arg Ser
	225	230	235
Ala Phe Ser	Lys Leu Leu Arg Ala Cys	Gly Glu Ile Glu Gly	Leu Glu
	245	250	255
Arg Val Arg	Phe Thr Ser Pro His	Pro Ala Glu Phe Thr	Ser Asp Val
	260	265	270
Ile Asp Ala	Met Ala Glu Thr Pro	Asn Ile Cys Pro Gln	Leu His Met
	275	280	285
Pro Leu Gln	Ser Gly Ser Asp Lys	Val Leu Lys Glu Met	Arg Arg Ser
	290	295	300
Tyr Arg Ser	Lys Lys Phe Leu Ser	Ile Leu Asp Glu Val	Arg Ala Lys
	305	310	315
Ile Pro His	Ala Ser Ile Thr Thr	Asp Ile Ile Val Gly	Phe Pro Gly
	325	330	335

Glu Thr Glu Glu Asp Phe Gln Ala Thr Leu Asp Val Val Lys Lys Ala
340 345 350

Arg Phe Thr Ser Ala Tyr Thr Phe Gln Tyr Ser Pro Arg Pro Gly Thr
355 360 365

Pro Ala Ala Glu Tyr Glu Asn Gln Leu Pro Lys Glu Val Val Gln Glu
370 375 380

Arg Tyr Glu Arg Leu Met Val Val Gln Glu Gln Val Cys Glu Glu Glu
385 390 395 400

Asn Gln Lys Leu Ile Gly Thr Thr Val Glu Leu Leu Val Gln Ala Gly
405 410 415

Gly Gly Arg Lys Asn Asp Ala Thr Lys Arg Met Ser Gly Arg Ala Arg
420 425 430

Asp Gly Arg Leu Val His Phe Ala Pro Glu Gly Asp Ile Asp Gly Glu
435 440 445

Ile Arg Pro Gly Asp Phe Val Thr Val Thr Val Thr Glu Ala Lys Pro
450 455 460

Phe Phe Leu Ile Ala Asp Ser Gly Val Gln Thr His Arg Arg Thr Lys
465 470 475 480

Ala Gly Asp Asn Ser Ala Val Gly Gln Val Pro Thr Thr Ala Pro Ile
485 490 495

Gly Val Gly Leu Gly Leu Pro Gln Ile Gly Ala Pro Lys Val Ala Pro
500 505 510

Ala Thr Glu Ser Ala Cys Cys Ser Ile Asn
515 520

<210> 1379

<211> 752

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(729)

<223> RXN02997

<400> 1379

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Pro Leu Pro Gly Gln Pro Phe Glu Gly Glu Ala Leu Thr Leu Ile Asn
1 5 10 15

gcc ctc ctc cac cac gcc gaa aac gtc gca gcc tcc aac ccc tgg aag 96
Ala Leu Leu His His Ala Glu Asn Val Ala Ala Ser Asn Pro Trp Lys
20 25 30

cgc acc acc ttc cac acc gct cac atg cac cct cca ggg agt aat gcg 144
Arg Thr Thr Phe His Thr Ala His Met His Pro Pro Gly Ser Asn Ala
35 40 45

gat tgt gac tac tgc ctg gtg ctg caa cgc cgc gga tac gtt aaa gcc 192
 Asp Cys Asp Tyr Cys Leu Val Leu Gln Arg Arg Gly Tyr Val Lys Ala
 50 55 60

cac gaa gaa atc caa caa acc atc ccg ctt cct tca ggt gac tgg tcc 240
 His Glu Glu Ile Gln Thr Ile Pro Leu Pro Ser Gly Asp Trp Ser
 65 70 75 80

gct gga gaa ttc acc gtg gtg gac gtt gaa ggc acc gcc ttc cca agc 288
 Ala Gly Glu Phe Thr Val Val Asp Val Glu Gly Thr Ala Phe Pro Ser
 85 90 95

gcg ctg atc ccc agc atc gtg gaa ctc caa cac cgc gca gcc ctc gat 336
 Ala Leu Ile Pro Ser Ile Val Glu Leu Gln His Arg Ala Ala Leu Asp
 100 105 110

gtg ccc cac gga aac tta agt gtt gcg cct gca cag tgg gat gaa cac 384
 Val Pro His Gly Asn Leu Ser Val Ala Pro Ala Thr Asp Glu His
 115 120 125

cgc ttg gcg cag caa tct gaa aga atc ctt aaa aca gga acg aaa ctg 432
 Arg Leu Ala Gln Gln Ser Glu Arg Ile Leu Lys Thr Gly Thr Lys Leu
 130 135 140

ttc acc gta ctg ttt gcc gaa gga tcc aca gtc gct gcc atg tcc tcc 480
 Phe Thr Val Leu Phe Ala Glu Gly Ser Thr Val Ala Ala Met Ser Ser
 145 150 155 160

atc gcg att ccc cca ggc tcc aac cct gac atc gcc gaa cag gga ctg 528
 Ile Ala Ile Pro Pro Gly Ser Asn Pro Asp Ile Ala Glu Gln Gly Leu
 165 170 175

acc atc gtg cac cca gat ttc aga ggc cgt ggt ctt gga acc gct gtg 576
 Thr Ile Val His Pro Asp Phe Arg Gly Arg Gly Leu Gly Thr Ala Val
 180 185 190

aaa tta gcg gga ctg tca cta ctt tcg agg tgc cac cca gaa att caa 624
 Lys Leu Ala Gly Leu Ser Leu Leu Ser Arg Cys His Pro Glu Ile Gln
 195 200 205

cgc gta gcc acc tca aat gca gta gac aac cat gcg atg ctg gcg att 672
 Arg Val Ala Thr Ser Asn Ala Val Asp Asn His Ala Met Leu Ala Ile
 210 215 220

aac cgc tcc ata ggg gca aca gag atc gcc cga acc acc ctg tgg gag 720
 Asn Arg Ser Ile Gly Ala Thr Glu Ile Ala Arg Thr Thr Leu Trp Glu
 225 230 235 240

aag aaa ctc taggtgatgg aattcgagac caa 752
 Lys Lys Leu

<210> 1380

<211> 243

<212> PRT

<213> Corynebacterium glutamicum

<400> 1380

Pro Leu Pro Gly Gln Pro Phe Glu Gly Glu Ala Leu Thr Leu Ile Asn

1

5

10

15

Ala Leu Leu His His Ala Glu Asn Val Ala Ala Ser Asn Pro Trp Lys
 20 25 30
 Arg Thr Thr Phe His Thr Ala His Met His Pro Pro Gly Ser Asn Ala
 35 40 45
 Asp Cys Asp Tyr Cys Leu Val Leu Gln Arg Arg Gly Tyr Val Lys Ala
 50 55 60
 His Glu Glu Ile Gln Gln Thr Ile Pro Leu Pro Ser Gly Asp Trp Ser
 65 70 75 80
 Ala Gly Glu Phe Thr Val Val Asp Val Glu Gly Thr Ala Phe Pro Ser
 85 90 95
 Ala Leu Ile Pro Ser Ile Val Glu Leu Gln His Arg Ala Ala Leu Asp
 100 105 110
 Val Pro His Gly Asn Leu Ser Val Ala Pro Ala Gln Trp Asp Glu His
 115 120 125
 Arg Leu Ala Gln Gln Ser Glu Arg Ile Leu Lys Thr Gly Thr Lys Leu
 130 135 140
 Phe Thr Val Leu Phe Ala Glu Gly Ser Thr Val Ala Ala Met Ser Ser
 145 150 155 160
 Ile Ala Ile Pro Pro Gly Ser Asn Pro Asp Ile Ala Glu Gln Gly Leu
 165 170 175
 Thr Ile Val His Pro Asp Phe Arg Gly Arg Gly Leu Gly Thr Ala Val
 180 185 190
 Lys Leu Ala Gly Leu Ser Leu Leu Ser Arg Cys His Pro Glu Ile Gln
 195 200 205
 Arg Val Ala Thr Ser Asn Ala Val Asp Asn His Ala Met Leu Ala Ile
 210 215 220
 Asn Arg Ser Ile Gly Ala Thr Glu Ile Ala Arg Thr Thr Leu Trp Glu
 225 230 235 240
 Lys Lys Leu

<210> 1381

<211> 553

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(553)

<223> RXN03001

<400> 1381

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acgctacgac atctaactac tttaaaagga cgaaaaatatt atg gac tgg tta acc 115

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Met Asp Trp Leu Thr
1 5

att cct ctt ttc ctc gtt aat gaa atc ctt gcg gtt ccg gct ttc ctc 163
Ile Pro Leu Phe Leu Val Asn Glu Ile Leu Ala Val Pro Ala Phe Leu
10 15 20

atc ggt atc atc acc gcc gtg gga ttg ggt gcc atg ggg cgt tcc gtc 211
Ile Gly Ile Ile Thr Ala Val Gly Leu Gly Ala Met Gly Arg Ser Val
25 30 35

ggt cag gtt atc ggt gga gca atc aaa gca acg ttg ggc ttt ttg ctc 259
Gly Gln Val Ile Gly Gly Ala Ile Lys Ala Thr Leu Gly Phe Leu Leu
40 45 50

att ggt gcg ggt gcc acg ttg gtc act gcc tcc ctg gag cca ctg ggt 307
Ile Gly Ala Gly Ala Thr Leu Val Thr Ala Ser Leu Glu Pro Leu Gly
55 60 65

gcg atg atc atg ggt gcc aca gcc atg cgt ggt gtt gtc cca acg aat 355
Ala Met Ile Met Gly Ala Thr Gly Met Arg Gly Val Val Pro Thr Asn
70 75 80 85

gaa gcc atc gcc gga atc gca cag gct gaa tac gcc gcg cag gtg gcg 403
Glu Ala Ile Ala Gly Ile Ala Gln Ala Glu Tyr Gly Ala Gln Val Ala
90 95 100

tgg ctg atg att ctg gcc ttc gcc atc tct ttg gtg ttg gct cgt ttc 451
Trp Leu Met Ile Leu Gly Phe Ala Ile Ser Leu Val Leu Ala Arg Phe
105 110 115

acc aac ctg cgt tat gtc ttg ctc aac gga cac cac gtg ctg ttg atg 499
Thr Asn Leu Arg Tyr Val Leu Leu Asn Gly His His Val Leu Leu Met
120 125 130

tgc acc atg ctc acc atg gtc ttg gcc acc gga aga gtt gat gcg tgg 547
Cys Thr Met Leu Thr Met Val Leu Ala Thr Gly Arg Val Asp Ala Trp
135 140 145

atc ttc 553
Ile Phe
150

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<210> 1382

<211> 151

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1382

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Met Asp Trp Leu Thr Ile Pro Leu Phe Leu Val Asn Glu Ile Leu Ala
1 5 10 15

Val Pro Ala Phe Leu Ile Gly Ile Ile Thr Ala Val Gly Leu Gly Ala
20 25 30

Met Gly Arg Ser Val Gly Gln Val Ile Gly Gly Ala Ile Lys Ala Thr
35 40 45

Leu Gly Phe Leu Leu Ile Gly Ala Gly Ala Thr Leu Val Thr Ala Ser
50 55 60

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Leu Glu Pro Leu Gly Ala Met Ile Met Gly Ala Thr Gly Met Arg Gly
65 70 75 80

Val Val Pro Thr Asn Glu Ala Ile Ala Gly Ile Ala Gln Ala Glu Tyr
85 90 95

Gly Ala Gln Val Ala Trp Leu Met Ile Leu Gly Phe Ala Ile Ser Leu
100 105 110

Val Leu Ala Arg Phe Thr Asn Leu Arg Tyr Val Leu Leu Asn Gly His
115 120 125

His Val Leu Leu Met Cys Thr Met Leu Thr Met Val Leu Ala Thr Gly
130 135 140

Arg Val Asp Ala Trp Ile Phe
145 150

<210> 1383

<211> 891

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(868)

<223> RXN03005

<400> 1383

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taacaagcat cttcccactc tcgttacgg agtttctcac atg tct cac aag ttt 115
Met Ser His Lys Phe
1 5

tcc cgc cgt gct ttc gca gta ctg acc gct gcc gca att tcc act tcc 163
Ser Arg Arg Ala Phe Ala Val Leu Thr Ala Ala Ile Ser Thr Ser
10 15 20

gct ttc gca acc act gct ccg tct gcg att gca gag cca gtt cta atg 211
Ala Phe Ala Thr Thr Ala Pro Ser Ala Ile Ala Glu Pro Val Leu Met
25 30 35

tgc cac tgc aga cga ttc cag cgt cgc aac ttc aga aaa ctc cct cga 259
Ser His Cys Arg Arg Phe Gln Arg Arg Asn Phe Arg Lys Leu Pro Arg
40 45 50

ctg ggg ctt caa ggc ttc ctg gcg cac cta tgt cac cgg acc ttg gac 307
Leu Gly Leu Gln Gly Phe Leu Ala His Leu Cys His Arg Thr Leu Asp
55 60 65

tgg tgg aac cgt gac gca act ggc ggt gca act gtc aac gaa gat gga 355
Trp Trp Asn Arg Asp Ala Thr Gly Gly Ala Thr Val Asn Glu Asp Gly
70 75 80 85

acc tac aac ttc acc ctc gga act ggc tcc aat tac gac gtc gac acc 403
Thr Tyr Asn Phe Thr Leu Gly Thr Gly Ser Asn Tyr Asp Val Asp Thr
90 95 100

gag aag ggc cag ctg aac tac gaa gga act gtt gcc ttc gcc agt gac 451
 Glu Lys Gly Gln Leu Asn Tyr Glu Gly Thr Val Ala Phe Ala Ser Asp
 105 110 115

 gct cac ggc ttc aac atc acc ttg tcc aac ccg cag atc acc gtc gag 499
 Ala His Gly Phe Asn Ile Thr Leu Ser Asn Pro Gln Ile Thr Val Glu
 120 125 130

 ggc gac act gca act ttg agc gcc gag ctg tct gac aat gcc gct ccc 547
 Gly Asp Thr Ala Thr Leu Ser Ala Glu Leu Ser Asp Asn Ala Ala Pro
 135 140 145

 gaa gag acc tcc act act cgc gtt gat gtt gct gag ttc gaa ctg acc 595
 Glu Glu Thr Ser Thr Thr Arg Val Asp Val Ala Glu Phe Glu Leu Thr
 150 155 160 165

 gct cct gag gtt tca gaa acc gat gcg gac att acc tac acc tgg acc 643
 Ala Pro Glu Val Ser Glu Thr Asp Ala Asp Ile Thr Tyr Thr Trp Thr
 170 175 180

 gat gct tcc ggc act ttc ttg gag acc ctg cag cct gaa gaa ttg agc 691
 Asp Ala Ser Gly Thr Phe Leu Glu Thr Leu Gln Pro Glu Glu Leu Ser
 185 190 195

 cgt tac gca ggc cag gaa gcg gat gcg ctg agc ttc tcc atc acc gtg 739
 Arg Tyr Ala Gly Gln Glu Ala Asp Ala Leu Ser Phe Ser Ile Thr Val
 200 205 210

 gac aag gct tca gag aac cct tcc gat gat gtt gct acc gga tct tcc 787
 Asp Lys Ala Ser Glu Asn Pro Ser Asp Asp Val Ala Thr Gly Ser Ser
 215 220 225

 tcc agc ttc ctc tcc acc atc ttg aac ttc ctt cag cag ctg gcg agc 835
 Ser Ser Phe Leu Ser Thr Ile Leu Asn Phe Leu Gln Gln Leu Ala Ser
 230 235 240 245

 cca ctg ctc aag ctc ttc ggt tcg ctt tct tcc taaataatca gtaatgcccc 888
 Pro Leu Leu Lys Leu Phe Gly Ser Leu Ser Ser
 250 255

 acc 891

<210> 1384

<211> 256

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1384

Met Ser His Lys Phe Ser Arg Arg Ala Phe Ala Val Leu Thr Ala Ala
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Ala Ile Ser Thr Ser Ala Phe Ala Thr Thr Ala Pro Ser Ala Ile Ala
 20 25 30

Glu Pro Val Leu Met Ser His Cys Arg Arg Phe Gln Arg Arg Asn Phe
 35 40 45

Arg Lys Leu Pro Arg Leu Gly Leu Gln Gly Phe Leu Ala His Leu Cys
 50 55 60

His Arg Thr Leu Asp Trp Trp Asn Arg Asp Ala Thr Gly Gly Ala Thr
 65 70 75 80
 Val Asn Glu Asp Gly Thr Tyr Asn Phe Thr Leu Gly Thr Gly Ser Asn
 85 90 95
 Tyr Asp Val Asp Thr Glu Lys Gly Gln Leu Asn Tyr Glu Gly Thr Val
 100 105 110
 Ala Phe Ala Ser Asp Ala His Gly Phe Asn Ile Thr Leu Ser Asn Pro
 115 120 125
 Gln Ile Thr Val Glu Gly Asp Thr Ala Thr Leu Ser Ala Glu Leu Ser
 130 135 140
 Asp Asn Ala Ala Pro Glu Glu Thr Ser Thr Thr Arg Val Asp Val Ala
 145 150 155 160
 Glu Phe Glu Leu Thr Ala Pro Glu Val Ser Glu Thr Asp Ala Asp Ile
 165 170 175
 Thr Tyr Thr Trp Thr Asp Ala Ser Gly Thr Phe Leu Glu Thr Leu Gln
 180 185 190
 Pro Glu Glu Leu Ser Arg Tyr Ala Gly Gln Glu Ala Asp Ala Leu Ser
 195 200 205
 Phe Ser Ile Thr Val Asp Lys Ala Ser Glu Asn Pro Ser Asp Asp Val
 210 215 220
 Ala Thr Gly Ser Ser Ser Ser Phe Leu Ser Thr Ile Leu Asn Phe Leu
 225 230 235 240
 Gln Gln Leu Ala Ser Pro Leu Leu Lys Leu Phe Gly Ser Leu Ser Ser
 245 250 255

<210> 1385

<211> 448

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(448)

<223> RXN03009

<400> 1385

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accgtcatgg tttagogat caccgtttac cctgcactgc gtg gct aat atc gcc 115
 Val Ala Asn Ile Ala
 1 5

agc ttg tac gga ctg tgg gaa ggc agc aca tcc aca cca atc gaa cag 163
 Ser Leu Tyr Gly Leu Trp Glu Gly Ser Thr Ser Thr Pro Ile Glu Gln
 10 15 20

ctc gta cct gcg aaa ggt tcc agc ttt cgt ttg gtg agg tct ttt tac 211
 Leu Val Pro Ala Lys Gly Ser Ser Phe Arg Leu Val Arg Ser Phe Tyr
 25 30 35

agg cga att gac ggc caa gca gtt cag gct cgt ctc aag gag aag att 259
 Arg Arg Ile Asp Gly Gln Ala Val Gln Ala Arg Leu Lys Glu Lys Ile
 40 45 50

ctc aac acc gcg gaa aac ccg ctt cct cgc ttg gac att cca ggt aag 307
 Leu Asn Thr Ala Glu Asn Pro Leu Pro Arg Leu Asp Ile Pro Gly Lys
 55 60 65

gag cgc act gcg cag tac cca gaa aat ccg gat acc ttc gcc caa aaa 355
 Glu Arg Thr Ala Gln Tyr Pro Glu Asn Pro Asp Thr Phe Ala Gln Lys
 70 75 80 85

gca gct caa gaa att ctt gat gag ttc aga act cca ctg atc ggt gaa 403
 Ala Ala Gln Glu Ile Leu Asp Glu Phe Arg Thr Pro Leu Ile Gly Glu
 90 95 100

gaa gct gca gct cat gtt gag aaa acg aag acg att ttc tgg aag 448
 Glu Ala Ala Ala His Val Glu Lys Thr Lys Thr Ile Phe Trp Lys
 105 110 115

<210> 1386

<211> 116

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1386

Val Ala Asn Ile Ala Ser Leu Tyr Gly Leu Trp Glu Gly Ser Thr Ser
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Thr Pro Ile Glu Gln Leu Val Pro Ala Lys Gly Ser Ser Phe Arg Leu
 20 25 30

Val Arg Ser Phe Tyr Arg Arg Ile Asp Gly Gln Ala Val Gln Ala Arg
 35 40 45

Leu Lys Glu Lys Ile Leu Asn Thr Ala Glu Asn Pro Leu Pro Arg Leu
 50 55 60

Asp Ile Pro Gly Lys Glu Arg Thr Ala Gln Tyr Pro Glu Asn Pro Asp
 65 70 75 80

Thr Phe Ala Gln Lys Ala Ala Gln Glu Ile Leu Asp Glu Phe Arg Thr
 85 90 95

Pro Leu Ile Gly Glu Glu Ala Ala His Val Glu Lys Thr Lys Thr
 100 105 110

Ile Phe Trp Lys
 115

<210> 1387

<211> 360

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(337)

<223> RXN03010

<400> 1387

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cagcctggga ctcaatgcgt ggattacott cgggtcgcca gtg ccc acc gat aat 115
 Val Pro Thr Asp Asn
 1 5

ctt ttt ctc atc gtt gct gga att gcg tgg gtg ttg gca gga att ttg 163
 Leu Phe Leu Ile Val Ala Gly Ile Ala Trp Val Leu Ala Gly Ile Leu
 10 15 20

agc gtg ctg tcc atc ggc aag tac atg tca gca gta aat gag cga aag 211
 Ser Val Leu Ser Ile Gly Lys Tyr Met Ser Ala Val Asn Glu Arg Lys
 25 30 35

tgc aca ggc ttt tat aca gaa gtg cgg tgg aag aaa gcg ctc ttt act 259
 Ser Thr Gly Phe Tyr Thr Glu Val Pro Trp Lys Lys Ala Leu Phe Thr
 40 45 50

gcg aca gcc gtc cta ttg gtg ttt gct gtt gtg tgg tgg gcc ttg gat 307
 Ala Thr Ala Val Leu Leu Val Phe Ala Val Val Trp Ser Ala Leu Asp
 55 60 65

att gcc ctg tgg gta gga aag cag tca tgg tgaacacgtt gaactctaaa 357
 Ile Ala Leu Trp Val Gly Lys Gln Ser Trp
 70 75

acc 360

<210> 1388

<211> 79

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1388

Val Pro Thr Asp Asn Leu Phe Leu Ile Val Ala Gly Ile Ala Trp Val
 1 5 10 15

Leu Ala Gly Ile Leu Ser Val Leu Ser Ile Gly Lys Tyr Met Ser Ala
 20 25 30

Val Asn Glu Arg Lys Ser Thr Gly Phe Tyr Thr Glu Val Pro Trp Lys
 35 40 45

Lys Ala Leu Phe Thr Ala Thr Ala Val Leu Leu Val Phe Ala Val Val
 50 55 60

Trp Ser Ala Leu Asp Ile Ala Leu Trp Val Gly Lys Gln Ser Trp
 65 70 75

<210> 1389

<211> 324

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(301)

<223> RXN03011

<400> 1389

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atgaaaccaa ggggtaaaaa ctggtagtct cttocacgtc atg gca tac gaa act 115
 Met Ala Tyr Glu Thr
 1 5

gat tcc ctc aac cga cgc acc ctc ggg ccc gcg att gca agc gca gtc 163
 Asp Ser Leu Asn Arg Arg Thr Leu Gly Pro Ala Ile Ala Ser Ala Val
 10 15 20

gtg gga atc gcc gtc ggc gca gtc gca gta gtt ggg gtt tca atg atc 211
 Val Gly Ile Ala Val Gly Ala Val Ala Val Val Gly Val Ser Met Ile
 25 30 35

tca ggg cag gac act gtt ccc act ggt aac gcc gta act gca gac gat 259
 Ser Gly Gln Asp Thr Val Pro Thr Gly Asn Ala Val Thr Ala Asp Asp
 40 45 50

gcc ctg ctc ggt ggc cct gag tat ggt tca cgc gaa gca gac 301
 Ala Leu Leu Gly Gly Pro Glu Tyr Gly Ser Arg Glu Ala Asp
 55 60 65

taagaagcca cttcccgtt ttc 324

<210> 1390

<211> 67

<212> PRT

<213> Corynebacterium glutamicum

<400> 1390

Met Ala Tyr Glu Thr Asp Ser Leu Asn Arg Arg Thr Leu Gly Pro Ala
 1 5 10 15

Ile Ala Ser Ala Val Val Gly Ile Ala Val Gly Ala Val Ala Val Val
 20 25 30

Gly Val Ser Met Ile Ser Gly Gln Asp Thr Val Pro Thr Gly Asn Ala
 35 40 45

Val Thr Ala Asp Asp Ala Leu Leu Gly Gly Pro Glu Tyr Gly Ser Arg
 50 55 60

Glu Ala Asp
 65

<210> 1391

<211> 593

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(570)

<223> RXN03012

<400> 1391

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Thr	Thr	Ile	Asn	Ile	Ile	Ile	Thr	Asn	Gly	Ala	Ala	Pro	His	Pro	Thr	
1				5					10					15		

aat	ctc	aat	cgc	gca	gaa	att	cat	gat	cac	cta	ccc	ctc	act	gcc	tct	96
Asn	Leu	Asn	Arg	Ala	Glu	Ile	His	Asp	His	Leu	Pro	Leu	Thr	Ala	Ser	
			20					25					30			

gat	tcg	gag	cta	acc	cgc	ccc	tcc	cag	gaa	tca	gtt	ctc	tat	gac	cat	144
Asp	Ser	Glu	Leu	Thr	Arg	Pro	Ser	Gln	Glu	Ser	Val	Leu	Tyr	Asp	His	
		35				40						45				

gaa	tcc	gaa	act	gtc	ttg	cgc	acc	atg	gtc	atc	cct	gca	gac	ctg	cac	192
Glu	Ser	Glu	Thr	Val	Leu	Arg	Thr	Met	Val	Ile	Pro	Ala	Asp	Leu	His	
	50					55					60					

gtc	gct	atg	aag	cat	cta	gct	aaa	aaa	cac	aac	ctc	acg	gtc	aca	gag	240
Val	Ala	Met	Lys	His	Leu	Ala	Lys	Lys	His	Asn	Leu	Thr	Val	Thr	Glu	
65					70					75					80	

atc	tcg	cgc	atc	ctt	ctg	cag	cgc	tac	atc	gac	cgc	aat	att	aac	cat	288
Ile	Ser	Arg	Ile	Leu	Leu	Gln	Arg	Tyr	Ile	Asp	Arg	Asn	Ile	Asn	His	
				85					90					95		

gta	gag	caa	aac	cag	gct	gaa	tcc	gac	atg	gtg	gaa	gtc	ttt	gcc	agc	336
Val	Glu	Gln	Asn	Gln	Ala	Glu	Ser	Asp	Met	Val	Glu	Val	Phe	Ala	Ser	
			100					105					110			

caa	cca	acc	aat	gca	acc	gca	atg	atc	cct	gta	cct	gga	acc	agc	ttc	384
Gln	Pro	Thr	Asn	Ala	Thr	Ala	Met	Ile	Pro	Val	Pro	Gly	Thr	Ser	Phe	
			115				120					125				

agg	caa	ata	ttt	atc	aag	cac	agc	act	ggg	ttc	tgg	aaa	aac	att	gat	432
Arg	Gln	Ile	Phe	Ile	Lys	His	Ser	Thr	Gly	Phe	Trp	Lys	Asn	Ile	Asp	
	130					135					140					

cat	gat	ctt	gtc	gat	ctc	gac	gcc	tct	aag	acc	ccg	cgt	gta	cgc	gac	480
His	Asp	Leu	Val	Asp	Leu	Asp	Ala	Ser	Lys	Thr	Pro	Arg	Val	Arg	Asp	
145					150					155				160		

cgc	agt	gtc	tta	cca	caa	cct	caa	ctc	cac	aga	gcg	ttg	tta	tca	gat	528
Arg	Ser	Val	Leu	Pro	Gln	Pro	Gln	Leu	His	Arg	Ala	Leu	Leu	Ser	Asp	
			165					170						175		

gct	gat	atg	gct	cgc	ctt	gca	gca	caa	ctg	acc	gac	aaa	cac			570
Ala	Asp	Met	Ala	Arg	Leu	Ala	Ala	Gln	Leu	Thr	Asp	Lys	His			
			180					185					190			

taaaacctcc	acaacaagga	cat														593
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<210> 1392

<211> 190

<212> PRT

<213> Corynebacterium glutamicum

<400> 1392

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Thr Thr Ile Asn Ile Ile Ile Thr Asn Gly Ala Ala Pro His Pro Thr
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Asn Leu Asn Arg Ala Glu Ile His Asp His Leu Pro Leu Thr Ala Ser
          20          25          30
Asp Ser Glu Leu Thr Arg Pro Ser Gln Glu Ser Val Leu Tyr Asp His
          35          40          45
Glu Ser Glu Thr Val Leu Arg Thr Met Val Ile Pro Ala Asp Leu His
          50          55          60
Val Ala Met Lys His Leu Ala Lys Lys His Asn Leu Thr Val Thr Glu
          65          70          75          80
Ile Ser Arg Ile Leu Leu Gln Arg Tyr Ile Asp Arg Asn Ile Asn His
          85          90          95
Val Glu Gln Asn Gln Ala Glu Ser Asp Met Val Glu Val Phe Ala Ser
          100          105          110
Gln Pro Thr Asn Ala Thr Ala Met Ile Pro Val Pro Gly Thr Ser Phe
          115          120          125
Arg Gln Ile Phe Ile Lys His Ser Thr Gly Phe Trp Lys Asn Ile Asp
          130          135          140
His Asp Leu Val Asp Leu Asp Ala Ser Lys Thr Pro Arg Val Arg Asp
          145          150          155          160
Arg Ser Val Leu Pro Gln Pro Gln Leu His Arg Ala Leu Leu Ser Asp
          165          170          175
Ala Asp Met Ala Arg Leu Ala Ala Gln Leu Thr Asp Lys His
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<210> 1393

<211> 1662

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1639)

<223> RXN03017

<400> 1393

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                                     Met Leu Asp Ser Leu
                                     1          5

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aaa aat cgc ttc acc aaa gcg aaa ggt tct cat gga gtg ggg gag ggg 163
Lys Asn Arg Phe Thr Lys Ala Lys Gly Ser His Gly Val Gly Glu Gly
          10          15          20

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gct gtt tct ggc gat gca gca gta aag cca ctg cgc aaa gaa gaa cga 211
Ala Val Ser Gly Asp Ala Val Lys Pro Leu Arg Lys Glu Glu Arg
          25          30          35

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ctc gcc tca gtc att cag gaa acc gaa cca ggt gct gca gtc gag gtc	259
Leu Ala Ser Val Ile Gln Glu Thr Glu Pro Gly Ala Val Glu Val	
40 45 50	
atg cgt cgc aat gac gca ttc gct ttg cca ggt gag acc ggt tgg gta	307
Met Arg Arg Asn Asp Ala Phe Ala Leu Pro Gly Glu Thr Gly Trp Val	
55 60 65	
gtc atg ctg ttg cca act cac gat tca caa ttc ggt ggg ctc aac gct	355
Val Met Leu Leu Pro Thr His Asp Ser Gln Phe Gly Gly Leu Asn Ala	
70 75 80 85	
aag gaa aag aac cgc gag gat aaa ggc acg atc atc aac ctg gtg gtc	403
Lys Glu Lys Asn Arg Glu Asp Lys Gly Thr Ile Ile Asn Leu Val Val	
90 95 100	
aac gat gat att cat tcc gtt gtc act cca gaa ctt ctt gac agc gat	451
Asn Asp Asp Ile His Ser Val Val Thr Pro Glu Leu Leu Asp Ser Asp	
105 110 115	
gtg ctt ggt gtc att cct gat gca gat tct ttc gat cgc atg gat gag	499
Val Leu Gly Val Ile Pro Asp Ala Asp Ser Phe Asp Arg Met Asp Glu	
120 125 130	
ttt gat tta ctg cgt aac aaa gca cgc tgg cac tac gga gtg gct gca	547
Phe Asp Leu Leu Arg Asn Lys Ala Arg Trp His Tyr Gly Val Ala Ala	
135 140 145	
att gaa cct gac acg ggt gag ctg gtg gtg ttt aag gtg ccc gcg aaa	595
Ile Glu Pro Asp Thr Gly Glu Leu Val Val Phe Lys Val Pro Ala Lys	
150 155 160 165	
aat agc gct tcg gca cgc ggt gac att ttt tcc gag gtc ggc gat gtg	643
Asn Ser Ala Ser Ala Arg Gly Asp Ile Phe Ser Glu Val Gly Asp Val	
170 175 180	
ctt agc ggt gct gct gac ctc gaa gac gtg gtt gat ttt gag gtc att	691
Leu Ser Gly Ala Ala Asp Leu Glu Asp Val Val Asp Phe Glu Val Ile	
185 190 195	
gcc acc ttc cta gag gtg ctg aat gag acc tct gag gtg gat att gat	739
Ala Thr Phe Leu Glu Val Leu Asn Glu Thr Ser Glu Val Asp Ile Asp	
200 205 210	
gac gaa gat ggc gac gtg cct tat ggt ctt gag ggt gtc aat gca gcg	787
Asp Glu Asp Gly Asp Val Pro Tyr Gly Leu Glu Gly Val Asn Ala Ala	
215 220 225	
gga gtt atc acg gat gac ctc att cgc gag aag ctt gat gtg gat tcc	835
Gly Val Ile Thr Asp Asp Leu Ile Arg Glu Lys Leu Asp Val Asp Ser	
230 235 240 245	
tat ccg agc agt gca gag atc att gac aat att gtg cat gtg ttc acc	883
Tyr Pro Ser Ser Ala Glu Ile Ile Asp Asn Ile Val His Val Phe Thr	
250 255 260	
aag ttg cag ggc aag cat cat gtg gca cca cag ccg gtg ctt cac agc	931
Lys Leu Gln Gly Lys His His Val Ala Pro Gln Pro Val Leu His Ser	
265 270 275	

gca gac gta gtg gat gtt gat gca cag gag tcc cat gac aca gtg gtt 979
 Ala Asp Val Val Asp Val Asp Ala Gln Glu Ser His Asp Thr Val Val
 280 285 290

att gag agc cct gat gat gtc gca cta gca gaa cag gtg gat gta ccg 1027
 Ile Glu Ser Pro Asp Asp Val Ala Leu Ala Glu Val Asp Val Pro
 295 300 305

gat ttc agt gat gga ttt ggt att gac gat gcc gag gtt act gag cca 1075
 Asp Phe Ser Asp Gly Phe Gly Ile Asp Asp Ala Glu Val Thr Glu Pro
 310 315 320 325

gag gat gag gag gtt gtc gaa gca aca gct gat gca gat cct ttt ggt 1123
 Glu Asp Glu Glu Val Val Glu Ala Thr Ala Asp Ala Asp Pro Phe Gly
 330 335 340

gat gta gca gaa gac gat cct ttc ggc agt gat gat gaa cca gat ttt 1171
 Asp Val Ala Glu Asp Asp Pro Phe Gly Ser Asp Asp Glu Pro Asp Phe
 345 350 355

ggt gca tcc gat gtt gtt gct gca ccg gca cct gta gcc gcc atg tcc 1219
 Gly Ala Ser Asp Val Val Ala Ala Pro Ala Pro Val Ala Gly Met Ser
 360 365 370

gat gag cag atc cag gcg ctg att cgt ggt gtg tct gag tcc gtg caa 1267
 Asp Glu Gln Ile Gln Ala Leu Ile Arg Gly Val Ser Glu Ser Val Gln
 375 380 385

gca aag act ggt tca gaa ctt aat gct ttg cga gaa gaa ctt gca caa 1315
 Ala Lys Thr Gly Ser Glu Leu Asn Ala Leu Arg Glu Glu Leu Ala Gln
 390 395 400 405

gca ctg gct tac aat ccg gtt cag gat tca cag gca gca ttg gca cag 1363
 Ala Leu Ala Tyr Asn Pro Val Gln Asp Ser Gln Ala Ala Leu Ala Gln
 410 415 420

gtg cac gca gct gat gcc cgc agc ttt gat gcc gat caa gtg ggt gat 1411
 Val His Ala Ala Asp Ala Arg Ser Phe Asp Ala Asp Gln Val Gly Asp
 425 430 435

gct gtc acc aaa cgt tat gtt aat gac gac ttg ggg ctg tat gtc gat 1459
 Ala Val Thr Lys Arg Tyr Val Asn Asp Asp Leu Gly Leu Tyr Val Asp
 440 445 450

gag gca aac ttc aat aat gct ttg acc agg gca ccg ttc cag gtg gcg 1507
 Glu Ala Asn Phe Asn Asn Ala Leu Thr Arg Ala Pro Phe Gln Val Ala
 455 460 465

atg ccg caa ttc cag gag act aca ccg tgg tta ggt gat cag ctt cgt 1555
 Met Pro Gln Phe Gln Glu Thr Thr Pro Trp Leu Gly Asp Gln Leu Arg
 470 475 480 485

aca ttg gtg gct gtg ttt aat ggt cag ctg ctt gat cag cat cag cgt 1603
 Thr Leu Val Ala Val Phe Asn Gly Gln Leu Leu Asp Gln His Gln Arg
 490 495 500

gac tac cga aga agt gcg cgc gat gta cat tgc gct taatgatcgc 1649
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<210> 1394

<211> 513

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1394

Met Leu Asp Ser Leu Lys Asn Arg Phe Thr Lys Ala Lys Gly Ser His
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 20 25 30

Arg Lys Glu Glu Arg Leu Ala Ser Val Ile Gln Glu Thr Glu Pro Gly
 35 40 45

Ala Ala Val Glu Val Met Arg Arg Asn Asp Ala Phe Ala Leu Pro Gly
 50 55 60

Glu Thr Gly Trp Val Val Met Leu Leu Pro Thr His Asp Ser Gln Phe
 65 70 75 80

Gly Gly Leu Asn Ala Lys Glu Lys Asn Arg Glu Asp Lys Gly Thr Ile
 85 90 95

Ile Asn Leu Val Val Asn Asp Asp Ile His Ser Val Val Thr Pro Glu
 100 105 110

Leu Leu Asp Ser Asp Val Leu Gly Val Ile Pro Asp Ala Asp Ser Phe
 115 120 125

Asp Arg Met Asp Glu Phe Asp Leu Leu Arg Asn Lys Ala Arg Trp His
 130 135 140

Tyr Gly Val Ala Ala Ile Glu Pro Asp Thr Gly Glu Leu Val Val Phe
 145 150 155 160

Lys Val Pro Ala Lys Asn Ser Ala Ser Ala Arg Gly Asp Ile Phe Ser
 165 170 175

Glu Val Gly Asp Val Leu Ser Gly Ala Ala Asp Leu Glu Asp Val Val
 180 185 190

Asp Phe Glu Val Ile Ala Thr Phe Leu Glu Val Leu Asn Glu Thr Ser
 195 200 205

Glu Val Asp Ile Asp Asp Glu Asp Gly Asp Val Pro Tyr Gly Leu Glu
 210 215 220

Gly Val Asn Ala Ala Gly Val Ile Thr Asp Asp Leu Ile Arg Glu Lys
 225 230 235 240

Leu Asp Val Asp Ser Tyr Pro Ser Ser Ala Glu Ile Ile Asp Asn Ile
 245 250 255

Val His Val Phe Thr Lys Leu Gln Gly Lys His His Val Ala Pro Gln
 260 265 270

Pro Val Leu His Ser Ala Asp Val Val Asp Val Asp Ala Gln Glu Ser
 275 280 285

His Asp Thr Val Val Ile Glu Ser Pro Asp Asp Val Ala Leu Ala Glu
290 295 300

Gln Val Asp Val Pro Asp Phe Ser Asp Gly Phe Gly Ile Asp Asp Ala
305 310 315 320

Glu Val Thr Glu Pro Glu Asp Glu Glu Val Val Glu Ala Thr Ala Asp
325 330 335

Ala Asp Pro Phe Gly Asp Val Ala Glu Asp Asp Pro Phe Gly Ser Asp
340 345 350

Asp Glu Pro Asp Phe Gly Ala Ser Asp Val Val Ala Ala Pro Ala Pro
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Val Ala Gly Met Ser Asp Glu Gln Ile Gln Ala Leu Ile Arg Gly Val
370 375 380

Ser Glu Ser Val Gln Ala Lys Thr Gly Ser Glu Leu Asn Ala Leu Arg
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Glu Glu Leu Ala Gln Ala Leu Ala Tyr Asn Pro Val Gln Asp Ser Gln
405 410 415

Ala Ala Leu Ala Gln Val His Ala Ala Asp Ala Arg Ser Phe Asp Ala
420 425 430

Asp Gln Val Gly Asp Ala Val Thr Lys Arg Tyr Val Asn Asp Asp Leu
435 440 445

Gly Leu Tyr Val Asp Glu Ala Asn Phe Asn Asn Ala Leu Thr Arg Ala
450 455 460

Pro Phe Gln Val Ala Met Pro Gln Phe Gln Glu Thr Thr Pro Trp Leu
465 470 475 480

Gly Asp Gln Leu Arg Thr Leu Val Ala Val Phe Asn Gly Gln Leu Leu
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<211> 2616

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(2593)

<223> FRXA02753

<400> 1395

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Met Leu Asp Ser Leu
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aaa aat cgc ttc acc aaa gcg aaa ggt tct cat gga gtg ggg gag ggg	163
Lys Asn Arg Phe Thr Lys Ala Lys Gly Ser His Gly Val Gly Glu Gly	
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gct gtt tct ggc gat gca gca gta aag cca ctg cgc aaa gaa gaa cga	211
Ala Val Ser Gly Asp Ala Ala Val Lys Pro Leu Arg Lys Glu Glu Arg	
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ctc gcc tca gtc att cag gaa acc gaa cca ggt gct gca gtc gag gtc	259
Leu Ala Ser Val Ile Gln Glu Thr Glu Pro Gly Ala Ala Val Glu Val	
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Met Arg Arg Asn Asp Ala Phe Ala Leu Pro Gly Glu Thr Gly Trp Val	
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Val Met Leu Leu Pro Thr His Asp Ser Gln Phe Gly Gly Leu Asn Ala	
70 75 80 85	
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Lys Glu Lys Asn Arg Glu Asp Lys Gly Thr Ile Ile Asn Leu Val Val	
90 95 100	
aac gat gat att cat tcc gtt gtc act cca gaa ctt ctt gac agc gat	451
Asn Asp Asp Ile His Ser Val Val Thr Pro Glu Leu Leu Asp Ser Asp	
105 110 115	
gtg ctt ggt gtc att cct gat gca gat tct ttc gat cgc atg gat gag	499
Val Leu Gly Val Ile Pro Asp Ala Asp Ser Phe Asp Arg Met Asp Glu	
120 125 130	
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Phe Asp Leu Leu Arg Asn Lys Ala Arg Trp His Tyr Gly Val Ala Ala	
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Ile Glu Pro Asp Thr Gly Glu Leu Val Val Phe Lys Val Pro Ala Lys	
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Asn Ser Ala Ser Ala Arg Gly Asp Ile Phe Ser Glu Val Gly Asp Val	
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Leu Ser Gly Ala Ala Asp Leu Glu Asp Val Val Asp Phe Glu Val Ile	
185 190 195	
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Ala Thr Phe Leu Glu Val Leu Asn Glu Thr Ser Glu Val Asp Ile Asp	
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gac gaa gat ggc gac gtg cct tat ggt ctt gag ggt gtc aat gca gcg	787
Asp Glu Asp Gly Asp Val Pro Tyr Gly Leu Glu Gly Val Asn Ala Ala	
215 220 225	
gga gtt atc acg gat gac ctc att cgc gag aag ctt gat gtg gat tcc	835
Gly Val Ile Thr Asp Asp Leu Ile Arg Glu Lys Leu Asp Val Asp Ser	

230	235	240	245	
tat ccg agc agt gca gag atc att gac aat att gtg cat gtg ttc acc				883
Tyr Pro Ser Ser Ala Glu Ile Ile Asp Asn Ile Val His Val Phe Thr	250	255	260	
aag ttg cag ggc aag cat cat gtg gca cca cag ccg gtg ctt cac agc				931
Lys Leu Gln Gly Lys His His Val Ala Pro Gln Pro Val Leu His Ser	265	270	275	
gca gac gta gtg gat gtt gat gca cag gag tcc cat gac aca gtg gtt				979
Ala Asp Val Val Asp Val Asp Ala Gln Glu Ser His Asp Thr Val Val	280	285	290	
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Ile Glu Ser Pro Asp Asp Val Ala Leu Ala Glu Gln Val Asp Val Pro	295	300	305	
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Asp Phe Ser Ser Asp Gly Phe Gly Ile Asp Asp Ala Glu Val Thr Glu Pro	310	315	320	325
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Glu Asp Glu Glu Val Val Glu Ala Thr Ala Asp Ala Asp Pro Phe Gly	330	335	340	
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Asp Val Ala Glu Asp Asp Pro Phe Gly Ser Asp Asp Glu Pro Asp Phe	345	350	355	
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Gly Ala Ser Asp Val Val Ala Ala Pro Ala Pro Val Ala Gly Met Ser	360	365	370	
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Asp Glu Gln Ile Gln Ala Leu Ile Arg Gly Val Ser Glu Ser Val Gln	375	380	385	
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Ala Lys Thr Gly Ser Glu Leu Asn Ala Leu Arg Glu Glu Leu Ala Gln	390	395	400	405
gca ctg gct tac aat ccg gtt cag gat tca cag gca gca ttg gca cag				1363
Ala Leu Ala Tyr Asn Pro Val Gln Asp Ser Gln Ala Ala Leu Ala Gln	410	415	420	
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Val His Ala Ala Asp Ala Arg Ser Phe Asp Ala Asp Gln Val Gly Asp	425	430	435	
gct gtc acc aaa cgt tat gtt aat gac gac ttg ggg ctg tat gtc gat				1459
Ala Val Thr Lys Arg Tyr Val Asn Asp Asp Leu Gly Leu Tyr Val Asp	440	445	450	
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Glu Ala Asn Phe Asn Asn Ala Leu Thr Arg Ala Pro Phe Gln Val Ala	455	460	465	
atg ccg caa ttc cag gag act aca ccg tgg tta ggt gat cag ctt cgt				1555
Met Pro Gln Phe Gln Glu Thr Thr Pro Trp Leu Gly Asp Gln Leu Arg	470	475	480	485

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cgt ttg gca tcg gtg aat gag cag aag ctt gct gca gat aat cgt gtg Arg Leu Ala Ser Val Asn Glu Gln Lys Leu Ala Ala Asp Asn Arg Val 680 685 690	2179
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 Ala Ser Glu Glu Arg Ala Glu Arg Glu Ile Thr Thr Ala Arg Leu Asp
 745 750 755

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 Glu Ala His Glu Ala Glu Ile Val Ile Glu Arg Asp Arg Ala Thr Gln
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gca gag gcg aac tcc atg acg ttt gtt gag tca gtc aag cag cag gat 2515
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 790 795 800 805

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 Arg Ser Asn Asn Ile Ile Leu Ile Ala Val Leu Ile Val Gly Leu Ile
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 825 830

tgt 2616

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<400> 1396
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 35 40 45

Ala Ala Val Glu Val Met Arg Arg Asn Asp Ala Phe Ala Leu Pro Gly
 50 55 60

Glu Thr Gly Trp Val Val Met Leu Leu Pro Thr His Asp Ser Gln Phe
 65 70 75 80

Gly Gly Leu Asn Ala Lys Glu Lys Asn Arg Glu Asp Lys Gly Thr Ile
 85 90 95

Ile Asn Leu Val Val Asn Asp Asp Ile His Ser Val Val Thr Pro Glu
 100 105 110

Leu Leu Asp Ser Asp Val Leu Gly Val Ile Pro Asp Ala Asp Ser Phe
 115 120 125

Asp Arg Met Asp Glu Phe Asp Leu Leu Arg Asn Lys Ala Arg Trp His
 130 135 140
 Tyr Gly Val Ala Ala Ile Glu Pro Asp Thr Gly Glu Leu Val Val Phe
 145 150 155 160
 Lys Val Pro Ala Lys Asn Ser Ala Ser Ala Arg Gly Asp Ile Phe Ser
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 Glu Val Gly Asp Val Leu Ser Gly Ala Ala Asp Leu Glu Asp Val Val
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 Asp Phe Glu Val Ile Ala Thr Phe Leu Glu Val Leu Asn Glu Thr Ser
 195 200 205
 Glu Val Asp Ile Asp Asp Glu Asp Gly Asp Val Pro Tyr Gly Leu Glu
 210 215 220
 Gly Val Asn Ala Ala Gly Val Ile Thr Asp Asp Leu Ile Arg Glu Lys
 225 230 235 240
 Leu Asp Val Asp Ser Tyr Pro Ser Ser Ala Glu Ile Ile Asp Asn Ile
 245 250 255
 Val His Val Phe Thr Lys Leu Gln Gly Lys His His Val Ala Pro Gln
 260 265 270
 Pro Val Leu His Ser Ala Asp Val Val Asp Val Asp Ala Gln Glu Ser
 275 280 285
 His Asp Thr Val Val Ile Glu Ser Pro Asp Asp Val Ala Leu Ala Glu
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 Gln Val Asp Val Pro Asp Phe Ser Asp Gly Phe Gly Ile Asp Asp Ala
 305 310 315 320
 Glu Val Thr Glu Pro Glu Asp Glu Glu Val Val Glu Ala Thr Ala Asp
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 Ala Asp Pro Phe Gly Asp Val Ala Glu Asp Asp Pro Phe Gly Ser Asp
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 Asp Glu Pro Asp Phe Gly Ala Ser Asp Val Val Ala Ala Pro Ala Pro
 355 360 365
 Val Ala Gly Met Ser Asp Glu Gln Ile Gln Ala Leu Ile Arg Gly Val
 370 375 380
 Ser Glu Ser Val Gln Ala Lys Thr Gly Ser Glu Leu Asn Ala Leu Arg
 385 390 395 400
 Glu Glu Leu Ala Gln Ala Leu Ala Tyr Asn Pro Val Gln Asp Ser Gln
 405 410 415
 Ala Ala Leu Ala Gln Val His Ala Ala Asp Ala Arg Ser Phe Asp Ala
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 Asp Gln Val Gly Asp Ala Val Thr Lys Arg Tyr Val Asn Asp Asp Leu
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 Gly Leu Tyr Val Asp Glu Ala Asn Phe Asn Asn Ala Leu Thr Arg Ala

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				485					490					495	
Asp	Gln	His	Gln	Arg	Asp	Tyr	Glu	Glu	Val	Arg	Ala	Met	Tyr	Ile	Ala
			500					505					510		
Leu	Asn	Asp	Arg	Ser	Asn	Leu	Glu	Ile	Ala	Arg	Asp	Leu	Gly	Leu	Asp
		515					520					525			
Asn	Lys	Asp	Ser	Glu	Phe	Tyr	Glu	Val	Tyr	Arg	Ala	Ile	Glu	Arg	Asp
		530					535				540				
Arg	Asp	Val	Met	Ala	Gly	Asp	Gln	Gln	Arg	Val	Glu	Ser	Glu	Arg	Arg
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Gln	Gln	Leu	Gln	Gln	Glu	Tyr	Glu	Ala	Asn	Arg	Glu	Glu	Tyr	Val	Met
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Ala	Lys	Ile	Ala	Glu	Gln	Arg	Val	Glu	Tyr	Asp	Arg	Arg	His	Met	Pro
			580					585					590		
Arg	His	Thr	Ala	Ser	Leu	Glu	Ala	Val	Gly	Arg	Glu	Leu	Thr	Ser	Leu
			595				600					605			
Arg	Asp	Arg	Thr	Ile	Glu	Asp	Tyr	Thr	Ala	Arg	Met	Asn	Thr	Leu	Arg
			610			615					620				
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625				630						635					640
Asp	Glu	Leu	Arg	Pro	Ile	Val	Glu	Arg	Gln	Ala	Glu	Leu	Gln	Arg	Ala
				645					650					655	
Ala	Phe	Asp	Gly	Phe	Ile	Val	Asp	Leu	Asp	Lys	Phe	Ile	Ala	Asp	His
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			675				680					685			
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			690			695					700				
Glu	Gly	Ile	Arg	Val	Glu	Thr	Asp	Lys	Met	Ile	Ala	Ser	Gln	Arg	Lys
705				710						715					720
Ala	Leu	Glu	Arg	Gln	Glu	Ala	Glu	Phe	Ala	Ala	Glu	Leu	Lys	Arg	Arg
				725					730					735	
Asp	Thr	Ile	Val	Ala	Ala	Ser	Glu	Glu	Arg	Ala	Glu	Arg	Glu	Ile	Thr
			740					745					750		
Thr	Ala	Arg	Leu	Asp	Ala	Glu	Ala	Ala	Leu	Lys	Arg	Met	Glu	Glu	Gln
			755			760						765			
Ile	Arg	Val	Asn	Asn	Glu	Ala	His	Glu	Ala	Glu	Ile	Val	Ile	Glu	Arg
			770			775					780				

Asp Arg Ala Thr Gln Ala Glu Ala Asn Ser Met Thr Phe Val Glu Ser
785 790 795 800

Val Lys Gln Gln Asp Arg Ser Asn Asn Ile Ile Leu Ile Ala Val Leu
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Ile Val Gly Leu Ile Ala Gly Met Val Ala Gly Ala Ala Phe Phe
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<210> 1397

<211> 1116

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1093)

<223> RXN03018

<400> 1397

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Val Thr Thr Glu Glu
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gtg cgc gcg atg tac att gcg ctt aat gat cgc tct aat ctt gag atc 163
Val Arg Ala Met Tyr Ile Ala Leu Asn Asp Arg Ser Asn Leu Glu Ile
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gct cgt gat ctt gga ctg gat aat aag gat tcc gaa ttc tac gag gtt 211
Ala Arg Asp Leu Gly Leu Asp Asn Lys Asp Ser Glu Phe Tyr Glu Val
25 30 35

tac cgt gcc att gag cgt gac cgc gat gtt atg gct ggt gat caa cag 259
Tyr Arg Ala Ile Glu Arg Asp Arg Asp Val Met Ala Gly Asp Gln Gln
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cgt gtg gag tca gag cgt cgt cag caa ttg cag cag gag tat gag gcg 307
Arg Val Glu Ser Glu Arg Arg Gln Gln Leu Gln Glu Tyr Glu Ala
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aac cgt gaa gaa tat gtc atg gca aag atc gcg gag cag cgc gtg gag 355
Asn Arg Glu Glu Tyr Val Met Ala Lys Ile Ala Glu Gln Arg Val Glu
70 75 80 85

tat gat cgc cgt cat atg cct cgc cat acc gca tca cta gaa gcg gta 403
Tyr Asp Arg Arg His Met Pro Arg His Thr Ala Ser Leu Glu Ala Val
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ggt cga gag ctg acg agc ctg cgg gat cgc acc att gag gat tac acc 451
Gly Arg Glu Leu Thr Ser Leu Arg Asp Arg Thr Ile Glu Asp Tyr Thr
105 110 115

gca cgc atg aac acg ctg cgt cgt gca cgt gct ggt gaa cgg gct aac 499
Ala Arg Met Asn Thr Leu Arg Arg Ala Arg Ala Glu Arg Ala Asn
120 125 130

gct gca gaa tct cgc att att gac gaa ttg cgc cgg att gtg gag cgc 547

Ala Ala Glu Ser Arg Ile Ile Asp Glu Leu Arg Pro Ile Val Glu Arg
 135 140 145

cag gca gaa ctg caa cga gca gct ttc gat ggt ttc att gtt gat ctt 595
 Gln Ala Glu Leu Gln Arg Ala Ala Phe Asp Gly Phe Ile Val Asp Leu
 150 155 160 165

gac aag ttt att gct gat cac cgc gaa gat gac ctg cgt ttg gca tgc 643
 Asp Lys Phe Ile Ala Asp His Arg Glu Asp Asp Leu Arg Leu Ala Ser
 170 175 180

gtg aat gag cag aag ctt gct gca gat aat cgt gtg gca cag ttg acc 691
 Val Asn Glu Gln Lys Leu Ala Ala Asp Asn Arg Val Ala Gln Leu Thr
 185 190 195

aag gaa gcc gaa gag cgc atc gag ggt atc cgc gtc gag acc gat aag 739
 Lys Glu Ala Glu Glu Arg Ile Glu Gly Ile Arg Val Glu Thr Asp Lys
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atg atc gcc tcc cag cgc aag gca ctt gag cgt cag gaa gcg gaa ttc 787
 Met Ile Ala Ser Gln Arg Lys Ala Leu Glu Arg Gln Glu Ala Glu Phe
 215 220 225

gca gca gag ctt aag cgt cgc gac act att gtc gct gca tgc gag gaa 835
 Ala Ala Glu Leu Lys Arg Arg Asp Thr Ile Val Ala Ala Ser Glu Glu
 230 235 240 245

cgt gct gag cgg gaa att acc aca gca cgt ctt gat gct gag gcg gcg 883
 Arg Ala Glu Arg Glu Ile Thr Thr Ala Arg Leu Asp Ala Glu Ala Ala
 250 255 260

ctc aag cgc atg gaa gag caa att cgt gta aat aat gag gcg cat gag 931
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 265 270 275

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 Ala Glu Ile Val Ile Glu Arg Asp Arg Ala Thr Gln Ala Glu Ala Asn
 280 285 290

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 Ile Ile Leu Ile Ala Val Leu Ile Val Gly Leu Ile Ala Gly Met Val
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<210> 1398

<211> 331

<212> PRT

<213> Corynebacterium glutamicum

<400> 1398

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 Ala Gly Asp Gln Gln Arg Val Glu Ser Glu Arg Arg Gln Gln Leu Gln
 50 55 60
 Gln Glu Tyr Glu Ala Asn Arg Glu Glu Tyr Val Met Ala Lys Ile Ala
 65 70 75 80
 Glu Gln Arg Val Glu Tyr Asp Arg Arg His Met Pro Arg His Thr Ala
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 Ser Leu Glu Ala Val Gly Arg Glu Leu Thr Ser Leu Arg Asp Arg Thr
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 Ile Glu Asp Tyr Thr Ala Arg Met Asn Thr Leu Arg Arg Ala Arg Ala
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 Gly Glu Arg Ala Asn Ala Ala Glu Ser Arg Ile Ile Asp Glu Leu Arg
 130 135 140
 Pro Ile Val Glu Arg Gln Ala Glu Leu Gln Arg Ala Ala Phe Asp Gly
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 165 170 175
 Leu Arg Leu Ala Ser Val Asn Glu Gln Lys Leu Ala Ala Asp Asn Arg
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 Val Ala Gln Leu Thr Lys Glu Ala Glu Glu Arg Ile Glu Gly Ile Arg
 195 200 205
 Val Glu Thr Asp Lys Met Ile Ala Ser Gln Arg Lys Ala Leu Glu Arg
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 Gln Glu Ala Glu Phe Ala Ala Glu Leu Lys Arg Arg Asp Thr Ile Val
 225 230 235 240
 Ala Ala Ser Glu Glu Arg Ala Glu Arg Glu Ile Thr Thr Ala Arg Leu
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 Asp Ala Glu Ala Ala Leu Lys Arg Met Glu Glu Gln Ile Arg Val Asn
 260 265 270
 Asn Glu Ala His Glu Ala Glu Ile Val Ile Glu Arg Asp Arg Ala Thr
 275 280 285
 Gln Ala Glu Ala Asn Ser Met Thr Phe Val Glu Ser Val Lys Gln Gln
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 Asp Arg Ser Asn Asn Ile Ile Leu Ile Ala Val Leu Ile Val Gly Leu
 305 310 315 320
 Ile Ala Gly Met Val Ala Gly Ala Ala Phe Phe
 325 330

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Leu Asp Pro Arg Glu Asp Phe Ala Glu Cys Met Gln Leu Gln Val Leu
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gaa ccc atc gag gat ttg gat ttc act cca gtt cca ggc gtc gcc tca Glu Pro Ile Glu Asp Leu Asp Phe Thr Pro Val Pro Gly Val Ala Ser 200 205 210	739
cca ttt gaa gag gtc agc gcg aaa gat gag aaa ttc tct cca cgc cca Pro Phe Glu Glu Val Ser Ala Lys Asp Glu Lys Phe Ser Pro Arg Pro 215 220 225	787
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gag tct ttc gag gcc gct gaa atc aag gta act gag ttt ttt gga gaa Glu Ser Phe Glu Ala Ala Glu Ile Lys Val Thr Glu Phe Phe Gly Glu 265 270 275	931
cca gct gct cca gta gcg gaa tca ggc gta gaa gct ccc act ccg gaa Pro Ala Ala Pro Val Ala Glu Ser Gly Val Glu Ala Pro Thr Pro Glu 280 285 290	979
gct ccc acg gtt cct gaa gca gct aag ccc act ccg gcg aaa cct aag Ala Pro Thr Val Pro Glu Ala Ala Lys Pro Thr Pro Ala Lys Pro Lys 295 300 305	1027
act cca aag gca gag ccc caa aag caa gaa tcc ccc aag ccg gga act Thr Pro Lys Lys Ala Glu Pro Gln Lys Gln Glu Ser Pro Lys Pro Gly Thr 310 315 320 325	1075
cca aaa cca aaa gct cca agc cct gcg gat att cca ccg aaa gcc cca Pro Lys Pro Lys Ala Pro Ser Pro Ala Asp Ile Pro Pro Lys Ala Pro 330 335 340	1123
gct gac act gag gaa cat tcg gaa gtc gaa gct gaa atc gag gac tca Ala Asp Thr Glu Glu His Ser Glu Val Glu Ala Glu Ile Glu Asp Ser 345 350 355	1171
cgt cca aag atc ccc agc cct tcg atg atg gct ccc cgc cgc aag ctt Arg Pro Lys Ile Pro Ser Pro Ser Met Met Ala Pro Arg Arg Lys Leu 360 365 370	1219
cgt tcc cgc tac gtt ccg ctt ccc aac gaa gtg tgg gca aca gca gga Arg Ser Arg Tyr Val Pro Leu Pro Asn Glu Val Trp Ala Thr Ala Gly 375 380 385	1267
ttc caa act cct tac gat gtc ggg caa cag tac gca tcg tgg tgg ttt Phe Gln Thr Pro Tyr Asp Val Gly Gln Gln Tyr Ala Ser Trp Trp Phe 390 395 400 405	1315
gaa aac gca gct acc agc act caa aga gat cag gct cat cta ttg tct Glu Asn Ala Ala Thr Ser Thr Gln Arg Asp Gln Ala His Leu Leu Ser 410 415 420	1363
ggt ggc gga ctt cca cca gag atc gat cgc ccg ctt ctg cag ttt gct	1411

Gly Gly Gly Leu Pro Pro Glu Ile Asp Arg Pro Leu Leu Gln Phe Ala
 425 430 435

tgt gaa act ctc cac gaa tac acc ctg act gaa gcg cag cgc gta gct 1459
 Cys Glu Thr Leu His Glu Tyr Thr Leu Thr Glu Ala Gln Arg Val Ala
 440 445 450

tta cgc gat ggc ttt cac tcc gga atc cgt ggt gta ttg ctc aac cag 1507
 Leu Arg Asp Gly Phe His Ser Gly Ile Arg Gly Val Leu Leu Asn Gln
 455 460 465

cga gat agc tagaatcaca aaaaactggg gct 1539
 Arg Asp Ser
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<210> 1400

<211> 472

<212> PRT

<213> Corynebacterium glutamicum

<400> 1400

Met Leu Glu Arg Thr Gln Val Phe Val Asp Thr Ser Tyr Leu Leu Ala
 1 5 10 15

Ser Phe Tyr Asn Ser Trp Glu Thr Gly Ala Arg Ala Gln Leu Glu Ile
 20 25 30

Asp Leu Pro Glu Val Val Gly Val Leu Gly Arg Met Ile Glu Gln Gln
 35 40 45

Leu Lys Gln Pro Val Gln Arg Gln Met Trp Tyr Asp Gly Ile Pro Asp
 50 55 60

Ser Gly Pro His Arg Tyr Gln Arg Ala Leu Arg Thr Cys Asp Gly Val
 65 70 75 80

Gln Leu Arg Ala Gly Gln Leu Ile Glu Trp Gly Glu Arg Arg Thr Gln
 85 90 95

Lys Ala Val Asp Thr Arg Leu Val Ala Asp Leu Val Leu Ala Gly Val
 100 105 110

Arg Gly Gln Cys Ser Asp Ile Val Leu Val Ser Gly Asp Ala Asp Met
 115 120 125

Ile Pro Gly Val Gln Glu Ala Ala Asn Ala Gly Leu Arg Val His Leu
 130 135 140

Tyr Gly Phe Gly Trp Asp Ser Met Ser Ser Gln Leu Arg His Cys Cys
 145 150 155 160

Asp Thr Thr Thr Ile Leu Asp Pro Arg Glu Asp Phe Ala Glu Cys Met
 165 170 175

Gln Leu Gln Val Leu Glu Gly Pro Leu Pro Pro Val Val Arg Val Lys
 180 185 190

Pro Ile Asn Asp Ala Glu Pro Ile Glu Asp Leu Asp Phe Thr Pro Val
 195 200 205

Pro Gly Val Ala Ser Pro Phe Glu Glu Val Ser Ala Lys Asp Glu Lys
210 215 220

Phe Ser Pro Arg Pro Ser Glu Pro Ala Glu Ala Leu Ser Glu Gln Val
225 230 235 240

Cys Glu Ala Gln Tyr Glu Ile Ser Lys His Glu Gly Gln Thr Ala Asp
245 250 255

Ser Gly Glu Ile Thr Glu Ser Phe Glu Ala Ala Glu Ile Lys Val Thr
260 265 270

Glu Phe Phe Gly Glu Pro Ala Ala Pro Val Ala Glu Ser Gly Val Glu
275 280 285

Ala Pro Thr Pro Glu Ala Pro Thr Val Pro Glu Ala Ala Lys Pro Thr
290 295 300

Pro Ala Lys Pro Lys Thr Pro Lys Ala Glu Pro Gln Lys Gln Glu Ser
305 310 315 320

Pro Lys Pro Gly Thr Pro Lys Pro Lys Ala Pro Ser Pro Ala Asp Ile
325 330 335

Pro Pro Lys Ala Pro Ala Asp Thr Glu Glu His Ser Glu Val Glu Ala
340 345 350

Glu Ile Glu Asp Ser Arg Pro Lys Ile Pro Ser Pro Ser Met Met Ala
355 360 365

Pro Arg Arg Lys Leu Arg Ser Arg Tyr Val Pro Leu Pro Asn Glu Val
370 375 380

Trp Ala Thr Ala Gly Phe Gln Thr Pro Tyr Asp Val Gly Gln Gln Tyr
385 390 395 400

Ala Ser Trp Trp Phe Glu Asn Ala Ala Thr Ser Thr Gln Arg Asp Gln
405 410 415

Ala His Leu Leu Ser Gly Gly Gly Leu Pro Pro Glu Ile Asp Arg Pro
420 425 430

Leu Leu Gln Phe Ala Cys Glu Thr Leu His Glu Tyr Thr Leu Thr Glu
435 440 445

Ala Gln Arg Val Ala Leu Arg Asp Gly Phe His Ser Gly Ile Arg Gly
450 455 460

Val Leu Leu Asn Gln Arg Asp Ser
465 470

<210> 1401

<211> 996

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(973)

<223> RXN03025

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Ala Arg Leu Ala Glu Leu Arg Ala Glu Ala Leu Gly Thr Ser Ala Thr
230                      235                      240                      245

cct aag ggc cag cta gag gca ggt gtc gag gat gcg gaa gaa ctt atc      883
Pro Lys Gly Gln Leu Glu Ala Gly Val Glu Asp Ala Glu Glu Leu Ile
250                      255                      260

gac gaa acc tcc acc cct tca gct acc cca gaa acc gca agc cca gaa      931
Asp Glu Thr Ser Thr Pro Ser Ala Thr Pro Glu Thr Ala Ser Pro Glu
265                      270                      275

gct gat gct cca gaa gca tcc gca gac gag tcc gag aag aaa      973
Ala Asp Ala Pro Glu Ala Ser Ala Asp Glu Ser Glu Lys Lys
280                      285                      290

taacctaaac acaaaaaact ggg      996

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<210> 1402
<211> 291
<212> PRT
<213> Corynebacterium glutamicum

<400> 1402
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Asp Asn Lys Ile Asp Glu Asn Ala Asp Pro Lys Ile Gln Ile Gln Gln
20                      25                      30

Ala Thr Glu Ala Ala Gln Lys Gln His Gln Gln Ile Met Gln His Ala
35                      40                      45

Ser Gln Ile Ile Gly Gln Gln Lys Gln Leu Glu Met Lys Leu Asn Arg
50                      55                      60

Leu Val Thr Asp Arg Asp Lys Leu Gln Glu Gln Ala Arg Gln Ala Ile
65                      70                      75                      80

Gln Leu Ala Asp Lys Ser Ala Asn Glu Gly Asp Ser Val Lys Ala Gln
85                      90                      95

Glu Phe Asn Asn Thr Ala Glu Val Phe Ala Ser Gln Leu Val Ala Val
100                     105                     110

Glu Gln Gln Leu Glu Gln Thr Thr Ala Leu His Gln Gln Ala Glu Val
115                     120                     125

Ala Ala Lys Asp Ala Val Ala Lys Ser Lys Glu Ser Glu Met Arg Leu
130                     135                     140

Lys Glu Gln Met Ser Gln Ile Asp Ala Leu Arg Ala Gln Ala Asp Gln
145                     150                     155                     160

Ala Lys Met Gln Glu Ser Val Thr Lys Ser Met Asp Ser Leu Asn Gln
165                     170                     175

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Phe Gly Thr Gln Asp Ser Ser Val Pro Thr Leu Asp Ala Val Arg Glu
 180 185 190
 Lys Ile Glu Arg Arg Tyr Ala Asp Ala Leu Gly Ala Gln Glu Leu Thr
 195 200 205
 Gln Asn Thr Val Ser Asp Arg Met Ala Glu Ile Ala Gln Ser Gly Thr
 210 215 220
 Asp Met Arg Ala Ser Ala Arg Leu Ala Glu Leu Arg Ala Glu Ala Leu
 225 230 235 240
 Gly Thr Ser Ala Thr Pro Lys Gly Gln Leu Glu Ala Gly Val Glu Asp
 245 250 255
 Ala Glu Glu Leu Ile Asp Glu Thr Ser Thr Pro Ser Ala Thr Pro Glu
 260 265 270
 Thr Ala Ser Pro Glu Ala Asp Ala Pro Glu Ala Ser Ala Asp Glu Ser
 275 280 285
 Glu Lys Lys
 290

<210> 1403

<211> 174

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (17)..(151)

<223> RXN03027

<400> 1403

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 Met Glu Asn Val Tyr Glu Phe Leu Gly Asn Leu Asp
 1 5 10

gtc ctt tcc ggc tcc ggc ctc atc ggc tac gtc ttc gac ttc ctc ggc 100
 Val Leu Ser Gly Ser Gly Leu Ile Gly Tyr Val Phe Asp Phe Leu Gly
 15 20 25

gct tcc agc aag tgg gct ggc gca gtt gct gac ctc atc ggt ctg ctt 148
 Ala Ser Ser Lys Trp Ala Gly Ala Val Ala Asp Leu Ile Gly Leu Leu
 30 35 40

ggc taattaactt cgcccacggg caa 174
 Gly
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<210> 1404

<211> 45

<212> PRT

<213> Corynebacterium glutamicum

<400> 1404

Met Glu Asn Val Tyr Glu Phe Leu Gly Asn Leu Asp Val Leu Ser Gly
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Ser Gly Leu Ile Gly Tyr Val Phe Asp Phe Leu Gly Ala Ser Ser Lys
 20 25 30

Trp Ala Gly Ala Val Ala Asp Leu Ile Gly Leu Leu Gly
 35 40 45

<210> 1405

<211> 630

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (95)..(607)

<223> RXN03029

<400> 1405

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aaaaatccgg ttatgacatt aagtacctag gacaatg ttt gga gtg ggc tat tat 115
 Met Phe Gly Val Gly Tyr Tyr
 1 5

aca acc gcc cac cga ttg tcc acc ctg cag cgc ccc aac ttg cgc ggc 163
 Thr Thr Ala His Arg Leu Ser Thr Leu Gln Arg Pro Asn Leu Arg Gly
 10 15 20

atc ccc tta acc ttc gtg agc gtc gac cga gcc ggc aac atg tcc aaa 211
 Ile Pro Leu Thr Phe Val Ser Val Asp Arg Ala Gly Asn Met Ser Lys
 25 30 35

cgc caa tcc gcc acg ggc ttc cac ttc acc cat tac ggc ggc acc tgc 259
 Arg Gln Ser Ala Thr Gly Phe His Phe Thr His Tyr Gly Gly Thr Cys
 40 45 50 55

ccc ctg tgg aac gtg ttt gaa acc ttc acc aac ccc ggc caa gtg ctc 307
 Pro Leu Trp Asn Val Phe Glu Thr Phe Thr Asn Pro Gly Gln Val Leu
 60 65 70

cgc caa ttc gcg caa atg ccc gac gga cgc aac tac ctg tgg atc tca 355
 Arg Gln Phe Ala Gln Met Pro Asp Gly Arg Asn Tyr Leu Trp Ile Ser
 75 80 85

cgc acc gtg cga cac cac gaa gcc cgg ttc ggc gaa gta gac aaa atg 403
 Arg Thr Val Arg His His Glu Ala Arg Phe Gly Glu Val Asp Lys Met
 90 95 100

ttc gcc atc ggc ttg ggc tgc gaa gcg cgc cac gcc gac cgc act gtg 451
 Phe Ala Ile Gly Leu Gly Cys Glu Ala Arg His Ala Asp Arg Thr Val
 105 110 115

tac tcc cgc ggt ttc aac ctc cag gac ctc tcc acc gcc acc ccc atc 499
 Tyr Ser Arg Gly Phe Asn Leu Gln Asp Leu Ser Thr Ala Thr Pro Ile
 120 125 130 135

ggg tcc ggc tgc cga gtg tgc acc cgc gag aac tgc gcg cag cgc gca 547
 Gly Ser Gly Cys Arg Val Cys Thr Arg Glu Asn Cys Ala Gln Arg Ala
 140 145 150

ttc cca tcc gtc cac ggc cgc atc aac atc gac gcg cac gaa tcc act 595
 Phe Pro Ser Val His Gly Arg Ile Asn Ile Asp Ala His Glu Ser Thr
 155 160 165

atc gcg ccg tac taagaaaagg agcttgcttt acg 630
 Ile Ala Pro Tyr
 170

<210> 1406

<211> 171

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1406

Met Phe Gly Val Gly Tyr Tyr Thr Thr Ala His Arg Leu Ser Thr Leu
 1 5 10 15

Gln Arg Pro Asn Leu Arg Gly Ile Pro Leu Thr Phe Val Ser Val Asp
 20 25 30

Arg Ala Gly Asn Met Ser Lys Arg Gln Ser Ala Thr Gly Phe His Phe
 35 40 45

Thr His Tyr Gly Gly Thr Cys Pro Leu Trp Asn Val Phe Glu Thr Phe
 50 55 60

Thr Asn Pro Gly Gln Val Leu Arg Gln Phe Ala Gln Met Pro Asp Gly
 65 70 75 80

Arg Asn Tyr Leu Trp Ile Ser Arg Thr Val Arg His His Glu Ala Arg
 85 90 95

Phe Gly Glu Val Asp Lys Met Phe Ala Ile Gly Leu Gly Cys Glu Ala
 100 105 110

Arg His Ala Asp Arg Thr Val Tyr Ser Arg Gly Phe Asn Leu Gln Asp
 115 120 125

Leu Ser Thr Ala Thr Pro Ile Gly Ser Gly Cys Arg Val Cys Thr Arg
 130 135 140

Glu Asn Cys Ala Gln Arg Ala Phe Pro Ser Val His Gly Arg Ile Asn
 145 150 155 160

Ile Asp Ala His Glu Ser Thr Ile Ala Pro Tyr
 165 170

<210> 1407

<211> 789

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(789)

<223> RXN03031

<400> 1407

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1				5					10					15		
cgc	gcc	atc	caa	gaa	cgc	tac	tac	ttc	ctg	agc	atc	cgc	tac	ctc	gcc	96
Arg	Ala	Ile	Gln	Glu	Arg	Tyr	Tyr	Phe	Leu	Ser	Ile	Arg	Tyr	Leu	Ala	
			20					25				30				
tcc	atc	atg	atc	gcc	gtg	gcc	aaa	gca	gac	ccc	acc	ctg	tgg	gaa	gaa	144
Ser	Ile	Met	Ile	Ala	Val	Ala	Lys	Ala	Asp	Pro	Thr	Leu	Trp	Glu	Glu	
			35				40					45				
ctc	gac	ctg	cgc	atc	acc	gac	gcc	tta	aca	cca	gtc	acc	gca	ggg	gaa	192
Leu	Asp	Leu	Arg	Ile	Thr	Asp	Ala	Leu	Thr	Pro	Val	Thr	Ala	Gly	Glu	
			50			55					60					
gtg	atg	atc	caa	tcc	tcc	acc	ctg	tcc	aaa	cgc	atc	gcc	gcc	tgg	atc	240
Val	Met	Ile	Gln	Ser	Ser	Thr	Leu	Ser	Lys	Arg	Ile	Ala	Ala	Trp	Ile	
			65			70				75					80	
aaa	gaa	ctc	gac	ccc	gaa	ccc	aca	cca	gag	ccc	ata	ccg	aaa	gag	gac	288
Lys	Glu	Leu	Asp	Pro	Glu	Pro	Thr	Pro	Glu	Pro	Ile	Pro	Lys	Glu	Asp	
				85					90					95		
tat	gtt	cac	gtc	cac	acc	act	gat	gag	gcg	acc	tat	gtc	cgc	atc	aaa	336
Tyr	Val	His	Val	His	Thr	Thr	Asp	Glu	Ala	Thr	Tyr	Val	Arg	Ile	Lys	
				100					105					110		
atc	agc	ggc	ccc	aac	cgc	ctg	atc	ctc	aat	gac	atc	atc	acc	caa	ctc	384
Ile	Ser	Gly	Pro	Asn	Arg	Leu	Ile	Leu	Asn	Asp	Ile	Thr	Gln	Leu		
			115				120					125				
aaa	gac	aca	gac	acc	gag	gac	agc	ctg	cct	gaa	gcg	ctc	atg	gcg	ttc	432
Lys	Asp	Thr	Asp	Thr	Glu	Asp	Ser	Leu	Pro	Glu	Ala	Leu	Met	Ala	Phe	
			130			135					140					
ctg	atg	gag	aaa	atc	cag	tta	aag	atc	acc	aag	tac	ctt	ttc	acc	cca	480
Leu	Met	Glu	Lys	Ile	Gln	Leu	Lys	Ile	Thr	Lys	Tyr	Leu	Phe	Thr	Pro	
			145		150					155					160	
cat	aag	cac	cct	gag	cag	gtg	tgg	tca	ccg	gac	tac	ggt	gac	att	ggt	528
His	Lys	His	Pro	Glu	Gln	Val	Trp	Ser	Pro	Asp	Tyr	Gly	Asp	Ile	Gly	
				165				170						175		
ccc	gaa	gcc	tat	gcc	aat	gcc	acc	ctc	gtg	tgc	gcc	aag	gac	tta	gat	576
Pro	Glu	Ala	Tyr	Ala	Asn	Ala	Thr	Leu	Val	Cys	Ala	Lys	Asp	Leu	Asp	
			180				185						190			
gag	gtc	gct	gga	gcc	acg	gag	aag	agc	tac	acc	ccg	agt	gag	aag	atg	624
Glu	Val	Ala	Gly	Ala	Thr	Glu	Lys	Ser	Tyr	Thr	Pro	Ser	Glu	Lys	Met	
			195				200					205				
aaa	gcc	ctg	atc	aga	gct	cgg	gat	ggg	cat	tgc	cgc	ttc	cca	ggg	tgt	672
Lys	Ala	Leu	Ile	Arg	Ala	Arg	Asp	Gly	His	Cys	Arg	Phe	Pro	Gly	Cys	
			210			215				220						
tgc	gtc	ccg	gcg	agt	aaa	tgc	cag	gtc	gat	cac	att	atc	ccg	tgg	gcg	720
Cys	Val	Pro	Ala	Ser	Lys	Cys	Gln	Val	Asp	His	Ile	Ile	Pro	Trp	Ala	
			225			230				235					240	
gag	ggc	ggc	ccg	aca	gcg	gcg	tgg	aac	ctg	cag	ttg	ttg	tgc	cag	ccg	768
Glu	Gly	Gly	Pro	Thr	Ala	Ala	Trp	Asn	Leu	Gln	Leu	Leu	Cys	Gln	Arg	

245

250

255

cat cac aat atg aaa acc gat
 His His Asn Met Lys Thr Asp
 260

789

<210> 1408

<211> 263

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1408

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Arg Ala Ile Gln Glu Arg Tyr Tyr Phe Leu Ser Ile Arg Tyr Leu Ala
 20 25 30

Ser Ile Met Ile Ala Val Ala Lys Ala Asp Pro Thr Leu Trp Glu Glu
 35 40 45

Leu Asp Leu Arg Ile Thr Asp Ala Leu Thr Pro Val Thr Ala Gly Glu
 50 55 60

Val Met Ile Gln Ser Ser Thr Leu Ser Lys Arg Ile Ala Ala Trp Ile
 65 70 75 80

Lys Glu Leu Asp Pro Glu Pro Thr Pro Glu Pro Ile Pro Lys Glu Asp
 85 90 95

Tyr Val His Val His Thr Thr Asp Glu Ala Thr Tyr Val Arg Ile Lys
 100 105 110

Ile Ser Gly Pro Asn Arg Leu Ile Leu Asn Asp Ile Ile Thr Gln Leu
 115 120 125

Lys Asp Thr Asp Thr Glu Asp Ser Leu Pro Glu Ala Leu Met Ala Phe
 130 135 140

Leu Met Glu Lys Ile Gln Leu Lys Ile Thr Lys Tyr Leu Phe Thr Pro
 145 150 155 160

His Lys His Pro Glu Gln Val Trp Ser Pro Asp Tyr Gly Asp Ile Gly
 165 170 175

Pro Glu Ala Tyr Ala Asn Ala Thr Leu Val Cys Ala Lys Asp Leu Asp
 180 185 190

Glu Val Ala Gly Ala Thr Glu Lys Ser Tyr Thr Pro Ser Glu Lys Met
 195 200 205

Lys Ala Leu Ile Arg Ala Arg Asp Gly His Cys Arg Phe Pro Gly Cys
 210 215 220

Cys Val Pro Ala Ser Lys Cys Gln Val Asp His Ile Ile Pro Trp Ala
 225 230 235 240

Glu Gly Gly Pro Thr Ala Ala Trp Asn Leu Gln Leu Leu Cys Arg
 245 250 255

His His Asn Met Lys Thr Asp
260

<210> 1409

<211> 408

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(385)

<223> RXN03032

<400> 1409

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ccaactcgt aagcacacca tcattggcgtg gtgcgcgcgt atg acc gac ggg gac 115
Met Thr Asp Gly Asp
1 5

tta gac gct gat atc tca ccc cgc cag atc ggg ttg atg acc acc cga 163
Leu Asp Ala Asp Ile Ser Pro Arg Gln Ile Gly Leu Met Thr Thr Arg
10 15 20

acc gtg gtc gaa atc gtt cga cta cgc cac atg att gcc caa caa cta 211
Thr Val Val Glu Ile Val Arg Leu Arg His Met Ile Ala Gln Gln Leu
25 30 35

gaa aga gcc acg atc atg gaa aac gag tac ctc aaa gaa atc gca gcg 259
Glu Arg Ala Thr Ile Met Glu Asn Glu Tyr Leu Lys Glu Ile Ala Ala
40 45 50

ctg aag aaa gaa ctc gcg cac tac aag caa aaa gac cat cag aat caa 307
Leu Lys Lys Glu Leu Ala His Tyr Lys Gln Lys Asp His Gln Asn Gln
55 60 65

atg gtg atc gat atc ttg gga aaa gct att ggg acc agg ccc aat cct 355
Met Val Ile Asp Ile Leu Gly Lys Ala Ile Gly Thr Arg Pro Asn Pro
70 75 80 85

ggc gag ggc tta gac gag gag gac gcc acc taaacgtgga tgagcaacgc 405
Gly Glu Gly Leu Asp Glu Glu Asp Ala Thr
90 95

gcc 408

<210> 1410

<211> 95

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1410

Met Thr Asp Gly Asp Leu Asp Ala Asp Ile Ser Pro Arg Gln Ile Gly
1 5 10 15

Leu Met Thr Thr Arg Thr Val Val Glu Ile Val Arg Leu Arg His Met
20 25 30

Ile Ala Gln Gln Leu Glu Arg Ala Thr Ile Met Glu Asn Glu Tyr Leu

35	40	45
Lys Glu Ile Ala Ala Leu Lys	Lys Glu Leu Ala His Tyr Lys Gln Lys	
50	55	60
Asp His Gln Asn Gln Met Val Ile Asp Ile Leu Gly Lys Ala Ile Gly		
65	70	75
Thr Arg Pro Asn Pro Gly Glu Gly Leu Asp Glu Glu Asp Ala Thr		
	85	90
		95

<210> 1411
 <211> 683
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(660)
 <223> RXN03034

<400> 1411

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1 5 10 15	
caa aca cga ctc gag ttc atg cgg atc tac acc acc ctg ccg cac ggc	96
Gln Thr Arg Leu Glu Phe Met Arg Ile Tyr Thr Thr Leu Pro His Gly	
20 25 30	
tac cgc cag ccc ttc ctt aaa gcc aac aac atc ggc cac tgc acc gtt	144
Tyr Arg Gln Pro Phe Leu Lys Ala Asn Asn Ile Gly His Cys Thr Val	
35 40 45	
cga acc tgg cta gca gca ata agc acc ttc agc cga ctt ccc cat gct	192
Arg Thr Trp Leu Ala Ala Ile Ser Thr Phe Ser Arg Leu Pro His Ala	
50 55 60	
ttt gat gat gcc cac cgc ttc ggg atc gaa cgc acc acc cca gtc gac	240
Phe Asp Asp Ala His Arg Phe Gly Ile Glu Arg Thr Thr Pro Val Asp	
65 70 75 80	
gat gtc acc aca cta acg gct gat gac aaa cgt gac ctg gtc ata gga	288
Asp Val Thr Thr Leu Thr Ala Asp Asp Lys Arg Asp Leu Val Ile Gly	
85 90 95	
tac tta gct caa cca cac ggt cag gcc cag caa ttc ctc acg ttt tac	336
Tyr Leu Ala Gln Pro His Gly Gln Gly Gln Gln Phe Leu Thr Phe Tyr	
100 105 110	
caa ctc cgt aag cac acc atc atg gcc tgg tgc gcc gct atg acc gac	384
Gln Leu Arg Lys His Thr Ile Met Ala Trp Cys Ala Ala Met Thr Asp	
115 120 125	
ggg gac tta gac gct gat atc tca ccc cgc cag atc ggg ttg atg acc	432
Gly Asp Leu Asp Ala Asp Ile Ser Pro Arg Gln Ile Gly Leu Met Thr	
130 135 140	
acc cga acc gtg gtc gaa atc gtt cga cta cgc cac atg att gcc caa	480
Thr Arg Thr Val Val Glu Ile Val Arg Leu Arg His Met Ile Ala Gln	

[illegible]

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<210> 1412
<211> 220
<212> PRT
<213> Corynebacterium glutamicum
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400> 1412																	
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Gln	Thr	Arg	Leu	Glu	Phe	Met	Arg	Ile	Tyr	Thr	Thr	Leu	Pro	His	Gly		
			20					25					30				
Tyr	Arg	Gln	Pro	Phe	Leu	Lys	Ala	Asn	Asn	Ile	Gly	His	Cys	Thr	Val		
		35					40					45					
Arg	Thr	Trp	Leu	Ala	Ala	Ile	Ser	Thr	Phe	Ser	Arg	Leu	Pro	His	Ala		
	50					55					60						
Phe	Asp	Asp	Ala	His	Arg	Phe	Gly	Ile	Glu	Arg	Thr	Thr	Pro	Val	Asp		
65				70						75					80		
Asp	Val	Thr	Thr	Leu	Thr	Ala	Asp	Asp	Gly	Arg	Asp	Leu	Val	Ile	Gly		
				85				90						95			
Tyr	Leu	Ala	Gln	Pro	His	Gly	Gln	Gly	Gln	Gln	Phe	Leu	Thr	Phe	Tyr		
		100						105					110				
Gln	Leu	Arg	Lys	His	Thr	Ile	Met	Ala	Trp	Cys	Ala	Ala	Met	Thr	Asp		
		115					120					125					
Gly	Asp	Leu	Asp	Ala	Asp	Ile	Ser	Pro	Arg	Gln	Ile	Gly	Leu	Met	Thr		
	130					135					140						
Thr	Arg	Thr	Val	Val	Glu	Ile	Val	Arg	Leu	Arg	His	Met	Ile	Ala	Gln		
145					150					155				160			
Gln	Leu	Glu	Arg	Ala	Thr	Ile	Met	Glu	Asn	Glu	Tyr	Leu	Lys	Glu	Ile		
			165					170					175				
Ala	Ala	Leu	Lys	Lys	Glu	Leu	Ala	His	Tyr	Lys	Gln	Lys	Asp	His	Gln		

180

185

190

Asn Gln Met Val Ile Asp Ile Leu Gly Lys Ala Ile Gly Thr Arg Pro
 195 200 205

Asn Pro Gly Glu Gly Leu Asp Glu Glu Asp Ala Thr
 210 215 220

<210> 1413

<211> 408

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(385)

<223> FRXA00063

<400> 1413

cctgggtcata ggatacttag ctcaaccaca cggtcagggc cagcaattcc tcacgtttta 60

ccaactcgt aagcacacca tcatggcctg gtgcgccgct atg acc gac ggg gac 115
 Met Thr Asp Gly Asp
 1 5

tta gac gct gat atc tca ccc cgc cag atc ggg ttg atg acc acc cga 163
 Leu Asp Ala Asp Ile Ser Pro Arg Gln Ile Gly Leu Met Thr Thr Arg
 10 15 20

acc gtg gtc gaa atc gtt cga cta cgc cac atg att gcc caa caa cta 211
 Thr Val Val Glu Ile Val Arg Leu Arg His Met Ile Ala Gln Gln Leu
 25 30 35

gaa aga gcc acg atc atg gaa aac gag tac ctc aaa gaa atc gca gcg 259
 Glu Arg Ala Thr Ile Met Glu Asn Glu Tyr Leu Lys Glu Ile Ala Ala
 40 45 50

ctg aag aaa gaa ctc gcg cac tac aag caa aaa gac cat cag aat caa 307
 Leu Lys Lys Glu Leu Ala His Tyr Lys Gln Lys Asp His Gln Asn Gln
 55 60 65

atg gtg atc gat atc ttg gga aaa gct att ggg acc agg ccc aat cct 355
 Met Val Ile Asp Ile Leu Gly Lys Ala Ile Gly Thr Arg Pro Asn Pro
 70 75 80 85

ggc gag ggc tta gac gag gag gac gcc acc taaacgtgga tgagcaacgc 405
 Gly Glu Gly Leu Asp Glu Glu Asp Ala Thr
 90 95

gcc 408

<210> 1414

<211> 95

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1414

Met Thr Asp Gly Asp Leu Asp Ala Asp Ile Ser Pro Arg Gln Ile Gly
 1 5 10 15

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Leu Met Thr Thr Arg Thr Val Val Glu Ile Val Arg Leu Arg His Met
                20                      25                      30

Ile Ala Gln Gln Leu Glu Arg Ala Thr Ile Met Glu Asn Glu Tyr Leu
                35                      40                      45

Lys Glu Ile Ala Ala Leu Lys Lys Glu Leu Ala His Tyr Lys Gln Lys
                50                      55                      60

Asp His Gln Asn Gln Met Val Ile Asp Ile Leu Gly Lys Ala Ile Gly
                65                      70                      75                      80

Thr Arg Pro Asn Pro Gly Glu Gly Leu Asp Glu Glu Asp Ala Thr
                85                      90                      95

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<210> 1415

<211> 309

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(286)

<223> RXN03037

<400> 1415

cgctaaaaga caaatgacag cgaagctgca ttcggtatata cacctgaaga acactcttca 60

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ccactagcat tocaccaacg cctcggaag ggctatctcc atg tct gtt gac gat    115
                Met Ser Val Asp Asp
                1                      5

```

```

ctt tac gct gtt gct ctc gat act cac acc ggt aag cct atc ccc tgc    163
Leu Tyr Ala Val Ala Leu Asp Thr His Thr Gly Lys Pro Ile Pro Cys
                10                      15                      20

```

```

gta ctc tgt gaa aat gct cca cag att gtt atc tac gat ggt tgc tgc    211
Val Leu Cys Glu Asn Ala Pro Gln Ile Val Ile Tyr Asp Gly Cys Cys
                25                      30                      35

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tcg ctt gca tat acc caa gca ctt ggc gat ctc gcc gaa gcg gaa tac    259
Ser Leu Ala Tyr Thr Gln Ala Leu Gly Asp Leu Ala Glu Ala Glu Tyr
                40                      45                      50

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tac ggc gcc gat ctt gct gca gct gcc taaacaaact tcatagaacg    306
Tyr Gly Ala Asp Leu Ala Ala Ala
                55                      60

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aca 309

<210> 1416

<211> 62

<212> PRT

<213> Corynebacterium glutamicum

<400> 1416

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Met Ser Val Asp Asp Leu Tyr Ala Val Ala Leu Asp Thr His Thr Gly
1                      5                      10                      15

```


agc ggc aat tgc aac ctc gct gca tac gtt tta cca agc ttc cga gcc 547

Ser Gly Asn Cys Asn Leu Ala Ala Tyr Val Leu Pro Ser Phe Arg Ala
 135 140 145

cgc gga cat aga aga tgg agt cgc att gat cgc tcg ggc atg cgc ctg 595
 Pro Gly His Arg Arg Trp Ser Arg Ile Asp Pro Ser Gly Met Arg Leu
 150 155 160 165

gat taagaaanta aaaatctstg aca 621
 Asp

<210> 1418
 <211> 166
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1418
 Met Glu Gly Pro Glu Ala Phe Thr Val Ala Ala Ile Ala Ala Ala Ala
 1 5 10 15

Gly Val Ser Pro Arg Thr Phe His Asn Tyr Phe Pro Ser Arg Glu Asp
 20 25 30

Ala Leu Val Gln Phe Val Val Ile Arg Val Gln Glu Leu Thr Asp Gln
 35 40 45

Leu Tyr Glu Phe Pro Thr Ser Val Pro Pro Arg Asp Ala Ile Glu Gln
 50 55 60

Leu Val Ile Asn Gln Leu Arg Asp Gly Asp Asp Ala Met Asp Ser Phe
 65 70 75 80

Ser Ala Met Phe Arg Ile Gly Glu Ile Leu Glu Asn Leu Asp Pro Ile
 85 90 95

Lys Cys Val Ile Asp Lys Glu Arg Leu Ile Ala Pro Leu Leu Glu Phe
 100 105 110

Met Val Glu Arg Asp Lys Asp Leu Asp Lys Phe Asp Xaa Gly Asn Ser
 115 120 125

Asp Pro Phe Ala Cys Ser Gly Asn Cys Asn Leu Ala Ala Tyr Val Leu
 130 135 140

Pro Ser Phe Arg Ala Pro Gly His Arg Arg Trp Ser Arg Ile Asp Pro
 145 150 155 160

Ser Gly Met Arg Leu Asp
 165

<210> 1419
 <211> 627
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(604)
 <223> FRXA02892

400> 1419	accgaggaac tgaaggaaaa tgtaggtgtc ggggcttaga gaaacaaaaa aggctgctac	60	
gcggaacagca ttgtcacgtg ctgctgcgga gatgccttg	atg Met	gaa ggc cct gag Glu Gly Pro Glu	115
gcg ttc acg gtt gcg gcc att gca gct gca gcc ggg gtc tcc ccc agg	Ala Phe Thr Val Ala Ala Ile Ala Ala Gly Val Ser Pro Arg	10 15 20	163
act ttt cat aac tac ttc cct tct cgg gaa gac gca ttg gtg caa ttt	Thr Phe His Asn Tyr Phe Pro Ser Arg Glu Asp Ala Leu Val Gln Phe	25 30 35	211
gtg gtc att cgc gtt cag gaa ctc acg gat cag cta tac gag ttt cct	Val Val Ile Arg Val Gln Leu Leu Thr Asp Gln Leu Tyr Glu Phe Pro	40 45 50	259
aca agc gtg ccc cca cga gat gcc att gaa caa ttg gtg ata aac caa	Thr Ser Val Pro Pro Arg Asp Ala Ile Glu Gln Leu Val Ile Asn Gln	55 60 65	307
ttg cgg gat ggc gat gac gct atg gat tct ttc agc gca atg ttt cga	Leu Arg Asp Gly Asp Asn Ala Met Asp Ser Phe Ser Ala Met Phe Arg	70 75 80 85	355
atc ggt gag atc ctt gaa aat ctt gac ccc atc aag tgt gtt atc gat	Ile Gly Glu Ile Leu Glu Asn Leu Asp Pro Ile Lys Cys Val Ile Asp	90 95 100	403
aag gag cga ctc att gct ccg ttg ctt gag ttc atg gtt gaa cgt gac	Lys Glu Arg Leu Ile Ala Pro Leu Leu Glu Phe Met Val Glu Arg Asp	105 110 115	451
aaa gac ctt gac aag ttc gat gcg gca act ctg atc cat ttg cat gca	Lys Asp Leu Asp Lys Phe Asp Ala Ala Thr Leu Ile His Leu His Ala	120 125 130	499
gcg gca att gca acc tcg ctg cat acg ttt tac caa gct tcc gag ccc	Ala Ala Ile Ala Thr Ser Leu His Thr Phe Tyr Gln Ala Ser Glu Pro	135 140 145	547
cgg gac ata gaa gat gga gtc gca ttg atc cgt cgg gca tgc gcc tgg	Arg Asp Ile Glu Asp Gly Val Ala Leu Ile Arg Arg Ala Cys Ala Trp	150 155 160 165	595
att aag aaa taaaaattgt ggcgtgtgaa cct	Ile Lys Lys		627

<210> 1420

<211> 168

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1420

Met Glu Gly Pro Glu Ala Phe Thr Val Ala Ala Ile Ala Ala Ala Ala
1 5 10 15

Gly Val Ser Pro Arg Thr Phe His Asn Tyr Phe Pro Ser Arg Glu Asp
20 25 30

Ala Leu Val Gln Phe Val Val Ile Arg Val Gln Glu Leu Thr Asp Gln
35 40 45

Leu Tyr Glu Phe Pro Thr Ser Val Pro Pro Arg Asp Ala Ile Glu Gln
50 55 60

Leu Val Ile Asn Gln Leu Arg Asp Gly Asp Asp Ala Met Asp Ser Phe
65 70 75 80

Ser Ala Met Phe Arg Ile Gly Glu Ile Leu Glu Asn Leu Asp Pro Ile
85 90 95

Lys Cys Val Ile Asp Lys Glu Arg Leu Ile Ala Pro Leu Leu Glu Phe
100 105 110

Met Val Glu Arg Asp Lys Asp Leu Asp Lys Phe Asp Ala Ala Thr Leu
115 120 125

Ile His Leu His Ala Ala Ala Ile Ala Thr Ser Leu His Thr Phe Tyr
130 135 140

Gln Ala Ser Glu Pro Arg Asp Ile Glu Asp Gly Val Ala Leu Ile Arg
145 150 155 160

Arg Ala Cys Ala Trp Ile Lys Lys
165

<210> 1421

<211> 1096

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1096)

<223> RXN03045

<400> 1421

agcttttcta ttctgaaaaa tagccttgta ttcgaaaatt tgatcgggta tgggtggttg 60

tattagcaca ggggaactaaa ogggaaagg ggaagacacc atg agc atc acc aca 115
Met Ser Ile Thr Thr
1 5

cac gtc caa gca ctc acc aca gca ctc aac gcc atc gac aac cat ttg 163
His Val Gln Ala Leu Thr Thr Ala Leu Asn Ala Ile Asp Asn His Leu
10 15 20

gcc agc atg ctt gac cat ggt gtc acc cca gac caa tac aag gcc atc 211
Ala Ser Met Leu Asp His Gly Val Thr Pro Asp Gln Tyr Lys Ala Ile
25 30 35

gag ccc gac ctc atc gcc cta gaa cac acc atc aac cac cac gcc acc 259
Glu Pro Asp Leu Ile Ala Leu Glu His Thr Ile Asn His His Ala Thr
40 45 50

atc gcc gcc caa acc acc gcc ctc gcc gaa cgc acc aat gct gcg cag Ile Ala Ala Gln Thr Thr Ala Leu Ala Glu Arg Thr Asn Ala Ala Gln 55 60 65	307
tcg att ggc tcc acc cac ctc atc gac tac ctc acc acc acc ttc ggc Ser Ile Gly Ser Thr His Leu Ile Asp Tyr Leu Thr Thr Thr Phe Gly 70 75 80 85	355
cta tct aaa gca cgc gcc cac cac cgc atc aat ctc gcc cac tcc ctc Leu Ser Lys Ala Arg Ala His His Arg Ile Asn Leu Ala His Ser Leu 90 95 100	403
tac ccc ata ccg aag cca aac tct gga tct ggc aac ggc ggt aat ggt Tyr Pro Ile Pro Lys Pro Asn Ser Gly Ser Gly Asn Gly Gly Asn Gly 105 110 115	451
ggc aat ccc gac ggt ggt cct gat ggt ggc gac tcg ggt gat gac gac Gly Asn Pro Asp Gly Gly Pro Asp Gly Gly Asp Ser Gly Asp Asp Asp 120 125 130	499
tcc ggc gat gat gac ccc gac ccc gaa ccg gac aag cct gaa gac ggc Ser Gly Asp Asp Asp Pro Asp Pro Glu Pro Asp Lys Pro Glu Asp Gly 135 140 145	547
aaa cct gat agt gat aag ccc cgt agg cca cgg atc agc gcg gaa aaa Lys Pro Asp Ser Asp Lys Pro Arg Arg Pro Arg Ile Ser Ala Glu Lys 150 155 160 165	595
cac gcc atc atc acc gac gaa ctc gcc cgc ctc aac ccg aat acc aca His Ala Ile Ile Thr Asp Glu Leu Ala Arg Leu Asn Pro Asn Thr Thr 170 175 180	643
ccc agc gcc gag gaa ctg cgc aac caa gcc ctg agt cag gcg atc tgg Pro Ser Ala Glu Glu Leu Arg Asn Gln Ala Leu Ser Gln Ala Ile Trp 185 190 195	691
cgc acc cca gaa gac ctc cgc acg tgg cta cgc cac cag gtc acc acc Arg Thr Pro Glu Asp Leu Arg Thr Trp Leu Arg His Gln Val Thr Thr 200 205 210	739
gcg aac aaa aac aac ccc aac ccc atc acc gcc atg aaa agg cgc tac Ala Asn Lys Asn Asn Pro Asn Pro Ile Thr Ala Met Lys Arg Arg Tyr 215 220 225	787
ctc tca gta ggt aaa ccc gat gcc gac aac atg gtc cgc atc agc ggc Leu Ser Val Gly Lys Pro Asp Ala Asp Asn Met Val Arg Ile Ser Gly 230 235 240 245	835
ctc gtg ccc gca gcc acc gca gca ctg atc acc gcg aac acc gca ccg Leu Val Pro Ala Ala Thr Ala Ala Leu Ile Thr Ala Asn Thr Ala Pro 250 255 260	883
tta acc aaa cgc ggc aac ctc gtg gat cta cca gca gca gaa gat atg Leu Thr Lys Arg Gly Asn Leu Val Asp Leu Pro Ala Ala Glu Asp Met 265 270 275	931
cgc acc cgc ggg caa cgc cat gcg gac gcg ttg cat cac atc atg gag Arg Thr Arg Gly Gln Arg His Ala Asp Ala Leu His His Ile Met Glu 280 285 290	979
atc tac aac cac ggt att gtc acc cca gct cgt ggt gga aca gcc agc	1027

```

Ile Tyr Asn His Gly Ile Val Thr Pro Ala Arg Gly Gly Thr Ala Ser
 295                      300                      305

atc atc atc tcc atg acc acc gat gat ctt gac gag atc aac cac gcc 1075
Ile Ile Ile Ser Met Thr Thr Asp Asp Leu Asp Glu Ile Asn His Ala
 310                      315                      320                      325

aac agc agt ggt gaa agt ctg
Asn Ser Ser Gly Glu Ser Leu
                      330

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1096

<210> 1422

<211> 332

<212> PRT

<213> Corynebacterium glutamicum

<400> 1422

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Met Ser Ile Thr Thr His Val Gln Ala Leu Thr Thr Ala Leu Asn Ala
 1                      5                      10                      15

Ile Asp Asn His Leu Ala Ser Met Leu Asp His Gly Val Thr Pro Asp
 20                      25

Gln Tyr Lys Ala Ile Glu Pro Asp Leu Ile Ala Leu Glu His Thr Ile
 35                      40                      45

Asn His His Ala Thr Ile Ala Ala Gln Thr Thr Ala Leu Ala Glu Arg
 50                      55                      60

Thr Asn Ala Ala Gln Ser Ile Gly Ser Thr His Leu Ile Asp Tyr Leu
 65                      70                      75                      80

Thr Thr Thr Phe Gly Leu Ser Lys Ala Arg Ala His His Arg Ile Asn
 85                      90                      95

Leu Ala His Ser Leu Tyr Pro Ile Pro Lys Pro Asn Ser Gly Ser Gly
100                      105                      110

Asn Gly Gly Asn Gly Gly Asn Pro Asp Gly Gly Pro Asp Gly Gly Asp
115                      120                      125

Ser Gly Asp Asp Asp Ser Gly Asp Asp Asp Pro Asp Pro Glu Pro Asp
130                      135                      140

Lys Pro Glu Asp Gly Lys Pro Asp Ser Asp Lys Pro Arg Arg Pro Arg
145                      150                      155                      160

Ile Ser Ala Glu Lys His Ala Ile Ile Thr Asp Glu Leu Ala Arg Leu
165                      170                      175

Asn Pro Asn Thr Thr Pro Ser Ala Glu Glu Leu Arg Asn Gln Ala Leu
180                      185                      190

Ser Gln Ala Ile Trp Arg Thr Pro Glu Asp Leu Arg Thr Trp Leu Arg
195                      200                      205

His Gln Val Thr Thr Ala Asn Lys Asn Asn Pro Asn Pro Ile Thr Ala
210                      215                      220

Met Lys Arg Arg Tyr Leu Ser Val Gly Lys Pro Asp Ala Asp Asn Met

```

400> 1423																	
gcc tca att gct aat tcc acc ctg aat att cca gtg gga ttg gcc gcc	48																
Ala Ser Ile Ala Asn Ser Thr Leu Asn Ile Pro Val Gly Leu Gly Gly																	
1 5 10 15																	
tcc aat ttg ctg ctc aag gcg caa acc gcg acc cca tct gag cct gcg	96																
Ser Asn Leu Leu Lys Ala Gln Thr Ala Thr Pro Ser Glu Pro Ala																	
20 25 30																	
aat gct cag gac aaa ctg tac cgt ttc tgc atc gcc aat ggt aag agg	144																
Asn Ala Gln Asp Lys Leu Tyr Arg Phe Cys Ile Ala Asn Gly Lys Arg																	
35 40 45																	
gca ttt tcc gat gcg cag cga ttc ttg ctc aac gcc gac gag ctc gcg	192																
Ala Phe Ser Asp Ala Gln Arg Phe Leu Leu Asn Ala Asp Glu Leu Ala																	
50 55 60																	
gag ctt tct gat tat gag cgt ctg gct tat gcc atc acc ttg ctt gat	240																
Glu Leu Ser Asp Tyr Glu Arg Leu Ala Tyr Ala Ile Thr Leu Leu Asp																	
65 70 75 80																	
cag cct gga aaa gaa gca gaa gga cgc gaa ctt ttt cct ttc gga gct	288																
Gln Pro Gly Lys Glu Ala Glu Gly Arg Glu Leu Phe Pro Phe Gly Ala																	
85 90 95																	
tcg ccg cca ggg cta ccg cgc tgt cga ttt ctt gga atc cca gac tgt	336																
Ser Pro Pro Gly Leu Pro Arg Cys Arg Phe Leu Gly Ile Pro Asp Cys																	
100 105 110																	
tgaccacgtg aataaccocg atg	359																

<210> 1424
 <211> 112
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1424
 Ala Ser Ile Ala Asn Ser Thr Leu Asn Ile Pro Val Gly Leu Gly Gly
 1 5 10 15
 Ser Asn Leu Leu Leu Lys Ala Gln Thr Ala Thr Pro Ser Glu Pro Ala
 20 25 30
 Asn Ala Gln Asp Lys Leu Tyr Arg Phe Cys Ile Ala Asn Gly Lys Arg
 35 40 45
 Ala Phe Ser Asp Ala Gln Arg Phe Leu Leu Asn Ala Asp Glu Leu Ala
 50 55 60
 Glu Leu Ser Asp Tyr Glu Arg Leu Ala Tyr Ala Ile Thr Leu Leu Asp
 65 70 75 80
 Gln Pro Gly Lys Glu Ala Glu Gly Arg Glu Leu Phe Pro Phe Gly Ala
 85 90 95
 Ser Pro Pro Gly Leu Pro Arg Cys Arg Phe Leu Gly Ile Pro Asp Cys
 100 105 110

<210> 1425
 <211> 1539
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1516)
 <223> RXN03047

<400> 1425
 ctctaccac ttaaaatgga cgcattatcg caagataagg catgcttgga tgaatagatt 60
 ttaactcaac gtttactaaa cagaatcgga attaggagcc atg ctt gaa cgc aca 115
 Met Leu Glu Arg Thr
 1 5
 cag gta ttc gtg gat acg tcc tac ctg ctc gca agc ttt tac aac tct 163
 Gln Val Phe Val Asp Thr Ser Tyr Leu Leu Ala Ser Phe Tyr Asn Ser
 10 15 20
 tgg gag aca ggg gca cgt gcc caa tta gaa atc gac ctc ccc gaa gta 211
 Trp Glu Thr Gly Ala Arg Ala Gln Leu Glu Ile Asp Leu Pro Glu Val
 25 30 35
 gtc ggg gta tta gga agg atg att gaa caa caa ctt aaa cag cca gta 259
 Val Gly Val Leu Gly Arg Met Ile Glu Gln Gln Leu Lys Gln Pro Val
 40 45 50

caa cgc caa atg tgg tac gac gga atc ccc gat tcc ggc ccc cac cgc	307
Gln Arg Gln Met Trp Tyr Asp Gly Ile Pro Asp Ser Gly Pro His Arg	
55 60 65	
tat caa cga gca cta cgc acc tgc gat ggt gtg caa ctt cgt gct ggc	355
Tyr Gln Arg Ala Leu Arg Thr Cys Asp Gly Val Gln Leu Arg Ala Gly	
70 75 80 85	
caa tta att gaa tgg ggc gaa cgc cgc aca caa aag gca gta gat acc	403
Gln Leu Ile Glu Trp Gly Glu Arg Arg Thr Gln Lys Ala Val Asp Thr	
90 95 100	
cgc ctt gtt gca gac ctc gtt ctc gca ggt gtt cgc gga caa tgc tcc	451
Arg Leu Val Ala Asp Leu Val Leu Ala Gly Val Arg Gly Gln Cys Ser	
105 110 115	
gat atc gtg ctc gtc agt ggc gac gcc gac atg atc ccc ggt gtt caa	499
Asp Ile Val Leu Val Ser Gly Ala Asp Met Ile Pro Gly Val Gln	
120 125 130	
gaa gct gcc aat gca ggc ctt cgc gtt cac ctc tac ggc ttc ggc tgg	547
Glu Ala Ala Asn Ala Gly Leu Arg Val His Leu Tyr Gly Phe Gly Trp	
135 140 145	
gat tcc atg tcc tcc caa ctg cgc cac tgc tgt gac acc acc acc att	595
Asp Ser Met Ser Ser Gln Leu Arg His Cys Cys Asp Thr Thr Thr Ile	
150 155 160 165	
ttg gat cct cga gaa gat ttt gct gaa tgc atg cag ctg cag gtt ctc	643
Leu Asp Pro Arg Glu Asp Phe Ala Glu Cys Met Gln Leu Gln Val Leu	
170 175 180	
gaa ggt cca cta ccc cct gtc gtt cgg gta aag ccc atc aac gat gca	691
Glu Gly Pro Leu Pro Pro Val Val Arg Val Lys Pro Ile Asn Asp Ala	
185 190 195	
gaa ccc atc gag gat ttg gat ttc act cca gtt cca ggc gtc gcc tca	739
Glu Pro Ile Glu Asp Leu Asp Phe Thr Pro Val Pro Gly Val Ala Ser	
200 205 210	
cca ttt gaa gag gtc agc cgc aaa gat gag aaa ttc tct cca cgc cca	787
Pro Phe Glu Glu Val Ser Ala Lys Asp Glu Lys Phe Ser Pro Arg Pro	
215 220 225	
agt gaa cct gcc gaa gct ttg tgc gaa cag gtc tgt gaa cgc cag tat	835
Ser Glu Pro Ala Glu Ala Leu Ser Glu Gln Val Cys Glu Ala Gln Tyr	
230 235 240 245	
gag atc tcc aaa cac gaa ggt caa acc gct gat tca gga gaa atc acc	883
Glu Ile Ser Lys His Glu Gly Gln Thr Ala Asp Ser Gly Glu Ile Thr	
250 255 260	
gag tct ttc gag gcc gct gaa atc aag gta act gag ttt ttt gga gaa	931
Glu Ser Phe Glu Ala Ala Glu Ile Lys Val Thr Glu Phe Phe Gly Glu	
265 270 275	
cca gct gct cca gta cgc gaa tca ggc gta gaa gct ccc act cgc gaa	979
Pro Ala Ala Pro Val Ala Glu Ser Gly Val Glu Ala Pro Thr Pro Glu	
280 285 290	

gct ccc acg gtt cct gaa gca gct aag ccc act ccg gcg aaa cct aag 1027
 Ala Pro Thr Val Pro Glu Ala Ala Lys Pro Thr Pro Ala Lys Pro Lys
 295 300 305

act cca aag gca gag ccc caa aag caa gaa tcc ccc aag ccg gga act 1075
 Thr Pro Lys Ala Glu Pro Gln Lys Gln Glu Ser Pro Lys Pro Gly Thr
 310 315 320 325

cca aaa cca aaa gct cca agc cct gcg gat att cca ccg aaa gcc cca 1123
 Pro Lys Pro Lys Ala Pro Ser Pro Ala Asp Ile Pro Pro Lys Ala Pro
 330 335 340

gct gac act gag gaa cat tcg gaa gtc gaa gct gaa atc gag gac tca 1171
 Ala Asp Thr Glu Glu His Ser Glu Val Glu Ala Glu Ile Glu Asp Ser
 345 350 355

cgt cca aag atc ccc agc cct tcg atg atg gct ccc cgc cgc aag ctt 1219
 Arg Pro Lys Ile Pro Ser Pro Ser Met Met Ala Pro Arg Arg Lys Leu
 360 365 370

cgt tcc cgc tac gtt ccg ctt ccc aac gaa gtg tgg gca aca gca gga 1267
 Arg Ser Arg Tyr Val Pro Leu Pro Asn Glu Val Trp Ala Thr Ala Gly
 375 380 385

ttc caa act cct tac gat gtc ggg caa cag tac gca tcg tgg tgg ttt 1315
 Phe Gln Thr Pro Tyr Asp Val Gly Gln Gln Tyr Ala Ser Trp Trp Phe
 390 395 400 405

gaa aac gca gct acc agc act caa aga gat cag gct cat cta ttg tct 1363
 Glu Asn Ala Ala Thr Ser Thr Gln Arg Asp Gln Ala His Leu Leu Ser
 410 415 420

ggt ggc gga ctt cca cca gag atc gat cgc ccg ctt ctg cag ttt gct 1411
 Gly Gly Gly Leu Pro Pro Glu Ile Asp Arg Pro Leu Leu Gln Phe Ala
 425 430 435

tgt gaa act ctc cac gaa tac acc ctg act gaa gcg cag cgc gta gct 1459
 Cys Glu Thr Leu His Glu Tyr Thr Leu Thr Glu Ala Gln Arg Val Ala
 440 445 450

tta cgc gat ggc ttt cac tcc gga atc cgt ggt gta ttg ctc aac cag 1507
 Leu Arg Asp Gly Phe His Ser Gly Ile Arg Gly Val Leu Leu Asn Gln
 455 460 465

cga gat agc tagaatcaca aaaaactggg gct 1539
 Arg Asp Ser
 470

<210> 1426

<211> 472

<212> PRT

<213> Corynebacterium glutamicum

<400> 1426

Met Leu Glu Arg Thr Gln Val Phe Val Asp Thr Ser Tyr Leu Leu Ala
 1 5 10 15

Ser Phe Tyr Asn Ser Trp Glu Thr Gly Ala Arg Ala Gln Leu Glu Ile
 20 25 30

Asp Leu Pro Glu Val Val Gly Val Leu Gly Arg Met Ile Glu Gln Gln
 35 40 45
 Leu Lys Gln Pro Val Gln Arg Gln Met Trp Tyr Asp Gly Ile Pro Asp
 50 55 60
 Ser Gly Pro His Arg Tyr Gln Arg Ala Leu Arg Thr Cys Asp Gly Val
 65 70 75 80
 Gln Leu Arg Ala Gly Gln Leu Ile Glu Trp Gly Glu Arg Arg Thr Gln
 85 90 95
 Lys Ala Val Asp Thr Arg Leu Val Ala Asp Leu Val Leu Ala Gly Val
 100 105 110
 Arg Gly Gln Cys Ser Asp Ile Val Leu Val Ser Gly Asp Ala Asp Met
 115 120 125
 Ile Pro Gly Val Gln Glu Ala Ala Asn Ala Gly Leu Arg Val His Leu
 130 135 140
 Tyr Gly Phe Gly Trp Asp Ser Met Ser Ser Gln Leu Arg His Cys Cys
 145 150 155 160
 Asp Thr Thr Thr Ile Leu Asp Pro Arg Glu Asp Phe Ala Glu Cys Met
 165 170 175
 Gln Leu Gln Val Leu Glu Gly Pro Leu Pro Pro Val Val Arg Val Lys
 180 185 190
 Pro Ile Asn Asp Ala Glu Pro Ile Glu Asp Leu Asp Phe Thr Pro Val
 195 200 205
 Pro Gly Val Ala Ser Pro Phe Glu Glu Val Ser Ala Lys Asp Glu Lys
 210 215 220
 Phe Ser Pro Arg Pro Ser Glu Pro Ala Glu Ala Leu Ser Glu Gln Val
 225 230 235 240
 Cys Glu Ala Gln Tyr Glu Ile Ser Lys His Glu Gly Gln Thr Ala Asp
 245 250 255
 Ser Gly Glu Ile Thr Glu Ser Phe Glu Ala Ala Glu Ile Lys Val Thr
 260 265 270
 Glu Phe Phe Gly Glu Pro Ala Ala Pro Val Ala Glu Ser Gly Val Glu
 275 280 285
 Ala Pro Thr Pro Glu Ala Pro Thr Val Pro Glu Ala Ala Lys Pro Thr
 290 295 300
 Pro Ala Lys Pro Lys Thr Pro Lys Ala Glu Pro Gln Lys Gln Glu Ser
 305 310 315 320
 Pro Lys Pro Gly Thr Pro Lys Pro Lys Ala Pro Ser Pro Ala Asp Ile
 325 330 335
 Pro Pro Lys Ala Pro Ala Asp Thr Glu Glu His Ser Glu Val Glu Ala
 340 345 350
 Glu Ile Glu Asp Ser Arg Pro Lys Ile Pro Ser Pro Ser Met Met Ala

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355          360          365
Pro Arg Arg Lys Leu Arg Ser Arg Tyr Val Pro Leu Pro Asn Glu Val
370          375          380
Trp Ala Thr Ala Gly Phe Gln Thr Pro Tyr Asp Val Gly Gln Gln Tyr
385          390          395          400
Ala Ser Trp Trp Phe Glu Asn Ala Ala Thr Ser Thr Gln Arg Asp Gln
405          410          415
Ala His Leu Leu Ser Gly Gly Gly Leu Pro Pro Glu Ile Asp Arg Pro
420          425          430
Leu Leu Gln Phe Ala Cys Glu Thr Leu His Glu Tyr Thr Leu Thr Glu
435          440          445
Ala Gln Arg Val Ala Leu Arg Asp Gly Phe His Ser Gly Ile Arg Gly
450          455          460
Val Leu Leu Asn Gln Arg Asp Ser
465          470

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<210> 1427

<211> 1539

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1516)

<223> FRXA00036

<400> 1427

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ttaaactaac gtttactaaa cagaatcgga attaggagcc atg ctt gaa cgc aca 115
Met Leu Glu Arg Thr
1 5

```

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cag gta ttc gtg gat acg tcc tac ctg ctc gca agc ttt tac aac tot 163
Gln Val Phe Val Asp Thr Ser Tyr Leu Leu Ala Ser Phe Tyr Asn Ser
10 15 20

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tgg gag aca ggg gca cgt gcc caa tta gaa atc gac etc ccc gaa gta 211
Trp Glu Thr Gly Ala Arg Ala Gln Leu Glu Ile Asp Leu Pro Glu Val
25 30 35

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gtc ggg gta tta gga agg atg att gaa caa caa ctt aaa cag cca gta 259
Val Gly Val Leu Gly Arg Met Ile Glu Gln Gln Leu Pro Val
40 45 50

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caa cgc caa atg tgg tac gac gga atc ccc gat tcc ggc ccc cac cgc 307
Gln Arg Gln Met Trp Tyr Asp Gly Ile Pro Asp Ser Gly Pro His Arg
55 60 65

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tat caa cga gca cta cgc acc tgc gat ggt gtg caa ctt cgt gct ggc 355
Tyr Gln Arg Ala Leu Arg Thr Cys Asp Gly Val Gln Leu Arg Ala Gly
70 75 80 85

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caa tta att gaa tgg ggc gaa cgc cgc aca caa aag gca gta gat acc Gln Leu Ile Glu Trp Gly Glu Arg Arg Thr Gln Lys Ala Val Asp Thr	403
90 95 100	
cgc ctt gtt gca gac ctc gtt ctc gca ggt gtt cgc gga caa tgc tcc Arg Leu Val Ala Asp Leu Val Leu Ala Gly Val Arg Gly Gln Cys Ser	451
105 110 115	
gat atc gtg ctc gtc agt ggc gac gcc gac atg atc ccc ggt gtt caa Asp Ile Val Leu Val Ser Gly Asp Ala Asp Met Ile Pro Gly Val Gln	499
120 125 130	
gaa gct gcc aat gca ggc ctt cgc gtt cac ctc tac ggc ttc ggc tgg Glu Ala Ala Asn Ala Gly Leu Arg Val His Leu Tyr Gly Phe Gly Trp	547
135 140 145	
gat tcc atg tcc tcc caa ctg cgc cac tgc tgt gac acc acc acc att Asp Ser Met Ser Ser Gln Leu Arg His Cys Cys Asp Thr Thr Thr Ile	595
150 155 160 165	
ttg gat cct cga gaa gat ttt gct gaa tgc atg cag ctg cag gtt ctc Leu Asp Pro Arg Glu Asp Phe Ala Glu Cys Met Gln Leu Gln Val Leu	643
170 175 180	
gaa ggt cca cta ccc cct gtc gtt cgg gta aag ccc atc aac gat gca Glu Gly Pro Leu Pro Pro Val Val Arg Val Lys Pro Ile Asn Asp Ala	691
185 190 195	
gaa ccc atc gag gat ttg gat ttc act cca gtt cca ggc gtc gcc tca Glu Pro Ile Glu Asp Leu Asp Phe Thr Pro Val Pro Gly Val Ala Ser	739
200 205 210	
cca ttt gaa gag gtc agc gcg aaa gat gag aaa ttc tct cca cgc cca Pro Phe Glu Glu Val Ser Ala Lys Asp Glu Lys Phe Ser Pro Arg Pro	787
215 220 225	
agt gaa cct gcc gaa gct ttg tcg gaa cag gtc tgt gaa gcg cag tat Ser Glu Pro Ala Glu Ala Leu Ser Glu Gln Val Cys Glu Ala Gln Tyr	835
230 235 240 245	
gag atc tcc aaa cac gaa ggt caa acc gct gat tca gga gaa atc acc Glu Ile Ser Lys His Glu Gly Gln Thr Ala Asp Ser Gly Glu Ile Thr	883
250 255 260	
gag tct ttc gag gcc gct gaa atc aag gta act gag ttt ttt gga gaa Glu Ser Phe Glu Ala Ala Glu Ile Lys Val Thr Glu Phe Phe Gly Glu	931
265 270 275	
cca gct gct cca gta gcg gaa tca ggc gta gaa gct ccc act ccg gaa Pro Ala Ala Pro Val Ala Glu Ser Gly Val Glu Ala Pro Thr Pro Glu	979
280 285 290	
gct ccc acg gtt cct gaa gca gct aag ccc act ccg gcg aaa cct aag Ala Pro Thr Val Pro Glu Ala Ala Lys Pro Thr Pro Ala Lys Pro Lys	1027
295 300 305	
act cca aag gca gag ccc caa aag caa gaa tcc ccc aag ccg gga act Thr Pro Lys Ala Glu Pro Gln Lys Gln Glu Ser Pro Lys Pro Gly Thr	1075
310 315 320 325	
cca aaa cca aaa gct cca agc cct gcg gat att cca ccg aaa gcc cca	1123

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Pro Lys Pro Lys Ala Pro Ser Pro Ala Asp Ile Pro Pro Lys Ala Pro
      330                      335                      340

gct gac act gag gaa cat tcg gaa gtc gaa gct gaa atc gag gac tca 1171
Ala Asp Thr Glu Glu His Ser Glu Val Glu Ala Glu Ile Glu Asp Ser
      345                      350                      355

cgt cca aag atc ccc agc cct tcg atg atg gct ccc cgc cgc aag ctt 1219
Arg Pro Lys Ile Pro Ser Pro Ser Met Met Ala Pro Arg Arg Lys Leu
      360                      365                      370

cgt tcc cgc tac gtt ccg ctt ccc aac gaa gtg tgg gca aca gca gga 1267
Arg Ser Arg Tyr Val Pro Leu Pro Asn Glu Val Trp Ala Thr Ala Gly
      375                      380                      385

ttc caa act cct tac gat gtc ggg caa cag tac gca tcg tgg tgg ttt 1315
Phe Gln Thr Pro Tyr Asp Val Gly Gln Gln Tyr Ala Ser Trp Trp Phe
      390                      395                      400                      405

gaa aac gca gct acc agc act caa aga gat cag gct cat cta ttg tct 1363
Glu Asn Ala Ala Thr Ser Thr Gln Arg Asp Gln Ala His Leu Leu Ser
      410                      415                      420

ggt ggc gga ctt cca cca gag atc gat cgc ccg ctt ctg cag ttt gct 1411
Gly Gly Gly Leu Pro Pro Glu Ile Asp Arg Pro Leu Leu Gln Phe Ala
      425                      430                      435

tgt gaa act ctc cac gaa tac acc ctg act gaa gcg cag cgc gta gct 1459
Cys Glu Thr Leu His Glu Tyr Thr Leu Thr Glu Ala Gln Arg Val Ala
      440                      445                      450

* tta cgc gat ggc ttt cac tcc gga atc cgt ggt gta ttg ctc aac cag 1507
Leu Arg Asp Gly Phe His Ser Gly Ile Arg Gly Val Leu Leu Asn Gln
      455                      460                      465

cga gat agc tagaatcaca aaaaactggg gct 1539
Arg Asp Ser
470

<210> 1428
<211> 472
<212> PRT
<213> Corynebacterium glutamicum

<400> 1428
Met Leu Glu Arg Thr Gln Val Phe Val Asp Thr Ser Tyr Leu Leu Ala
  1                      5                      10                      15

Ser Phe Tyr Asn Ser Trp Glu Thr Gly Ala Arg Ala Gln Leu Glu Ile
                20                      25                      30

Asp Leu Pro Glu Val Val Gly Val Leu Gly Arg Met Ile Glu Gln Gln
      35                      40                      45

Leu Lys Gln Pro Val Gln Arg Gln Met Trp Tyr Asp Gly Ile Pro Asp
      50                      55                      60

Ser Gly Pro His Arg Tyr Gln Arg Ala Leu Arg Thr Cys Asp Gly Val
      65                      70                      75                      80

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Gln Leu Arg Ala Gly Gln Leu Ile Glu Trp Gly Glu Arg Arg Thr Gln
 85 90 95
 Lys Ala Val Asp Thr Arg Leu Val Ala Asp Leu Val Leu Ala Gly Val
 100 105 110
 Arg Gly Gln Cys Ser Asp Ile Val Leu Val Ser Gly Asp Ala Asp Met
 115 120 125
 Ile Pro Gly Val Gln Glu Ala Ala Asn Ala Gly Leu Arg Val His Leu
 130 135 140
 Tyr Gly Phe Gly Trp Asp Ser Met Ser Ser Gln Leu Arg His Cys Cys
 145 150 155 160
 Asp Thr Thr Thr Ile Leu Asp Pro Arg Glu Asp Phe Ala Glu Cys Met
 165 170 175
 Gln Leu Gln Val Leu Glu Gly Pro Leu Pro Pro Val Val Arg Val Lys
 180 185 190
 Pro Ile Asn Asp Ala Glu Pro Ile Glu Asp Leu Asp Phe Thr Pro Val
 195 200 205
 Pro Gly Val Ala Ser Pro Phe Glu Glu Val Ser Ala Lys Asp Glu Lys
 210 215 220
 Phe Ser Pro Arg Pro Ser Glu Pro Ala Glu Ala Leu Ser Glu Gln Val
 225 230 235 240
 Cys Glu Ala Gln Tyr Glu Ile Ser Lys His Glu Gly Gln Thr Ala Asp
 245 250 255
 Ser Gly Glu Ile Thr Glu Ser Phe Glu Ala Ala Glu Ile Lys Val Thr
 260 265 270
 Glu Phe Phe Gly Glu Pro Ala Ala Pro Val Ala Glu Ser Gly Val Glu
 275 280 285
 Ala Pro Thr Pro Glu Ala Pro Thr Val Pro Glu Ala Ala Lys Pro Thr
 290 295 300
 Pro Ala Lys Pro Lys Thr Pro Lys Ala Glu Pro Gln Lys Gln Glu Ser
 305 310 315 320
 Pro Lys Pro Gly Thr Pro Lys Pro Lys Ala Pro Ser Pro Ala Asp Ile
 325 330 335
 Pro Pro Lys Ala Pro Ala Asp Thr Glu Glu His Ser Glu Val Glu Ala
 340 345 350
 Glu Ile Glu Asp Ser Arg Pro Lys Ile Pro Ser Pro Ser Met Met Ala
 355 360 365
 Pro Arg Arg Lys Leu Arg Ser Arg Tyr Val Pro Leu Pro Asn Glu Val
 370 375 380
 Trp Ala Thr Ala Gly Phe Gln Thr Pro Tyr Asp Val Gly Gln Gln Tyr
 385 390 395 400
 Ala Ser Trp Trp Phe Glu Asn Ala Ala Thr Ser Thr Gln Arg Asp Gln

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                                405                410                415
Ala His Leu Leu Ser Gly Gly Gly Leu Pro Pro Glu Ile Asp Arg Pro
      420                425
Leu Leu Gln Phe Ala Cys Glu Thr Leu His Glu Tyr Thr Leu Thr Glu
      435                440                445
Ala Gln Arg Val Ala Leu Arg Asp Gly Phe His Ser Gly Ile Arg Gly
      450                455                460
Val Leu Leu Asn Gln Arg Asp Ser
      465                470

<210> 1429
<211> 996
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(973)
<223> RXN03048

<400> 1429
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ttagacacac gtaactaaaa cctcagggaa gtgactgata atg gct aat ccg ctc 115
                                         Met Ala Asn Pro Leu
                                         1                               5

agc aag ggc tgg aag tat ctc atg gca tgc ttc gac aac aag atc gat 163
Ser Lys Gly Trp Lys Tyr Leu Met Ala Ser Phe Asp Asn Lys Ile Asp
                        10                        15                        20

gag aat gca gat cca aag atc caa att cag caa gct aca gaa gct gcc 211
Glu Asn Ala Asp Pro Lys Ile Gln Ile Gln Gln Ala Thr Glu Ala Ala
                        25                        30                        35

cag aag cag cac cag cag att atg cag cac gct tct cag att atc ggt 259
Gln Lys Gln His Gln Gln Ile Met Gln His Ala Ser Gln Ile Ile Gly
                        40                        45                        50

cag cag aag cag ctt gag atg aaa ttg aac cgc ttg gtt act gac cgc 307
Gln Gln Lys Gln Leu Glu Met Lys Leu Asn Arg Leu Val Thr Asp Arg
                        55                        60                        65

gat aag ttg cag gaa cag gct cgt cag gca att cag ttg gca gat aag 355
Asp Lys Leu Gln Glu Gln Ala Arg Gln Ala Ile Gln Leu Ala Asp Lys
                        70                        75                        80                        85

tcc gca aac gaa ggc gac agt gtt aag gct cag gag ttc aac aac act 403
Ser Ala Asn Glu Gly Asp Ser Val Lys Ala Gln Glu Phe Asn Asn Thr
                        90                        95                        100

gct gag gtt ttt gct tcc cag ttg gta gct gtg gaa cag cag ttg gag 451
Ala Glu Val Phe Ala Ser Gln Leu Val Ala Val Glu Gln Gln Leu Glu
                        105                        110                        115

cag act act gcg ctt cat cag cag gct gag gtt gcg gcg aag gat gct 499

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Gln Thr Thr Ala Leu His Gln Gln Ala Glu Val Ala Ala Lys Asp Ala
 120 125 130
 gtt gcg aag tct aaa gag tct gag atg cgc ctg aaa gag cag atg tct 547
 Val Ala Lys Ser Lys Glu Ser Glu Met Arg Leu Lys Glu Gln Met Ser
 135 140 145
 cag att gat gct cta cgt gcg cag gct gat cag gcg aag atg cag gaa 595
 Gln Ile Asp Ala Leu Arg Ala Gln Ala Asp Gln Ala Lys Met Gln Glu
 150 155 160 165
 agt gtc act aag tct atg gat tct ttg aat cag ttt gcc act cag gat 643
 Ser Val Thr Lys Ser Met Asp Ser Leu Asn Gln Phe Gly Thr Gln Asp
 170 175 180
 tct tct gtt cct acc ctt gat gcg gtg cgt gag aag atc gag cgt cga 691
 Ser Ser Val Pro Thr Leu Asp Ala Val Arg Glu Lys Ile Glu Arg Arg
 185 190 195
 tac gca gat gct ttg gcc gcg cag gaa ctt acc cag aac act gtt agt 739
 Tyr Ala Asp Ala Leu Gly Ala Gln Glu Leu Thr Gln Asn Thr Val Ser
 200 205 210
 gat cgc atg gct gag att gcg cag tcc gcc acc gat atg cgg gcg tca 787
 Asp Arg Met Ala Glu Ile Ala Gln Ser Gly Thr Asp Met Arg Ala Ser
 215 220 225
 gct cgt ttg gct gaa ctt cgc gcg gag gcg ctg gcc acg tcc gca acg 835
 Ala Arg Leu Ala Glu Leu Arg Ala Glu Leu Gly Thr Ser Ala Thr
 230 235 240 245
 cct aag gcc cag cta gag gca ggt gtc gag gat gcg gaa gaa ctt atc 883
 Pro Lys Gly Gln Leu Glu Ala Gly Val Glu Asp Ala Glu Glu Leu Ile
 250 255 260
 gac gaa acc tcc acc cct tca gct acc cca gaa acc gca agc cca gaa 931
 Asp Glu Thr Ser Thr Pro Ser Ala Thr Pro Glu Thr Ala Ser Pro Glu
 265 270 275
 gct gat gct cca gaa gca tcc gca gac gag tcc gag aag aaa 973
 Ala Asp Ala Pro Glu Ala Ser Ala Asp Glu Ser Glu Lys Lys
 280 285 290
 taacctaacc acaaaaaaact ggg 996

<210> 1430

<211> 291

<212> PRT

<213> Corynebacterium glutamicum

<400> 1430

Met Ala Asn Pro Leu Ser Lys Gly Trp Lys Tyr Leu Met Ala Ser Phe
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Asp Asn Lys Ile Asp Glu Asn Ala Asp Pro Lys Ile Gln Ile Gln Gln
 20 25 30

Ala Thr Glu Ala Ala Gln Lys Gln His Gln Gln Ile Met Gln His Ala
 35 40 45

Ser Gln Ile Ile Gly Gln Gln Lys Gln Leu Glu Met Lys Leu Asn Arg
 50 55 60
 Leu Val Thr Asp Arg Asp Lys Leu Gln Glu Gln Ala Arg Gln Ala Ile
 65 70 75 80
 Gln Leu Ala Asp Lys Ser Ala Asn Glu Gly Asp Ser Val Lys Ala Gln
 85 90 95
 Glu Phe Asn Asn Thr Ala Glu Val Phe Ala Ser Gln Leu Val Ala Val
 100 105 110
 Glu Gln Gln Leu Glu Gln Thr Thr Ala Leu His Gln Gln Ala Glu Val
 115 120 125
 Ala Ala Lys Asp Ala Val Ala Lys Ser Lys Glu Ser Glu Met Arg Leu
 130 135 140
 Lys Glu Gln Met Ser Gln Ile Asp Ala Leu Arg Ala Gln Ala Asp Gln
 145 150 155 160
 Ala Lys Met Gln Glu Ser Val Thr Lys Ser Met Asp Ser Leu Asn Gln
 165 170 175
 Phe Gly Thr Gln Asp Ser Ser Val Pro Thr Leu Asp Ala Val Arg Glu
 180 185 190
 Lys Ile Glu Arg Arg Tyr Ala Asp Ala Leu Gly Ala Gln Glu Leu Thr
 195 200 205
 Gln Asn Thr Val Ser Asp Arg Met Ala Glu Ile Ala Gln Ser Gly Thr
 210 215 220
 Asp Met Arg Ala Ser Ala Arg Leu Ala Glu Leu Arg Ala Glu Ala Leu
 225 230 235 240
 Gly Thr Ser Ala Thr Pro Lys Gly Gln Leu Glu Ala Gly Val Glu Asp
 245 250 255
 Ala Glu Glu Leu Ile Asp Glu Thr Ser Thr Pro Ser Ala Thr Pro Glu
 260 265 270
 Thr Ala Ser Pro Glu Ala Asp Ala Pro Glu Ala Ser Ala Asp Glu Ser
 275 280 285
 Glu Lys Lys
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<210> 1431

<211> 996

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(973)

<223> FRXA00037

<400> 1431

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ttagacacac gtaactaaaa cctcagggaa gtgactgata atg gct aat ccg ctc 115
 Met Ala Asn Pro Leu
 1 5

agc aag ggc tgg aag tat ctc atg gca tgc ttc gac aac aag atc gat 163
 Ser Lys Gly Trp Lys Tyr Leu Met Ala Ser Phe Asp Asn Lys Ile Asp
 10 15 20

gag aat gca gat cca aag atc caa att cag caa gct aca gaa gct gcc 211
 Glu Asn Ala Asp Pro Lys Ile Gln Ile Gln Gln Ala Thr Glu Ala Ala
 25 30 35

cag aag cag cac cag cag att atg cag cac gct tct cag att atc ggt 259
 Gln Lys Gln His Gln Gln Ile Met Gln His Ala Ser Gln Ile Ile Gly
 40 45 50

cag cag aag cag ctt gag atg aaa ttg aac cgc ttg gtt act gac cgc 307
 Gln Gln Lys Lys Leu Glu Met Lys Leu Asn Arg Leu Val Thr Asp Arg
 55 60 65

gat aag ttg cag gaa cag gct cgt cag gca att cag ttg gca gat aag 355
 Asp Lys Leu Gln Glu Gln Ala Arg Gln Ala Ile Gln Leu Ala Asp Lys
 70 75 80 85

tcc gca aac gaa ggc gac agt gtt aag gct cag gag ttc aac aac act 403
 Ser Ala Asn Glu Gly Asp Ser Val Lys Ala Gln Glu Phe Asn Asn Thr
 90 95 100

gct gag gtt ttt gct tcc cag ttg gta gct gtg gaa cag cag ttg gag 451
 Ala Glu Val Phe Ala Ser Gln Leu Val Ala Val Glu Gln Gln Leu Glu
 105 110 115

cag act act gcg ctt cat cag cag gct gag gtt gcg gcg aag gat gct 499
 Gln Thr Thr Ala Leu His Gln Gln Ala Glu Val Ala Ala Lys Asp Ala
 120 125 130

gtt gcg aag tct aaa gag tct gag atg cgc ctg aaa gag cag atg tct 547
 Val Ala Lys Ser Lys Glu Ser Glu Met Arg Leu Lys Glu Gln Met Ser
 135 140 145

cag att gat gct cta cgt gcg cag gct gat cag gcg aag atg cag gaa 595
 Gln Ile Asp Ala Leu Arg Ala Gln Ala Asp Gln Ala Lys Met Gln Glu
 150 155 160 165

agt gtc act aag tct atg gat tct ttg aat cag ttt ggc act cag gat 643
 Ser Val Thr Lys Ser Met Asp Ser Leu Asn Gln Phe Gly Thr Gln Asp
 170 175 180

tct tct gtt cct acc ctt gat gcg gtg cgt gag aag atc gag cgt cga 691
 Ser Ser Val Pro Thr Leu Asp Ala Val Arg Glu Lys Ile Glu Arg Arg
 185 190 195

tac gca gat gct ttg ggc gcg cag gaa ctt acc cag aac act gtt agt 739
 Tyr Ala Asp Ala Leu Gly Ala Gln Glu Leu Thr Gln Asn Thr Val Ser
 200 205 210

gat cgc atg gct gag att gcg cag tcc ggc acc gat atg cgc gcg tca 787
 Asp Arg Met Ala Glu Ile Ala Gln Ser Gly Thr Asp Met Arg Ala Ser
 215 220 225

gct cgt ttg gct gaa ctt cgc gcg gag gcg ctg ggc acg tcc gca acg 835
 Ala Arg Leu Ala Glu Leu Arg Ala Glu Ala Leu Gly Thr Ser Ala Thr 245
 230 235 240

cct aag ggc cag cta gag gca ggt gtc gag gat gcg gaa gaa ctt atc 883
 Pro Lys Gly Gln Leu Glu Ala Gly Val Glu Asp Ala Glu Glu Leu Ile 260
 250 255 260

gac gaa acc tcc acc cct tca gct acc cca gaa acc gca agc cca gaa 931
 Asp Glu Thr Ser Thr Pro Ser Ala Thr Pro Glu Thr Ala Ser Pro Glu 275
 265 270 275

gct gat gct cca gaa gca tcc gca gac gag tcc gag aag aaa 973
 Ala Asp Ala Pro Glu Ala Ser Ala Asp Glu Ser Glu Lys Lys 290
 280 285 290

taacctaaac acaaaaaaact ggg 996

<210> 1432

<211> 291

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1432

Met Ala Asn Pro Leu Ser Lys Gly Trp Lys Tyr Leu Met Ala Ser Phe
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Asp Asn Lys Ile Asp Glu Asn Ala Asp Pro Lys Ile Gln Ile Gln Gln
 20 25 30

Ala Thr Glu Ala Ala Gln Lys Gln His Gln Gln Ile Met Gln His Ala
 35 40 45

Ser Gln Ile Ile Gly Gln Gln Lys Gln Leu Glu Met Lys Leu Asn Arg
 50 55 60

Leu Val Thr Asp Arg Asp Lys Leu Gln Glu Gln Ala Arg Gln Ala Ile
 65 70 75 80

Gln Leu Ala Asp Lys Ser Ala Asn Glu Gly Asp Ser Val Lys Ala Gln
 85 90 95

Glu Phe Asn Asn Thr Ala Glu Val Phe Ala Ser Gln Leu Val Ala Val
 100 105 110

Glu Gln Gln Leu Glu Gln Thr Thr Ala Leu His Gln Gln Ala Glu Val
 115 120 125

Ala Ala Lys Asp Ala Val Ala Lys Ser Lys Glu Ser Glu Met Arg Leu
 130 135 140

Lys Glu Gln Met Ser Gln Ile Asp Ala Leu Arg Ala Gln Ala Asp Gln
 145 150 155 160

Ala Lys Met Gln Glu Ser Val Thr Lys Ser Met Asp Ser Leu Asn Gln
 165 170 175

Phe Gly Thr Gln Asp Ser Ser Val Pro Thr Leu Asp Ala Val Arg Glu
 180 185 190

Lys Ile Glu Arg Arg Tyr Ala Asp Ala Leu Gly Ala Gln Glu Leu Thr
 195 200 205
 Gln Asn Thr Val Ser Asp Arg Met Ala Glu Ile Ala Gln Ser Gly Thr
 210 215 220
 Asp Met Arg Ala Ser Ala Arg Leu Ala Glu Leu Arg Ala Glu Ala Leu
 225 230 235 240
 Gly Thr Ser Ala Thr Pro Lys Gly Gln Leu Glu Ala Gly Val Glu Asp
 245 250 255
 Ala Glu Glu Leu Ile Asp Glu Thr Ser Thr Pro Ser Ala Thr Pro Glu
 260 265 270
 Thr Ala Ser Pro Glu Ala Asp Ala Pro Glu Ala Ser Ala Asp Glu Ser
 275 280 285
 Glu Lys Lys
 290

<210> 1433
 <211> 1066
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1066)
 <223> RXN03050

<400> 1433
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 agagtgggtg gtaacaacac ggggaaagg ggaagacacc atg agc atc acc aca 115
 Met Ser Ile Thr Thr
 1 5
 cac gtc caa gca ctc acc aca gca ctc aac gcc atc gac aac cat ttg 163
 His Val Gln Ala Leu Thr Thr Ala Leu Asn Ala Ile Asp Asn His Leu
 10 15 20
 gcc agc atg ctc gac cat ggt gtc acc cca gac caa tac aag gcc atc 211
 Ala Ser Met Leu Asp His Gly Val Thr Pro Asp Gln Tyr Lys Ala Ile
 25 30 35
 gag ccc gac ctc atc gcc cta gaa cac acc atc aac cac cac gcc acc 259
 Glu Pro Asp Leu Ile Ala Leu Glu His Thr Ile Asn His His Ala Thr
 40 45 50
 atc gcc gcc caa acc aca gcc ctc gcc gaa cgc acc aac gcc gcc cac 307
 Ile Ala Ala Gln Thr Thr Ala Leu Ala Glu Arg Thr Asn Ala Ala His
 55 60 65
 acc att ggc tcc acc cac ctc atc gac tac ctc acc acc acc ttc gga 355
 Thr Ile Gly Ser Thr His Leu Ile Asp Tyr Leu Thr Thr Thr Phe Gly
 70 75 80 85
 cta tcc aaa gca cgc gcc cac cac cgc atc aat ctc gcc cac tcc ctc 403
 Leu Ser Lys Ala Arg Ala His His Arg Ile Asn Leu Ala His Ser Leu

	90	95	100	
	tac ccc ata ccg aag cca aac cct gga tct ggc aac ggc ggt aat ggt			451
	Tyr Pro Ile Pro Lys Pro Asn Pro Gly Ser Gly Asn Gly Gly Asn Gly			
	105	110	115	
	ggc aat ccc gac ggc ggt cct gat ggt ggc gac tcg ggt gat gac gac			499
	Gly Asn Pro Asp Gly Gly Pro Asp Gly Gly Asp Ser Gly Asp Asp Asp			
	120	125	130	
	tcc ggc gac gat gac ccc gac ccc gaa ccg gac aag cct gaa gac ggc			547
	Ser Gly Asp Asp Asp Pro Asp Pro Glu Pro Asp Lys Pro Glu Asp Gly			
	135	140	145	
	aaa cct gat ggt gat aag cct cgt ggg cca cgg atc agc gcg gaa aaa			595
	Lys Pro Asp Gly Asp Lys Pro Arg Gly Pro Arg Ile Ser Ala Glu Lys			
	150	155	160	165
	cac gcc atc atc acc gac gaa ctc gcc cgc ctc aac ccg aat acc aca			643
	His Ala Ile Ile Thr Asp Glu Leu Ala Arg Leu Asn Pro Asn Thr Thr			
	170	175	180	
	ccc agc gcc gag gag cta cgc acc caa gcc ctg agt caa gcg atc tgg			691
	Pro Ser Ala Glu Glu Leu Arg Thr Gln Ala Leu Ser Gln Ala Ile Trp			
	185	190	195	
	cgc acc cca gaa gac ctc cgc acg tgg cta cgc cac cac gtc acc acc			739
	Arg Thr Pro Glu Asp Leu Arg Thr Trp Leu Arg His His Val Thr Thr			
	200	205	210	
	gcc aat aaa aac aac ccc aac ccc atc acc gcc atg aaa agg cgc tac			787
	Ala Asn Lys Asn Asn Pro Asn Pro Ile Thr Ala Met Lys Arg Arg Tyr			
	215	220	225	
	ctc gct gta ggt aaa ccc gat gcc gac aac atg gtc cgc atc agc ggc			835
	Leu Ala Val Gly Lys Pro Asp Ala Asp Asn Met Val Arg Ile Ser Gly			
	230	235	240	245
	ctc gtg ccc gca gcc acc gca gca ctg atc acc gcg aac acc gca ccg			883
	Leu Val Pro Ala Ala Thr Ala Ala Leu Ile Thr Ala Asn Thr Ala Pro			
	250	255	260	
	tta acc aaa cgc ggc aac ctc gtg gat cta ccc gca gca gaa gat atg			931
	Leu Thr Lys Arg Gly Asn Leu Val Asp Leu Pro Ala Ala Glu Asp Met			
	265	270	275	
	cgc acc cgc ggg caa cgc cat gcg gac gcg ttg cat cac atc atg gag			979
	Arg Thr Arg Gly Gln Arg His Ala Asp Ala Leu His His Ile Met Glu			
	280	285	290	
	atc tac aac cac ggt att gtc acc cca gct cgt ggt gga aca gcc agc			1027
	Ile Tyr Asn His Gly Ile Val Thr Pro Ala Arg Gly Gly Thr Ala Ser			
	295	300	305	
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<210> 1434

<211> 322

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1434

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Gln	Tyr	Lys	Ala	Ile	Glu	Pro	Asp	Leu	Ile	Ala	Leu	Glu	His	Thr	Ile
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Asn	His	His	Ala	Thr	Ile	Ala	Ala	Gln	Thr	Thr	Ala	Leu	Ala	Glu	Arg
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Thr	Asn	Ala	Ala	His	Thr	Ile	Gly	Ser	Thr	His	Leu	Ile	Asp	Tyr	Leu
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Thr	Thr	Thr	Phe	Gly	Leu	Ser	Lys	Ala	Arg	Ala	His	His	Arg	Ile	Asn
				85					90					95	

Leu	Ala	His	Ser	Leu	Tyr	Pro	Ile	Pro	Lys	Pro	Asn	Pro	Gly	Ser	Gly
			100					105					110		

Asn	Gly	Gly	Asn	Gly	Gly	Asn	Pro	Asp	Gly	Gly	Pro	Asp	Gly	Gly	Asp
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Ser	Gly	Asp	Asp	Asp	Ser	Gly	Asp	Asp	Asp	Pro	Asp	Pro	Glu	Pro	Asp
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Lys	Pro	Glu	Asp	Gly	Lys	Pro	Asp	Gly	Asp	Lys	Pro	Arg	Gly	Pro	Arg
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Ile	Ser	Ala	Glu	Lys	His	Ala	Ile	Ile	Thr	Asp	Glu	Leu	Ala	Arg	Leu
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Asn	Pro	Asn	Thr	Thr	Pro	Ser	Ala	Glu	Glu	Leu	Arg	Thr	Gln	Ala	Leu
			180					185					190		

Ser	Gln	Ala	Ile	Trp	Arg	Thr	Pro	Glu	Asp	Leu	Arg	Thr	Trp	Leu	Arg
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His	His	Val	Thr	Thr	Ala	Asn	Lys	Asn	Asn	Pro	Asn	Pro	Ile	Thr	Ala
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Met	Lys	Arg	Arg	Tyr	Leu	Ala	Val	Gly	Lys	Pro	Asp	Ala	Asp	Asn	Met
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Val	Arg	Ile	Ser	Gly	Leu	Val	Pro	Ala	Ala	Thr	Ala	Ala	Leu	Ile	Thr
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Ala	Ala	Glu	Asp	Met	Arg	Thr	Arg	Gly	Gln	Arg	His	Ala	Asp	Ala	Leu
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His	His	Ile	Met	Glu	Ile	Tyr	Asn	His	Gly	Ile	Val	Thr	Pro	Ala	Arg
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Glu Ile

<210> 1435

<211> 1558

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (12)..(1535)

<223> RXN03053

<400> 1435

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Leu Val Thr Asn Gly Leu Asn Asp Val Ala Gly Glu Tyr Val Gly Val
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Met Arg Gly Asp Val Asn Asn Ser Ala Val Leu Phe Asp Val Asp Arg
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tgg tcg gga cat gtc gta tgc gca gat agc tcg att aat aca tca cca 194
Trp Ser Gly His Val Val Cys Ala Asp Ser Ser Ile Asn Thr Ser Pro
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cta ctt aag cgt ccc cgt gtc gtt gac atg tgg ggg tcg aag att tct 242
Leu Leu Lys Arg Pro Arg Val Val Asp Met Trp Gly Ser Lys Ile Ser
          65                70                75

cag gca gcg cta ctg aat aac cgt cgc gta gtg cac ctg gtg ctc aat 290
Gln Ala Ala Leu Leu Asn Asn Arg Arg Val Val His Leu Val Leu Asn
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ggt gcc aag ctc gat gaa atg gga cca aag cta gaa tcc atg acc gct 338
Gly Ala Lys Leu Asp Glu Met Gly Pro Lys Leu Glu Ser Met Thr Ala
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cat gtg gat atg act agc gga gat ctc aac atg ttc gag ctg ttt ggt 386
His Val Asp Met Thr Ser Gly Asp Leu Asn Met Phe Glu Leu Phe Gly
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Lys Gln Glu Asp Glu Leu Ser Leu Tyr Ser Thr His Met Asp Lys Ile
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gtg ttt atg acc gag cag gca ttg ggc gat aag acc tct gag ctg gcg 482
Val Phe Met Thr Glu Gln Ala Leu Gly Asp Lys Thr Ser Glu Leu Ala
          145                150                155

cta ttg cgc gga aag ctc aaa gaa att att aca gcc ttt tat gtg gat 530
Leu Leu Arg Gly Lys Leu Lys Glu Ile Ile Thr Ala Phe Tyr Val Asp
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Leu Val Gly Val Pro His Glu Gln Ile Pro Leu Ser Val Phe Val	
190 195 200 205	
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Ser Tyr Leu Asp Gln Glu Tyr Glu Arg Gln Lys Tyr Glu Gly Thr Lys	
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Asp Pro Glu Met Phe Arg Ala Ile Ser Val Leu Arg Leu Thr Tyr Lys	
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Gly Ile Asp Ser Val Asn Ser Ala Arg Arg Val Ile Tyr Asp Phe Ser	
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Gly Val Leu Arg Arg Gly Ala Gly Val Ala Met Ala Gln Leu Val Asn	
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Val Ile Gly Phe Ala Val Glu Thr Leu Gly Gln Gly Asp Val Val Ile	
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Ile His Gly Ala Asp Gly Ile Val Asp Val Asp Val Gln Asp Tyr Leu	
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Ala Asn Gln Phe Ala Tyr Met Ala Glu Arg Gly Gly Arg Val Ala Tyr	
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Leu Tyr Ser Ser Met Asp Ala Met Leu Gly Thr Val Gly Phe Asn Gln	
335 340 345	
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Phe Gln Arg Ala Ala Tyr Thr Ile Leu Gly Pro Met Asn Val Asp Ser	
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Val Asp Thr Tyr Gln Ser Leu Ile Asn Ser Gln Ile Pro Met Asp Leu	
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Ala Arg Leu Val Thr Thr Gln Asn Ser Gly Ala Ser Tyr Leu Arg Arg	
385 390 395	
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Gly Ser Thr Asn Val Val Phe Glu Thr Asn Leu Ala Leu Gly Val Asn	
400 405 410	

cct tat atg gag cag cgt cgc aag att gaa gca cag cga ggt cag cga 1298
 Pro Tyr Met Glu Gln Arg Arg Lys Ile Glu Ala Gln Arg Gly Gln Arg
 415 420 425

cga tcc aag cga gac aag cac tac ggt ggt ggc acg acg atg gtg ggc 1346
 Arg Ser Lys Arg Asp Lys His Tyr Gly Gly Thr Thr Met Val Gly
 430 435 440 445

aca gcg gat ctt gat gtt gtc gca att cag gcg aag gcc gag cac cgc 1394
 Thr Ala Asp Leu Asp Val Val Ala Ile Gln Ala Lys Ala Glu His Arg
 450 455 460

gaa gag cgc ttt gat gag aaa tct gcg cgc aag atg aag gag ctt gat 1442
 Glu Glu Arg Phe Asp Glu Lys Ser Ala Arg Lys Met Lys Glu Leu Asp
 465 470 475

gat gta gaa gcg aaa gaa cta gct ttg aaa act ggg ccg aag aat ctt 1490
 Asp Val Glu Ala Lys Glu Leu Ala Leu Lys Thr Gly Pro Lys Asn Leu
 480 485 490

gat gat gcg ctt gca cag gtg gag aag aag cgc ctg gcg aag cgg 1535
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 <212> PRT
 <213> *Corynebacterium glutamicum*

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 35 40 45
 His Val Val Cys Ala Asp Ser Ser Ile Asn Thr Ser Pro Leu Leu Lys
 50 55 60
 Arg Pro Arg Val Val Asp Met Trp Gly Ser Lys Ile Ser Gln Ala Ala
 65 70 75 80
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 85 90 95
 Leu Asp Glu Met Gly Pro Lys Leu Glu Ser Met Thr Ala His Val Asp
 100 105 110
 Met Thr Ser Gly Asp Leu Asn Met Phe Glu Leu Phe Gly Lys Gln Glu
 115 120 125
 Asp Glu Leu Ser Leu Tyr Ser Thr His Met Asp Lys Ile Val Phe Met
 130 135 140
 Thr Glu Gln Ala Leu Gly Asp Lys Thr Ser Glu Leu Ala Leu Leu Arg

145 150 155 160
 Gly Lys Leu Lys Glu Ile Ile Thr Ala Phe Tyr Val Asp Met Lys Met
 165 170 175
 Trp Ala Leu Asn Ala Gly Glu Asn Arg Asp Lys Leu Arg Leu Val Gly
 180 185 190
 Val Pro His Glu Gln Ile Pro Leu Leu Ser Val Phe Val Ser Tyr Leu
 195 200 205
 Asp Gln Glu Tyr Glu Arg Gln Lys Tyr Glu Gly Thr Lys Asp Pro Glu
 210 215 220
 Met Phe Arg Ala Ile Ser Val Leu Arg Leu Thr Tyr Lys Asp Leu Leu
 225 230 235 240
 Asp Thr His Gly Asp Leu Phe Asn Gln His Thr Ala Asp Gly Ile Asp
 245 250 255
 Ser Val Asn Ser Ala Arg Arg Val Ile Tyr Asp Phe Ser Gly Val Leu
 260 265 270
 Arg Arg Gly Ala Gly Val Ala Met Ala Gln Leu Val Asn Val Ile Gly
 275 280 285
 Phe Ala Val Glu Thr Leu Gly Gln Gly Asp Val Val Ile Ile His Gly
 290 295 300
 Ala Asp Gly Ile Val Asp Val Asp Val Gln Asp Tyr Leu Ala Asn Gln
 305 310 315 320
 Phe Ala Tyr Met Ala Glu Arg Gly Gly Arg Val Ala Tyr Leu Tyr Ser
 325 330 335
 Ser Met Asp Ala Met Leu Gly Thr Val Gly Phe Asn Gln Phe Gln Arg
 340 345 350
 Ala Ala Tyr Thr Ile Leu Gly Pro Met Asn Val Asp Ser Val Asp Thr
 355 360 365
 Tyr Gln Ser Leu Ile Asn Ser Gln Ile Pro Met Asp Leu Ala Arg Leu
 370 375 380
 Val Thr Thr Gln Asn Ser Gly Ala Ser Tyr Leu Arg Arg Gly Ser Thr
 385 390 395 400
 Asn Val Val Phe Glu Thr Asn Leu Ala Leu Gly Val Asn Pro Tyr Met
 405 410 415
 Glu Gln Arg Arg Lys Ile Glu Ala Gln Arg Gly Gln Arg Arg Ser Lys
 420 425 430
 Arg Asp Lys His Tyr Gly Gly Gly Thr Thr Met Val Gly Thr Ala Asp
 435 440 445
 Leu Asp Val Val Ala Ile Gln Ala Lys Ala Glu His Arg Glu Glu Arg
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 Phe Asp Glu Lys Ser Ala Arg Lys Met Lys Glu Leu Asp Asp Val Glu
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Leu Ala Gln Val Glu Lys Lys Arg Leu Ala Lys Arg
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<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(1536)

<223> FRXA02885

<400> 1437

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 Ser Leu Val Thr Asn Gly Leu Asn Asp Val Ala Gly Glu Tyr Val Gly
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gtc atg cgt ggc gat gtc aac aac tcc gct gtg ctt ttt gat gtg gat 144
 Val Met Arg Gly Asp Val Asn Asn Ser Ala Val Leu Phe Asp Val Asp
 35 40 45

cgc tgg tcg gga cat gtc gta tgc gca gat agc tcg att aat aca tca 192
 Arg Trp Ser Gly His Val Val Cys Ala Asp Ser Ser Ile Asn Thr Ser
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cca cta ctt aag cgt ccc cgt gtc gtt gac atg tgg ggg tcg aag att 240
 Pro Leu Leu Lys Arg Pro Arg Val Val Asp Met Trp Gly Ser Lys Ile
 65 70 75 80

tct cag gca cgc cta ctg aat aac cgt cgc gta gtg cac ctg gtg ctc 288
 Ser Gln Ala Ala Leu Leu Asn Asn Arg Arg Val Val His Leu Val Leu
 85 90 95

aat ggt gcc aag ctc gat gaa atg gga cca aag cta gaa tcc atg acc 336
 Asn Gly Ala Lys Leu Asp Glu Met Gly Pro Lys Leu Glu Ser Met Thr
 100 105 110

gct cat gtg gat atg act agc gga gat ctc aac atg ttc gag ctg ttt 384
 Ala His Val Asp Met Thr Ser Gly Asp Leu Asn Met Phe Glu Leu Phe
 115 120 125

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 Gly Lys Gln Glu Asp Glu Leu Ser Leu Tyr Ser Thr His Met Asp Lys
 130 135 140

atc gtg ttt atg acc gag cag gca ttg ggc gat aag acc tct gag ctg 480
 Ile Val Phe Met Thr Glu Gln Ala Leu Gly Asp Lys Thr Ser Glu Leu
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 Ala Leu Leu Arg Gly Lys Leu Lys Glu Ile Ile Thr Ala Phe Tyr Val

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Val	Ser	Tyr	Leu	Asp	Gln	Glu	Tyr	Glu	Arg	Gln	Lys	Tyr	Glu	Gly	Thr					
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aaa	gac	cct	gaa	atg	ttt	cgt	gcc	att	tct	gtg	ctg	cga	ctg	acc	tat	720				
Lys	Asp	Pro	Glu	Met	Phe	Arg	Ala	Ile	Ser	Val	Leu	Arg	Leu	Thr	Tyr					
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Lys	Asp	Leu	Leu	Asp	Thr	His	Gly	Asp	Leu	Phe	Asn	Gln	His	Thr	Ala					
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Leu	Ala	Asn	Gln	Phe	Ala	Tyr	Met	Ala	Glu	Arg	Gly	Gly	Arg	Val	Ala					
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Tyr	Leu	Tyr	Ser	Ser	Met	Asp	Ala	Met	Leu	Gly	Thr	Val	Gly	Phe	Asn					
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Gln	Phe	Gln	Arg	Ala	Ala	Tyr	Thr	Ile	Leu	Gly	Pro	Met	Asn	Val	Asp					
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Leu	Ala	Arg	Leu	Val	Thr	Thr	Gln	Asn	Ser	Gly	Ala	Ser	Tyr	Leu	Arg					
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Arg	Gly	Ser	Ser	Asn	Val	Val	Phe	Glu	Thr	Asn	Leu	Ala	Leu	Gly	Val					
405										410					415					

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Arg Arg Ser Lys Arg Asp Lys His Tyr Gly Gly Gly Thr Thr Met Val
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ggc aca gcg gat ctt gat gtt gtc gca att cag gcg aag gcc gag cac 1392
Gly Thr Ala Asp Leu Asp Val Val Ala Ile Gln Ala Lys Ala Glu His
450 455 460

cgc gaa gag cgc ttt gat gag aaa tct gcg cgc aag atg aag gag ctt 1440
Arg Glu Glu Arg Phe Asp Glu Lys Ser Ala Arg Lys Met Lys Glu Leu
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485 490 495

ctt gat gat gcg ctt gca cag gtg gag aag aag cgc ctg gcg aag cgg 1536
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<400> 1438
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35 40 45
Arg Trp Ser Gly His Val Val Cys Ala Asp Ser Ser Ile Asn Thr Ser
50 55 60
Pro Leu Leu Lys Arg Pro Arg Val Val Asp Met Trp Gly Ser Lys Ile
65 70 75 80
Ser Gln Ala Ala Leu Asn Asn Arg Arg Val Val His Leu Val Leu
85 90 95
Asn Gly Ala Lys Leu Asp Glu Met Gly Pro Lys Leu Glu Ser Met Thr
100 105 110
Ala His Val Asp Met Thr Ser Gly Asp Leu Asn Met Phe Glu Leu Phe
115 120 125
Gly Lys Gln Glu Asp Glu Leu Ser Leu Tyr Ser Thr His Met Asp Lys
130 135 140

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Ile Val Phe Met Thr Glu Gln Ala Leu Gly Asp Lys Thr Ser Glu Leu
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 Asp Met Lys Met Trp Ala Leu Asn Ala Gly Glu Asn Arg Asp Lys Leu
 180 185 190
 Arg Leu Val Gly Val Pro His Glu Gln Ile Pro Leu Ser Val Phe
 195 200 205
 Val Ser Tyr Leu Asp Gln Glu Tyr Glu Arg Gln Lys Tyr Glu Gly Thr
 210 215 220
 Lys Asp Pro Glu Met Phe Arg Ala Ile Ser Val Leu Arg Leu Thr Tyr
 225 230 235 240
 Lys Asp Leu Leu Asp Thr His Gly Asp Leu Phe Asn Gln His Thr Ala
 245 250 255
 Asp Gly Ile Asp Ser Val Asn Ser Ala Arg Arg Val Ile Tyr Asp Phe
 260 265 270
 Ser Gly Val Leu Arg Arg Gly Ala Gly Val Ala Met Ala Gln Leu Val
 275 280 285
 Asn Val Ile Gly Phe Ala Val Glu Thr Leu Gly Gln Gly Asp Val Val
 290 295 300
 Ile Ile His Gly Ala Asp Gly Ile Val Asp Val Asp Val Gln Asp Tyr
 305 310 315 320
 Leu Ala Asn Gln Phe Ala Tyr Met Ala Glu Arg Gly Gly Arg Val Ala
 325 330 335
 Tyr Leu Tyr Ser Ser Met Asp Ala Met Leu Gly Thr Val Gly Phe Asn
 340 345 350
 Gln Phe Gln Arg Ala Ala Tyr Thr Ile Leu Gly Pro Met Asn Val Asp
 355 360 365
 Ser Val Asp Thr Tyr Gln Ser Leu Ile Asn Ser Gln Ile Pro Met Asp
 370 375 380
 Leu Ala Arg Leu Val Thr Thr Gln Asn Ser Gly Ala Ser Tyr Leu Arg
 385 390 395 400
 Arg Gly Ser Thr Asn Val Val Phe Glu Thr Asn Leu Ala Leu Gly Val
 405 410 415
 Asn Pro Tyr Met Glu Gln Arg Arg Lys Ile Glu Ala Gln Arg Gly Gln
 420 425 430
 Arg Arg Ser Lys Arg Asp Lys His Tyr Gly Gly Gly Thr Met Val
 435 440 445
 Gly Thr Ala Asp Leu Asp Val Val Ala Ile Gln Ala Lys Ala Glu His
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 Arg Glu Glu Arg Phe Asp Glu Lys Ser Ala Arg Lys Met Lys Glu Leu

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(529)
 <223> RXN03055

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 Met Tyr Ser Asp Lys
 1 5
 ctg att ctc ttg ttc ctt tct gag cag gat tca agc tat gaa tgc tgc 163
 Leu Ile Leu Leu Phe Leu Ser Glu Gln Asp Ser Ser Tyr Glu Cys Cys
 10 15 20
 gta ggt tta tta gat ggc tca gat gga cgt gat tat att gaa aag ctt 211
 Val Gly Leu Leu Asp Gly Ser Asp Gly Arg Asp Tyr Ile Glu Lys Leu
 25 30 35
 ctg aag ggt agg aag ctg aag aac cat ttt ctt gaa tgg gaa gat att 259
 Leu Lys Gly Arg Lys Leu Lys Asn His Phe Leu Glu Trp Glu Asp Ile
 40 45 50
 aac aag gct gat gtt gct cgt gaa gaa ata tat aaa ggg caa ttg gtg 307
 Asn Lys Ala Asp Val Ala Arg Glu Glu Ile Tyr Lys Gly Gln Leu Val
 55 60 65
 cat ctg gtg ttt gtg acg gct ctt tcc acg cct ggt gaa att tct ttt 355
 His Leu Val Phe Val Thr Ala Leu Ser Thr Pro Gly Glu Ile Ser Phe
 70 75 80 85
 gtt ttt cca ggt caa tct ctt atg agt gca aca ctc gaa gaa gac ttt 403
 Val Phe Pro Gly Gln Ser Leu Met Ser Ala Thr Leu Glu Glu Asp Phe
 90 95 100
 gct gcg ctt gtg ctc gaa gag gag cgc aca tca ttt aga cct gaa ctg 451
 Ala Ala Leu Val Leu Glu Glu Glu Arg Thr Ser Phe Arg Pro Glu Leu
 105 110 115
 tct cac ctg tgg tca ctc ccc gta ggg tgg gta gct ccg ggg ctt gag 499
 Ser His Leu Trp Ser Leu Pro Val Gly Trp Val Ala Pro Gly Leu Glu
 120 125 130

ggt ttc gtg gag cgt aat tcc gag gca gct tgaaccaccg cttctctgagc 549
 Gly Phe Val Glu Arg Asn Ser Glu Ala Ala
 135 140

cgg 552

<210> 1440

<211> 143

<212> PRT

<213> Corynebacterium glutamicum

<400> 1440

Met Tyr Ser Asp Lys Leu Ile Leu Leu Phe Leu Ser Glu Gln Asp Ser
 1 5 10 15

Ser Tyr Glu Cys Cys Val Gly Leu Leu Asp Gly Ser Asp Gly Arg Asp
 20 25 30

Tyr Ile Glu Lys Leu Leu Lys Gly Arg Lys Leu Lys Asn His Phe Leu
 35 40 45

Glu Trp Glu Asp Ile Asn Lys Ala Asp Val Ala Arg Glu Glu Ile Tyr
 50 55 60

Lys Gly Gln Leu Val His Leu Val Phe Val Thr Ala Leu Ser Thr Pro
 65 70 75 80

Gly Glu Ile Ser Phe Val Phe Pro Gly Gln Ser Leu Met Ser Ala Thr
 85 90 95

Leu Glu Glu Asp Phe Ala Ala Leu Val Leu Glu Glu Glu Arg Thr Ser
 100 105 110

Phe Arg Pro Glu Leu Ser His Leu Trp Ser Leu Pro Val Gly Trp Val
 115 120 125

Ala Pro Gly Leu Glu Gly Phe Val Glu Arg Asn Ser Glu Ala Ala
 130 135 140

<210> 1441

<211> 552

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(529)

<223> FRXA00261

<400> 1441

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accgtagtta acataagga tggaatagga gaattgcggc atg tat tcc gac aag 115
 Met Tyr Ser Asp Lys
 1 5

ctg att ctc ttg ttc ctt tct gag cag gat tca agc tat gaa tgc tgc 163
 Leu Ile Leu Leu Phe Leu Ser Glu Gln Asp Ser Ser Tyr Glu Cys Cys
 10 15 20

gta ggt tta tta gat ggc tca gat gga cgt gat tat att gaa aag ctt 211
 Val Gly Leu Leu Asp Gly Ser Asp Gly Arg Asp Tyr Ile Glu Lys Leu
 25 30 35

ctg aag ggt agg aag ctg aag aac cat ttt ctt gaa tgg gaa gat att 259
 Leu Lys Gly Arg Lys Leu Lys Asn His Phe Leu Glu Trp Glu Asp Ile
 40 45 50

aac aag gct gat gtt gct cgt gaa gaa ata tat aaa ggg caa ttg gtg 307
 Asn Lys Ala Asp Val Ala Arg Glu Glu Ile Tyr Lys Gly Gln Leu Val
 55 60 65

cat ctg gtg ttt gtg acg gct ctt tcc acg cct ggt gaa att tct ttt 355
 His Leu Val Phe Val Thr Ala Leu Ser Thr Pro Gly Glu Ile Ser Phe
 70 75 80 85

gtt ttt cca ggt caa tct ctc atg agt gca aca ctc gaa gaa gac ttt 403
 Val Phe Pro Gly Gln Ser Leu Met Ser Ala Thr Leu Glu Glu Asp Phe
 90 95 100

gct gca ctt gtg ctc gaa gag gag cgc aca tca ttt aga cct gat ctg 451
 Ala Ala Leu Val Leu Glu Glu Glu Arg Thr Ser Phe Arg Pro Asp Leu
 105 110 115

tct cac ttg tgg tca ctc ccc gta ggg tgg gta gct ccg ggg ctt gag 499
 Ser His Leu Trp Ser Leu Pro Val Gly Trp Val Ala Pro Gly Leu Glu
 120 125 130

ggt ttc gtg gag cgt aat tca gag gca gct tgaaccaccg ctctttgagc 549
 Gly Phe Val Glu Arg Asn Ser Glu Ala Ala
 135 140

cgg 552

<210> 1442
 <211> 143
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 1442
 Met Tyr Ser Asp Lys Leu Ile Leu Leu Phe Leu Ser Glu Gln Asp Ser
 1 5 10 15

Ser Tyr Glu Cys Cys Val Gly Leu Leu Asp Gly Ser Asp Gly Arg Asp
 20 25 30

Tyr Ile Glu Lys Leu Leu Lys Gly Arg Lys Leu Lys Asn His Phe Leu
 35 40 45

Glu Trp Glu Asp Ile Asn Lys Ala Asp Val Ala Arg Glu Glu Ile Tyr
 50 55 60

Lys Gly Gln Leu Val His Leu Val Phe Val Thr Ala Leu Ser Thr Pro
 65 70 75 80

Gly Glu Ile Ser Phe Val Phe Pro Gly Gln Ser Leu Met Ser Ala Thr
 85 90 95

Leu Glu Glu Asp Phe Ala Ala Leu Val Leu Glu Glu Glu Arg Thr Ser

100 105 110

Phe Arg Pro Asp Leu Ser His Leu Trp Ser Leu Pro Val Gly Trp Val
115 120 125

Ala Pro Gly Leu Glu Gly Phe Val Glu Arg Asn Ser Glu Ala Ala
130 135 140

<210> 1443
<211> 552
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(529)
<223> FRXA02888

<400> 1443
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accgtagtta acataaggaa tggaatagga gaattgcggc atg tat tcc gac aag 115
Met Tyr Ser Asp Lys
1 5

ctg att ctc ttg ttc ctt tct gag cag gat tca agc tat gaa tgc tgc 163
Leu Ile Leu Leu Phe Leu Ser Glu Gln Asp Ser Ser Tyr Glu Cys Cys
10 15 20

gta ggt tta tta gat ggc tca gat gga cgt gat tat att gaa aag ctt 211
Val Gly Leu Leu Asp Gly Ser Asp Gly Arg Asp Tyr Ile Glu Lys Leu
25 30 35

ctg aag ggt agg aag ctg aag aac cat ttt ctt gaa tgg gaa gat att 259
Leu Lys Gly Arg Lys Leu Lys Asn His Phe Leu Glu Trp Glu Asp Ile
40 45 50

aac aag gct gat gtt gct cgt gaa gaa ata tat aaa ggg caa ttg gtg 307
Asn Lys Ala Asp Val Ala Arg Glu Glu Ile Tyr Lys Gly Gln Leu Val
55 60 65

cat ctg gtg ttt gtg acg gct ctt tcc acg cct ggt gaa att tct ttt 355
His Leu Val Phe Val Thr Ala Leu Ser Thr Pro Gly Glu Ile Ser Phe
70 75 80 85

gtt ttt cca ggt caa tct ctt atg agt gca aca ctc gaa gaa gac ttt 403
Val Phe Pro Gly Gln Ser Leu Met Ser Ala Thr Leu Glu Glu Asp Phe
90 95 100

gct gcg ctt gtg ctc gaa gag gag cgc aca tca ttt aga cct gaa ctg 451
Ala Ala Leu Val Leu Glu Glu Glu Arg Thr Ser Phe Arg Pro Glu Leu
105 110 115

tct cac ctg tgg tca ctc ccc gta ggg tgg gta gct cgg ggg ctt gag 499
Ser His Leu Trp Ser Leu Pro Val Gly Trp Val Ala Pro Gly Leu Glu
120 125 130

ggt ttc gtg gag cgt aat tcc gag gca gct tgaaccaccg ctttctgagc 549
Gly Phe Val Glu Arg Asn Ser Glu Ala Ala
135 140

cgg

552

<210> 1444

<211> 143

<212> PRT

<213> Corynebacterium glutamicum

<400> 1444

Met Tyr Ser Asp Lys Leu Ile Leu Leu Phe Leu Ser Glu Gln Asp Ser
 1 5 10 15

Ser Tyr Glu Cys Cys Val Gly Leu Leu Asp Gly Ser Asp Gly Arg Asp
 20 25 30

Tyr Ile Glu Lys Leu Leu Lys Gly Arg Lys Leu Lys Asn His Phe Leu
 35 40 45

Glu Trp Glu Asp Ile Asn Lys Ala Asp Val Ala Arg Glu Glu Ile Tyr
 50 55 60

Lys Gly Gln Leu Val His Leu Val Phe Val Thr Ala Leu Ser Thr Pro
 65 70 75 80

Gly Glu Ile Ser Phe Val Phe Pro Gly Gln Ser Leu Met Ser Ala Thr
 85 90 95

Leu Glu Glu Asp Phe Ala Ala Leu Val Leu Glu Glu Glu Arg Thr Ser
 100 105 110

Phe Arg Pro Glu Leu Ser His Leu Trp Ser Leu Pro Val Gly Trp Val
 115 120 125

Ala Pro Gly Leu Glu Gly Phe Val Glu Arg Asn Ser Glu Ala Ala
 130 135 140

<210> 1445

<211> 603

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(580)

<223> RXN03059

<400> 1445

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aaatcttgcc cacgatgaac ggaattgagg atattgccta atg aat tcc ggt tcc 115
 Met Asn Ser Gly Ser
 1 5

aca atg cgc aga atc agt ctg cgc aat att ggc gcg cac aag gtc agg 163
 Thr Met Arg Arg Ile Ser Leu Arg Asn Ile Gly Ala His Lys Val Arg
 10 15 20

ctg ttt ttg aca gtt ctg gca gtg gtg ctc ggc acg tct ttt gtt tcc 211
 Leu Phe Leu Thr Val Leu Ala Val Val Leu Gly Thr Ser Phe Val Ser

25

30

35

ggc gcg atg atg ttt acc aac gcg ctg tcc tcc act ttt gat gag gct 259
 Gly Ala Met Met Phe Thr Asn Ala Leu Ser Ser Thr Phe Asp Glu Ala
 40 45 50

att gcc agc agc ttt gac gcc gtg gat gtg gtg gtt tca cca aac ggt 307
 Ile Ala Ser Ser Phe Asp Gly Val Asp Val Val Val Ser Pro Asn Gly
 55 60 65

gca tca gag gtg cag ggt gtt cct gtt gag acg gtt gaa tct ttg cgt 355
 Ala Ser Glu Val Gln Gly Val Pro Val Glu Thr Val Glu Ser Leu Arg
 70 75 80 85

gag gat tcc cgc atc aac cat ctc aac atc aac ggt tcc cag act gtc 403
 Glu Asp Ser Arg Ile Asn His Leu Asn Ile Asn Gly Ser Gln Thr Val
 90 95 100

gtt ctg gcg gat gct gat tcc aag gca att caa acg act ggg gga tct 451
 Val Leu Ala Asp Ala Asp Ser Lys Ala Ile Gln Thr Thr Gly Gly Ser
 105 110 115

tcg tta agc att tat tac agc gcg gac gac gcg gtt gcc cag gca cct 499
 Ser Leu Ser Ile Tyr Tyr Ser Ala Asp Asp Ala Val Ala Gln Ala Pro
 120 125 130

gaa ttg gct gag gga gag gca ccg act gcc acc gaa gag gtg ctt gcc 547
 Glu Leu Ala Glu Gly Glu Ala Pro Thr Gly Thr Glu Glu Val Leu Ala
 135 140 145

tcg aag gcg gcc gct gag gcg aat gcc ctg gag taggggacca gatcttggtc 600
 Ser Lys Ala Gly Ala Glu Ala Asn Gly Leu Glu
 150 155 160

gtg 603

<210> 1446

<211> 160

<212> PRT

<213> Corynebacterium glutamicum

<400> 1446

Met Asn Ser Gly Ser Thr Met Arg Arg Ile Ser Leu Arg Asn Ile Gly
 1 5 10 15

Ala His Lys Val Arg Leu Phe Leu Thr Val Leu Ala Val Val Leu Gly
 20 25 30

Thr Ser Phe Val Ser Gly Ala Met Met Phe Thr Asn Ala Leu Ser Ser
 35 40 45

Thr Phe Asp Glu Ala Ile Ala Ser Ser Phe Asp Gly Val Asp Val Val
 50 55 60

Val Ser Pro Asn Gly Ala Ser Glu Val Gln Gly Val Pro Val Glu Thr
 65 70 75 80

Val Glu Ser Leu Arg Glu Asp Ser Arg Ile Asn His Leu Asn Ile Asn
 85 90 95

Gly Ser Gln Thr Val Val Leu Ala Asp Ala Ser Lys Ala Ile Gln
 100 105 110

Thr Thr Gly Gly Ser Ser Leu Ser Ile Tyr Tyr Ser Ala Asp Asp Ala
 115 120 125

Val Ala Gln Ala Pro Glu Leu Ala Glu Gly Glu Ala Pro Thr Gly Thr
 130 135 140

Glu Glu Val Leu Ala Ser Lys Ala Gly Ala Glu Ala Asn Gly Leu Glu
 145 150 155 160

<210> 1447

<211> 603

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(580)

<223> FRXA02899

<400> 1447

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aaatcttgcc cacgatgaac ggaattgagg atattgccta atg aat tcc ggt tcc 115
 Met Asn Ser Gly Ser
 1 5

aca atg cgc aga atc agt ctg cgc aat att gcc gcg cac aag gtc agg 163
 Thr Met Arg Arg Ile Ser Leu Arg Asn Ile Gly Ala His Lys Val Arg
 10 15 20

ctg ttt ttg aca gtt ctg gca gtg gtg ctc gcc acg tct ttt gtt tcc 211
 Leu Phe Leu Thr Val Leu Ala Val Val Leu Gly Thr Ser Phe Val Ser
 25 30 35

ggc gcg atg atg ttt acc aac gcg ctg tcc tcc act ttt gat gag gct 259
 Gly Ala Met Met Phe Thr Asn Ala Leu Ser Ser Thr Phe Asp Glu Ala
 40 45 50

att gcc agc agc ttt gac gcc gtg gat gtg gtg gtt tca cca aac ggt 307
 Ile Ala Ser Ser Phe Asp Gly Val Asp Val Val Val Ser Pro Asn Gly
 55 60 65

gca tca gag gtg cag ggt gtt cct gtt gag acg gtt gaa tct ttg cgt 355
 Ala Ser Glu Val Gln Gly Val Pro Val Glu Thr Val Glu Ser Leu Arg
 70 75 80 85

gag gat tcc cgc atc aac cat ctc aac atc aac ggt tcc cag act gtc 403
 Glu Asp Ser Arg Ile Asn His Leu Asn Ile Asn Gly Ser Gln Thr Val
 90 95 100

gtt ctg gcg gat gct gat tcc aag gca att caa acg act ggg gga tcg 451
 Val Leu Ala Asp Ala Asp Ser Lys Ala Ile Gln Thr Thr Gly Gly Ser
 105 110 115

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tcg tta agc att tat tac agc gcg gac gac gcg gtt gcc cag gca cct 499
Ser Leu Ser Ile Tyr Tyr Ser Ala Asp Asp Ala Val Ala Gln Ala Pro
      120                      125                      130

gaa ttg gct gag gga gag gca ccg act ggc acc gaa gag gtg ctt gcc 547
Glu Leu Ala Glu Gly Glu Ala Pro Thr Gly Thr Glu Glu Val Leu Ala
      135                      140                      145

tcg aag gcg ggc gct gag gcg aat ggc ctg gag tagggggacca gatcttggtc 600
Ser Lys Ala Gly Ala Glu Ala Asn Gly Leu Glu
      150                      155                      160

gtg 603

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<210> 1448
 <211> 160
 <212> PRT
 <213> Corynebacterium glutamicum

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<400> 1448
Met Asn Ser Gly Ser Thr Met Arg Arg Ile Ser Leu Arg Asn Ile Gly
  1                      5                      10                      15

Ala His Lys Val Arg Leu Phe Leu Thr Val Leu Ala Val Val Leu Gly
      20                      25                      30

Thr Ser Phe Val Ser Gly Ala Met Met Phe Thr Asn Ala Leu Ser Ser
      35                      40                      45

Thr Phe Asp Glu Ala Ile Ala Ser Ser Phe Asp Gly Val Asp Val Val
      50                      55                      60

Val Ser Pro Asn Gly Ala Ser Glu Val Gln Gly Val Pro Val Glu Thr
      65                      70                      75                      80

Val Glu Ser Leu Arg Glu Asp Ser Arg Ile Asn His Leu Asn Ile Asn
      85                      90                      95

Gly Ser Gln Thr Val Val Leu Ala Asp Ala Asp Ser Lys Ala Ile Gln
      100                      105                      110

Thr Thr Gly Gly Ser Ser Leu Ser Ile Tyr Tyr Ser Ala Asp Asp Ala
      115                      120                      125

Val Ala Gln Ala Pro Glu Leu Ala Glu Gly Glu Ala Pro Thr Gly Thr
      130                      135                      140

Glu Glu Val Leu Ala Ser Lys Ala Gly Ala Glu Ala Asn Gly Leu Glu
      145                      150                      155                      160

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<210> 1449
 <211> 622
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(622)

<223> RXN03062

<400> 1449

gatgagtatt ctctccgagg caacgaagtt aatatgtcca tgagggcgaa gttgtagaca 60

atatttggcc catatggata attgacagga gtttaacgcc atg gaa acc cca acc 115
 Met Glu Thr Pro Thr
 1 5

caa gac atg gat gtc cgc tgg tta tac acc caa agc cag ctc aaa ctc 163
 Gln Asp Met Asp Val Arg Trp Leu Tyr Thr Gln Ser Gln Leu Lys Leu
 10 15 20

cgc gaa att ctc ccc aca aac aaa acc ttc gat gtc atc caa atc agc 211
 Arg Glu Ile Leu Pro Thr Asn Lys Thr Phe Asp Val Ile Gln Ile Ser
 25 30 35

gaa ctc gtt gac ccc acc gac ttc atc agg ccc aac agc gtg gtc tta 259
 Glu Leu Val Asp Pro Thr Asp Phe Ile Arg Pro Asn Ser Val Val Leu
 40 45 50

tcc gtt ggc atc gcc ttc gca gaa acg ccc gac ggg ctt cgc gat tgg 307
 Ser Val Gly Ile Ala Phe Ala Glu Thr Pro Asp Gly Leu Arg Asp Trp
 55 60 65

gca cac cga ctc gcc gac gca ggg gtc atc gcg atc ggg ttc ggc tcc 355
 Ala His Arg Leu Ala Asp Ala Gly Val Ile Ala Ile Gly Phe Gly Ser
 70 75 80 85

ggc ctc acc ttc cca cag gtt ccg cag gcg ctt atc gac gcc tcc ctc 403
 Gly Leu Thr Phe Pro Gln Val Pro Gln Ala Leu Ile Asp Ala Ser Leu
 90 95 100

cac ctt ggc ctc gcc ctc ttt gaa gtc ccc cgt gaa att cca ttt atc 451
 His Leu Gly Leu Gly Leu Phe Glu Val Pro Arg Glu Ile Pro Phe Ile
 105 110 115

tcg atc acc tcc agc gtg cgt gat gag caa acc cgc cgt gcc ggc cgc 499
 Ser Ile Thr Ser Ser Val Arg Asp Glu Gln Thr Arg Arg Ala Gly Arg
 120 125 130

ctg caa caa gaa ctc ctc ctg gaa cag gaa cgg ctt aac tcc atc gcc 547
 Leu Gln Gln Glu Leu Leu Leu Glu Gln Glu Arg Leu Asn Ser Ile Ala
 135 140 145

atc tcc ggt ggc atc gaa gcc ctg tgc cgt gct gcc gcc gac tat ttg 595
 Ile Ser Gly Gly Ile Glu Ala Leu Cys Arg Ala Ala Ala Asp Tyr Leu
 150 155 160 165

ggc ggt gca gta acc atc gtg gac agc 622
 Gly Gly Ala Val Thr Ile Val Asp Ser
 170

<210> 1450

<211> 174

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1450

Met Glu Thr Pro Thr Gln Asp Met Asp Val Arg Trp Leu Tyr Thr Gln
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Ser Gln Leu Lys Leu Arg Glu Ile Leu Pro Thr Asn Lys Thr Phe Asp
 20 25 30

Val Ile Gln Ile Ser Glu Leu Val Asp Pro Thr Asp Phe Ile Arg Pro
 35 40 45

Asn Ser Val Val Leu Ser Val Gly Ile Ala Phe Ala Glu Thr Pro Asp
 50 55 60

Gly Leu Arg Asp Trp Ala His Arg Leu Ala Asp Ala Gly Val Ile Ala
 65 70 75 80

Ile Gly Phe Gly Ser Gly Leu Thr Phe Pro Gln Val Pro Gln Ala Leu
 85 90 95

Ile Asp Ala Ser Leu His Leu Gly Leu Gly Leu Phe Glu Val Pro Arg
 100 105 110

Glu Ile Pro Phe Ile Ser Ile Thr Ser Ser Val Arg Asp Glu Gln Thr
 115 120 125

Arg Arg Ala Gly Arg Leu Gln Glu Leu Leu Leu Glu Gln Glu Arg
 130 135 140

Leu Asn Ser Ile Ala Ile Ser Gly Gly Ile Glu Ala Leu Cys Arg Ala
 145 150 155 160

Ala Ala Asp Tyr Leu Gly Gly Ala Val Thr Ile Val Asp Ser
 165 170

<210> 1451

<211> 786

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(763)

<223> RXN03066

<400> 1451

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cgaaatcacc gcggcgtaat agcaccagct taaaaacott atg aca tca gac aaa 115
 Met Thr Ser Asp Lys
 1 5

gac act gaa caa ttg gaa gcg gca ggc act gaa att tta atg cct cgc 163
 Asp Thr Glu Gln Leu Glu Ala Ala Gly Thr Glu Ile Leu Met Pro Arg
 10 15 20

cgc cgt ccg gca cag cag cgc agt cgt gaa cga ttc aat cga atc ctc 211
 Arg Arg Pro Ala Gln Gln Arg Ser Arg Glu Arg Phe Asn Arg Ile Leu
 25 30 35

acc gct gcg cgt tca gtg ott gtc gat cta ggt ttt gaa tcg ttc acg 259

Thr Ala Ala Arg Ser Val Leu Val Asp Leu Gly Phe Glu Ser Phe Thr
 40 45 50
 ttt gat gaa gtc gct aag cgt gca gag gta cgc atc ggc acg ctg tac 307
 Phe Asp Glu Val Ala Lys Arg Ala Glu Val Pro Ile Gly Thr Leu Tyr
 55 60 65
 caa ttc ttt gcc aat aag tat gta ttg atc tgc gaa ttg gat cgt gtg 355
 Gln Phe Phe Ala Asn Lys Tyr Val Leu Ile Cys Glu Leu Asp Arg Val
 70 75 80 85
 gat acc gca gaa gct gtc cgc gag ttg aag aaa ttc tcc gat cag gtt 403
 Asp Thr Ala Glu Ala Val Ala Glu Leu Lys Lys Phe Ser Asp Gln Val
 90 95 100
 cct gcg ttg cag tgg ccg gat atc ctt gat gaa ttc att gag cac ttg 451
 Pro Ala Leu Gln Trp Pro Asp Ile Leu Asp Glu Phe Ile Glu His Leu
 105 110 115
 gct agg ctc tgg cgc gat gat ccg tct cgg cgg gcc gtg tgg cat gcc 499
 Ala Arg Leu Trp Arg Asp Asp Pro Ser Arg Arg Ala Val Trp His Ala
 120 125 130
 atc cag tcc acg ccg gca act cgt gcg aca gct gcg gcg acg gaa aaa 547
 Ile Gln Ser Thr Pro Ala Thr Arg Ala Thr Ala Ala Thr Glu Lys
 135 140 145
 gag atg ctg gaa atc atc gcg gaa gtt atg cgc ccg ctt gcc cgc ggt 595
 Glu Met Leu Glu Ile Ile Ala Glu Val Met Arg Pro Leu Ala Arg Gly
 150 155 160 165
 gcc ggc tac gag gag cgc atg tca ctg gcg gga ttg ctg gtg cac acg 643
 Ala Gly Tyr Glu Glu Arg Met Ser Leu Ala Gly Leu Leu Val His Thr
 170 175 180
 gta agt tcc ctg ctt aac tat gcc gtg cgt gat gtc aat agt tcc gaa 691
 Val Ser Ser Leu Leu Asn Tyr Ala Val Arg Asp Val Asn Ser Ser Glu
 185 190 195
 gag gat ttc gac agc atc gtg gaa gaa ata aaa cga atg ctg att tct 739
 Glu Asp Phe Asp Ser Ile Val Glu Glu Ile Lys Arg Met Leu Ile Ser
 200 205 210
 tac ctc ttc tcc gtg gct act gga tagtcaacac gcacgttcca ccg 786
 Tyr Leu Phe Ser Val Ala Thr Gly
 215 220

<210> 1452

<211> 221

<212> FRT

<213> Corynebacterium glutamicum

<400> 1452

Met Thr Ser Asp Lys Asp Thr Glu Gln Leu Glu Ala Ala Gly Thr Glu
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Ile Leu Met Pro Arg Arg Arg Pro Ala Gln Gln Arg Ser Arg Glu Arg
 20 25 30

Phe Asn Arg Ile Leu Thr Ala Ala Arg Ser Val Leu Val Asp Leu Gly

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35              40              45
Phe Glu Ser Phe Thr Phe Asp Glu Val Ala Lys Arg Ala Glu Val Pro
50              55              60
Ile Gly Thr Leu Tyr Gln Phe Phe Ala Asn Lys Tyr Val Leu Ile Cys
65              70              75
Glu Leu Asp Arg Val Asp Thr Ala Glu Ala Val Ala Glu Leu Lys Lys
85              90              95
Phe Ser Asp Gln Val Pro Ala Leu Gln Trp Pro Asp Ile Leu Asp Glu
100             105             110
Phe Ile Glu His Leu Ala Arg Leu Trp Arg Asp Asp Pro Ser Arg Arg
115             120             125
Ala Val Trp His Ala Ile Gln Ser Thr Pro Ala Thr Arg Ala Thr Ala
130             135             140
Ala Ala Thr Glu Lys Glu Met Leu Glu Ile Ile Ala Glu Val Met Arg
145             150             155
Pro Leu Ala Arg Gly Ala Gly Tyr Glu Glu Arg Met Ser Leu Ala Gly
165             170             175
Leu Leu Val His Thr Val Ser Ser Leu Leu Asn Tyr Ala Val Arg Asp
180             185             190
Val Asn Ser Ser Glu Glu Asp Phe Asp Ser Ile Val Glu Ile Lys
195             200             205
Arg Met Leu Ile Ser Tyr Leu Phe Ser Val Ala Thr Gly
210             215             220

<210> 1453
<211> 786
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(763)
<223> FRXA02876

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cgaaatcacc gggcgtaat agcaccagct taaaaacott atg aca tca gac aaa 115
Met Thr Ser Asp Lys
1 5

gac act gaa caa ttg gaa gcg gca ggc act gaa att tta atg oct cgc 163
Asp Thr Glu Gln Leu Glu Ala Ala Gly Thr Glu Ile Leu Met Pro Arg
10 15 20

cgc cgt ccg gca cag cag cgc agt cgt gaa cga ttc aat cga atc ctc 211
Arg Arg Pro Ala Gln Gln Arg Ser Arg Glu Arg Phe Asn Arg Ile Leu
25 30 35

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acc gct gcg cgt tca gtg ctt gtc gat cta ggt ttt gaa tcg ttc acg 259
 Thr Ala Ala Arg Ser Val Leu Val Asp Leu Gly Phe Glu Ser Phe Thr
 40 45 50

ttt gat gaa gtc gct aag cgt gca gag gta ccg atc ggc acg ctg tac 307
 Phe Asp Glu Val Ala Lys Arg Ala Glu Val Pro Ile Gly Thr Leu Tyr
 55 60 65

caa ttc ttt gcc aat aag tat gta ttg atc tgc gaa ttg gat cgt gtg 355
 Gln Phe Phe Ala Asn Lys Tyr Val Leu Ile Cys Glu Leu Asp Arg Val
 70 75 80 85

gat acc gca gaa gct gtc gcg gag ttg aag aaa ttc tcc gat cag gtt 403
 Asp Thr Ala Glu Ala Val Ala Glu Leu Lys Lys Phe Ser Asp Gln Val
 90 95 100

cct gcg ttg cag tgg ccg gat atc ctt gat gaa ttc att gag cac ttg 451
 Pro Ala Leu Gln Trp Pro Asp Ile Leu Asp Glu Phe Ile Glu His Leu
 105 110 115

gct agg ctc tgg cgc gat gat ccg tct cgg cgg gcc gtg tgg cat gcc 499
 Ala Arg Leu Trp Arg Asp Asp Pro Ser Arg Arg Ala Val Trp His Ala
 120 125 130

atc cag tcc acg ccg gca act cgt gcg aca gct gcg gcg acg gaa aaa 547
 Ile Gln Ser Thr Pro Ala Thr Arg Ala Thr Ala Ala Thr Glu Lys
 135 140 145

gag atg ctg gaa atc atc gcg gaa gtt atg cgc ccg ctt gcc cgc ggt 595
 Glu Met Leu Glu Ile Ile Ala Glu Val Met Arg Pro Leu Ala Arg Gly
 150 155 160 165

gcc ggc tac gag gag cgc atg tca ctg gcg gga ttg ctg gtg cac acg 643
 Ala Gly Tyr Glu Glu Arg Met Ser Leu Ala Gly Leu Leu Val His Thr
 170 175 180

gta agt tcc ctg ctt aac tat gcc gtg cgt gat gtc aat agt tcc gaa 691
 Val Ser Ser Leu Leu Asn Tyr Ala Val Arg Asp Val Asn Ser Ser Glu
 185 190 195

gag gat ttc gac agc atc gtg gaa gaa atc aaa cga atg ctg att tct 739
 Glu Asp Phe Asp Ser Ile Val Glu Glu Ile Lys Arg Met Leu Ile Ser
 200 205 210

tac ctc ttc tcc gtg gct act gga tagtcaacac gcacgtcgcc acc 786
 Tyr Leu Phe Ser Val Ala Thr Gly
 215 220

<210> 1454

<211> 221

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1454

Met Thr Ser Asp Lys Asp Thr Glu Gln Leu Glu Ala Ala Gly Thr Glu
 1 5 10 15Ile Leu Met Pro Arg Arg Arg Pro Ala Gln Gln Arg Ser Arg Glu Arg
 20 25 30

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Phe Asn Arg Ile Leu Thr Ala Ala Arg Ser Val Leu Val Asp Leu Gly
   35                               40                   45
Phe Glu Ser Phe Thr Phe Asp Glu Val Ala Lys Arg Ala Glu Val Pro
   50                               55                   60
Ile Gly Thr Leu Tyr Gln Phe Phe Ala Asn Lys Tyr Val Leu Ile Cys
   65                               70                   75                   80
Glu Leu Asp Arg Val Asp Thr Ala Glu Ala Val Ala Glu Leu Lys Lys
   85                               90                   95
Phe Ser Asp Gln Val Pro Ala Leu Gln Trp Pro Asp Ile Leu Asp Glu
  100                               105                   110
Phe Ile Glu His Leu Ala Arg Leu Trp Arg Asp Asp Pro Ser Arg Arg
  115                               120                   125
Ala Val Trp His Ala Ile Gln Ser Thr Pro Ala Thr Arg Ala Thr Ala
  130                               135                   140
Ala Ala Thr Glu Lys Glu Met Leu Glu Ile Ile Ala Glu Val Met Arg
  145                               150                   155                   160
Pro Leu Ala Arg Gly Ala Gly Tyr Glu Glu Arg Met Ser Leu Ala Gly
  165                               170                   175
Leu Leu Val His Thr Val Ser Ser Leu Leu Asn Tyr Ala Val Arg Asp
  180                               185                   190
Val Asn Ser Ser Glu Glu Asp Phe Asp Ser Ile Val Glu Glu Ile Lys
  195                               200                   205
Arg Met Leu Ile Ser Tyr Leu Phe Ser Val Ala Thr Gly
  210                               215                   220

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<210> 1455

<211> 294

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(271)

<223> RXN03067

<400> 1455

ttgctgttgt tggcatttcc ccgcatccgg tggacaagct ggtaagttcc gtgaggacca 60

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tgagctgaac ttccctcttc ttcccgatga ggacaagtct gtg atg act gcg tgg      115
Val Met Thr Ala Trp
                               1                   5

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ggc ggc ttt ggt gag aag aag aat tac ggc aag att gtt cag ggt gta      163
Gly Ala Phe Gly Glu Lys Lys Asn Tyr Gly Lys Ile Val Gln Gly Val
                               10                   15                   20

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att cgt tcc aca ttc ctc atc aat gct gac gga act gtt ggc atg gcg      211
Ile Arg Ser Thr Phe Leu Ile Asn Ala Asp Gly Thr Val Gly Met Ala
                               25                   30                   35

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aag tac aat gtt cgt gca act ggt cac gtg gag cgc atc gtc cgc gaa 259
 Lys Tyr Asn Val Arg Ala Thr Gly His Val Glu Arg Ile Val Arg Glu
 40 45 50

atc acc gcg gcg taatagcacc agcttaaaaa cct 294
 Ile Thr Ala Ala
 55

<210> 1456

<211> 57

<212> PRT

<213> Corynebacterium glutamicum

<400> 1456

Val Met Thr Ala Trp Gly Ala Phe Gly Glu Lys Lys Asn Tyr Gly Lys
 1 5 10 15

Ile Val Gln Gly Val Ile Arg Ser Thr Phe Leu Ile Asn Ala Asp Gly
 20 25 30

Thr Val Gly Met Ala Lys Tyr Asn Val Arg Ala Thr Gly His Val Glu
 35 40 45

Arg Ile Val Arg Glu Ile Thr Ala Ala
 50 55

<210> 1457

<211> 143

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(120)

<223> RXN03068

<400> 1457

acc aag gaa gca tgc gat ttc cgt gat tct ttg agc aac ctc aac gat 48
 Thr Lys Glu Ala Cys Asp Phe Arg Asp Ser Leu Ser Asn Leu Asn Asp
 1 5 10 15

ctc gac att gct gtt gtt ggc att tcc ccg gat ccg gtg gac aag ctg 96
 Leu Asp Ile Ala Val Val Gly Ile Ser Pro Asp Pro Val Asp Lys Leu
 20 25 30

gta agt tcc gtg agg acc atg agc tgaacttccc tcttctttcc gat 143
 Val Ser Ser Val Arg Thr Met Ser
 35 40

<210> 1458

<211> 40

<212> PRT

<213> Corynebacterium glutamicum

<400> 1458

Thr Lys Glu Ala Cys Asp Phe Arg Asp Ser Leu Ser Asn Leu Asn Asp
 1 5 10 15

Leu Asp Ile Ala Val Val Gly Ile Ser Pro Asp Pro Val Asp Lys Leu
 20 25 30

Val Ser Ser Val Arg Thr Met Ser
 35 40

<210> 1459

<211> 753

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(730)

<223> RXN03073

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aaagggtgcc caattgtttc atgccgtgag ttttgcatat atg gac tcc gta aat 115
 Met Asp Ser Val Asn
 1 5

gtc ctg ctc att ggc ata atc gtc gcg att gct gct ttg ctg cct cgc 163
 Val Leu Leu Ile Gly Ile Ile Val Ala Ala Leu Leu Pro Arg
 10 15 20

aag ggt aaa tat ggg cca atc gcc acg cta ctg gtt gcc ggc gat tgg 211
 Lys Gly Lys Tyr Gly Pro Ile Ala Thr Leu Leu Val Ala Gly Asp Trp
 25 30 35

ctt ggc gtt ttc ctc ctc agt att ttg gtg atg ctc gtt ttt gat gga 259
 Leu Gly Val Phe Leu Leu Ser Ile Leu Val Met Leu Val Phe Asp Gly
 40 45 50

cta gag gat tta gtt cag ggc ttt ttg gat tca atc tgg ttc gga gtc 307
 Leu Glu Asp Leu Val Gln Gly Phe Leu Asp Ser Ile Trp Phe Gly Val
 55 60 65

atc ctt ctt gta act ggc atc gtt tcc ttc gtt gcg aca ctg gtt tct 355
 Ile Leu Leu Val Thr Gly Ile Val Ser Phe Val Ala Thr Leu Val Ser
 70 75 80 85

aaa acc gac agc act aga aag ctt gat gga ttc cta gcg cca gta aaa 403
 Lys Thr Asp Ser Thr Arg Lys Leu Asp Gly Phe Leu Ala Pro Val Lys
 90 95 100

act cct agt tgg aaa act gtt gga gcc gga ttg atc ctt gga atc gtt 451
 Thr Pro Ser Trp Lys Thr Val Gly Ala Gly Leu Ile Leu Gly Ile Val
 105 110 115

cag tca gcg aca tct gta cct ttt tat gca ggg ctt gga tat ttg agc 499
 Gln Ser Ala Thr Ser Val Pro Phe Tyr Ala Gly Leu Gly Tyr Leu Ser
 120 125 130

gtt ggc aat ttc agt cca gaa att agg tat ggc gga ctt gtg gtc tat 547
 Val Gly Asn Phe Ser Pro Glu Ile Arg Tyr Gly Gly Leu Val Val Tyr
 135 140 145

gcg acc ttg gct ctg agt ctg ccg att atc gtg gca att ctc gtt gga 595
 Ala Thr Leu Ala Leu Ser Leu Pro Ile Ile Val Ala Ile Leu Val Gly
 150 155 160 165

atg gtt cgc aaa tac cct gaa agt cct gtt ggt agg ttg ttt gaa ctg 643
 Met Val Arg Lys Tyr Pro Glu Ser Pro Val Gly Arg Leu Phe Glu Leu
 170 175 180

att ggt caa aat aaa gag aga gtc acc aaa tgg tcg ggc tat ctc gtg 691
 Ile Gly Gln Asn Lys Glu Arg Val Thr Lys Trp Ser Gly Tyr Leu Val
 185 190 195

tca ctg gtt ctg tgc ata atg ggc att act tcg atc ctg taactagcgc 740
 Ser Leu Val Leu Cys Ile Met Gly Ile Thr Ser Ile Leu
 200 205 210

atgtactcat gag 753

<210> 1460

<211> 210

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1460

Met Asp Ser Val Asn Val Leu Leu Ile Gly Ile Ile Val Ala Ile Ala
 1 5 10 15

Ala Leu Leu Pro Arg Lys Gly Lys Tyr Gly Pro Ile Ala Thr Leu Leu
 20 25 30

Val Ala Gly Asp Trp Leu Gly Val Phe Leu Leu Ser Ile Leu Val Met
 35 40 45

Leu Val Phe Asp Gly Leu Glu Asp Leu Val Gln Gly Phe Leu Asp Ser
 50 55 60

Ile Trp Phe Gly Val Ile Leu Leu Val Thr Gly Ile Val Ser Phe Val
 65 70 75 80

Ala Thr Leu Val Ser Lys Thr Asp Ser Thr Arg Lys Leu Asp Gly Phe
 85 90 95

Leu Ala Pro Val Lys Thr Pro Ser Trp Lys Thr Val Gly Ala Gly Leu
 100 105 110

Ile Leu Gly Ile Val Gln Ser Ala Thr Ser Val Pro Phe Tyr Ala Gly
 115 120 125

Leu Gly Tyr Leu Ser Val Gly Asn Phe Ser Pro Glu Ile Arg Tyr Gly
 130 135 140

Gly Leu Val Val Tyr Ala Thr Leu Ala Leu Ser Leu Pro Ile Ile Val
 145 150 155 160

Ala Ile Leu Val Gly Met Val Arg Lys Tyr Pro Glu Ser Pro Val Gly
 165 170 175

Arg Leu Phe Glu Leu Ile Gly Gln Asn Lys Glu Arg Val Thr Lys Trp
 180 185 190

Ser Gly Tyr Leu Val Ser Leu Val Leu Cys Ile Met Gly Ile Thr Ser
 195 200 205
 Ile Leu
 210

<210> 1461

<211> 574

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(574)

<223> FRXA02905

<400> 1461

cgaaacatct aggcaccccg acttttatgt cccctgcttga gttgaaaact gctgtcgatc 60

aaaggtgccc caattgtttc atgccgtgag ttttgcatta atg gac tcc gta aat 115
 Met Asp Ser Val Asn
 1 5

gtc ctg ctc att ggc ata atc gtc gcg att gct gct ttg ctg cct cgc 163
 Val Leu Leu Ile Gly Ile Ile Val Ala Ile Ala Ala Leu Leu Pro Arg
 10 15 20

aag ggt aaa tat ggg cca atc gcc acg cta ctg gtt gcc ggc gat tgg 211
 Lys Gly Lys Tyr Gly Pro Ile Ala Thr Leu Leu Val Ala Gly Asp Trp
 25 30 35

ctt ggc gtt ttc ctc ctc agt att ttg gtg atg ctc gtt ttt gat gga 259
 Leu Gly Val Phe Leu Leu Ser Ile Leu Val Met Leu Val Phe Asp Gly
 40 45 50

cta gag gat tta gtt cag ggc ttt ttg gat tca atc tgg ttc gga gtc 307
 Leu Glu Asp Leu Val Gln Gly Phe Leu Asp Ser Ile Trp Phe Gly Val
 55 60 65

atc ctt ctt gta act ggc atc gtt tcc ttc gtt gcg aca ctg gtt tct 355
 Ile Leu Leu Val Thr Gly Ile Val Ser Phe Val Ala Thr Leu Val Ser
 70 75 80 85

aaa acc gac agc act aga aag ctt gat gga ttc cta gcg cca gta aaa 403
 Lys Thr Asp Ser Thr Arg Lys Leu Asp Gly Phe Leu Ala Pro Val Lys
 90 95 100

act cct agt tgg aaa act gtt gga gcc gga ttg atc ctt gga atc gtt 451
 Thr Pro Ser Trp Lys Thr Val Gly Ala Gly Leu Ile Leu Gly Ile Val
 105 110 115

cag tca gcg aca tct gta cct ttt tat gca ggg ctt gga tat ttg agc 499
 Gln Ser Ala Thr Ser Val Pro Phe Tyr Ala Gly Leu Gly Tyr Leu Ser
 120 125 130

gtt ggc aat ttc agt cca gaa att agg tat ggc gga ctt gtg gtc tat 547
 Val Gly Asn Phe Ser Pro Glu Ile Arg Tyr Gly Gly Leu Val Val Tyr
 135 140 145

gcg acc ttg gct ctg agt ctg ccg att 574

Ala Thr Leu Ala Leu Ser Leu Pro Ile
150 155

<210> 1462

<211> 158

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1462

Met Asp Ser Val Asn Val Leu Leu Ile Gly Ile Ile Val Ala Ile Ala
1 5 10 15

Ala Leu Leu Pro Arg Lys Gly Lys Tyr Gly Pro Ile Ala Thr Leu Leu
20 25 30

Val Ala Gly Asp Trp Leu Gly Val Phe Leu Leu Ser Ile Leu Val Met
35 40 45

Leu Val Phe Asp Gly Leu Glu Asp Leu Val Gln Gly Phe Leu Asp Ser
50 55 60

Ile Trp Phe Gly Val Ile Leu Leu Val Thr Gly Ile Val Ser Phe Val
65 70 75 80

Ala Thr Leu Val Ser Lys Thr Asp Ser Thr Arg Lys Leu Asp Gly Phe
85 90 95

Leu Ala Pro Val Lys Thr Pro Ser Trp Lys Thr Val Gly Ala Gly Leu
100 105 110

Ile Leu Gly Ile Val Gln Ser Ala Thr Ser Val Pro Phe Tyr Ala Gly
115 120 125

Leu Gly Tyr Leu Ser Val Gly Asn Phe Ser Pro Glu Ile Arg Tyr Gly
130 135 140

Gly Leu Val Val Tyr Ala Thr Leu Ala Leu Ser Leu Pro Ile
145 150 155

<210> 1463

<211> 474

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(451)

<223> RXN03085

<400> 1463

taagcaggat tacgacaagc gccaaagatat caagcgctgc accgaagaac gcgaagtcac 60

cogtgagctc ggccgctgc ttaagggaat caacgcgtaa atg agt att cac atc 115
Met Ser Ile His Ile
1 5

gca aaa gtc cac gac gtc ctc aaa ggt gaa aaa acc tac gga acc acc 163
Ala Lys Val His Asp Val Leu Lys Gly Glu Lys Thr Tyr Gly Thr Thr
10 15 20

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att ttg gtg gat cgg ctc tgg cca cgc ggt gtg aaa aaa gac gac ctt 211
ile leu val asp arg leu trp pro arg gly val lys lys asp asp leu
      25                      30                      35

gag cca gac ctc tgg ctc aaa agc gtc gcc ccc aca acc gaa ctc cga 259
glu pro asp leu trp leu lys ser val ala pro thr thr glu leu arg
      40                      45                      50

aaa tgg ttc ggc cac gac cca gct aaa ttc tcc gaa ttc agc acc cgt 307
lys trp phe gly his asp pro ala lys phe ser glu phe ser thr arg
      55                      60                      65

tac acc gaa gag ctc aac gcc agc aac gac aaa gac cta gag acg ctt 355
tyr thr glu glu leu asn ala ser asn asp lys asp leu glu thr leu
      70                      75                      80                      85

gtc gac gcc acc tcc cgc cac ccc gta acc ctc ctc tac ggt gct gcc 403
val asp ala thr ser arg his pro val thr leu leu tyr gly ala ala
      90                      95                      100

gac cgc gac cac aac cac gcc att gtt cta gcc aag tgg cta aag aaa 451
asp arg asp his asn his ala ile val leu ala lys trp leu lys lys
      105                      110                      115

taactccttg caaatagttg caa 474

<210> 1464
<211> 117
<212> PRT
<213> Corynebacterium glutamicum

<400> 1464
Met Ser Ile His Ile Ala Lys Val His Asp Val Leu Lys Gly Glu Lys
  1                      5                      10                      15

Thr Tyr Gly Thr Thr Ile Leu Val Asp Arg Leu Trp Pro Arg Gly Val
      20                      25                      30

Lys Lys Asp Asp Leu Glu Pro Asp Leu Trp Leu Lys Ser Val Ala Pro
      35                      40                      45

Thr Thr Glu Leu Arg Lys Trp Phe Gly His Asp Pro Ala Lys Phe Ser
      50                      55                      60

Glu Phe Ser Thr Arg Tyr Thr Glu Glu Leu Asn Ala Ser Asn Asp Lys
      65                      70                      75                      80

Asp Leu Glu Thr Leu Val Asp Ala Thr Ser Arg His Pro Val Thr Leu
      85                      90                      95

Leu Tyr Gly Ala Ala Asp Arg Asp His Asn His Ala Ile Val Leu Ala
      100                      105                      110

Lys Trp Leu Lys Lys
      115

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<210> 1465

<211> 1181

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(1158)

<223> RXN03089

<400> 1465

cac	tcc	ctc	tac	ccc	ata	ccg	aag	cca	aac	tct	gga	tct	ggc	aac	ggc	48
His	Ser	Leu	Tyr	Pro	Ile	Pro	Lys	Pro	Asn	Ser	Gly	Ser	Gly	Asn	Gly	
1				5					10					15		

ggc	aat	ggc	ggc	aat	ccc	gat	ggc	ggc	cct	gat	ggc	ggc	gac	tcg	ggc	96
Gly	Asn	Gly	Gly	Asn	Pro	Asp	Gly	Gly	Pro	Asp	Gly	Gly	Asp	Ser	Gly	
			20				25						30			

gat	gac	gac	tcc	ggc	gat	gat	gac	ccc	gac	ccc	gaa	ccg	gac	aag	cct	144
Asp	Asp	Asp	Ser	Gly	Asp	Asp	Asp	Pro	Asp	Pro	Glu	Pro	Asp	Lys	Pro	
			35				40					45				

gaa	gac	ggc	aaa	cct	gat	agt	gat	aag	ccc	cgt	agg	cca	ccg	atc	agc	192
Glu	Asp	Gly	Lys	Pro	Asp	Ser	Asp	Lys	Pro	Arg	Arg	Pro	Arg	Ile	Ser	
			50			55					60					

gcg	gaa	aaa	cac	gcc	atc	atc	acc	gac	gaa	ctc	gcc	cgc	ctc	aac	ccg	240
Ala	Glu	Lys	His	Ala	Ile	Ile	Thr	Asp	Glu	Leu	Ala	Arg	Leu	Asn	Pro	
					70					75					80	

aat	acc	aca	ccc	agc	gcc	gag	gaa	cta	cgc	acc	caa	gcc	ctg	agt	caa	288
Asn	Thr	Thr	Pro	Ser	Ala	Glu	Glu	Leu	Arg	Thr	Gln	Ala	Leu	Ser	Gln	
				85					90					95		

gcg	atc	tgg	cgc	acc	cca	gaa	gac	ctc	cgc	acg	tgg	cta	cgc	cac	cag	336
Ala	Ile	Trp	Arg	Thr	Pro	Glu	Asp	Leu	Arg	Thr	Trp	Leu	Arg	His	Gln	
			100				105						110			

gtc	acc	acc	gcg	aac	aaa	aac	aac	ccc	aac	ccc	atc	acc	gcc	atg	aaa	384
Val	Thr	Thr	Ala	Asn	Lys	Asn	Pro	Pro	Asn	Pro	Ile	Thr	Ala	Met	Lys	
			115			120						125				

agg	cgc	tac	ctc	tca	gta	ggc	aaa	ccc	gat	gcc	gac	aac	atg	gtc	cgc	432
Arg	Arg	Tyr	Leu	Ser	Val	Gly	Lys	Pro	Asp	Ala	Asp	Asn	Met	Val	Arg	
			130			135					140					

atc	agc	ggc	ctc	gtg	ccc	gca	gcc	acc	gca	gca	ctg	atc	acc	gcg	aac	480
Ile	Ser	Gly	Leu	Val	Pro	Ala	Ala	Thr	Ala	Ala	Leu	Ile	Thr	Ala	Asn	
					150					155					160	

acc	gca	ccg	tta	acc	aaa	cgt	ggc	aac	ctc	gtg	gat	cta	cca	gca	gca	528
Thr	Ala	Pro	Leu	Thr	Lys	Arg	Gly	Asn	Leu	Val	Asp	Leu	Pro	Ala	Ala	
				165				170						175		

gaa	gat	atg	cgc	acc	cgc	ggg	caa	cgc	cat	gcg	gat	gcg	ttg	cat	cac	576
Glu	Asp	Met	Arg	Thr	Arg	Gly	Gln	Arg	His	Ala	Asp	Ala	Leu	His	His	
			180				185						190			

atc	atg	gag	atc	tac	aac	cac	ggc	att	gtc	acc	cca	gct	cgt	ggc	gga	624
Ile	Met	Glu	Ile	Tyr	Asn	His	Gly	Ile	Val	Thr	Pro	Ala	Arg	Gly	Gly	
			195				200					205				

aca gcc agc atc atc atc tcc atg acc acc gat gat ctt gac gag atc 672
 Thr Ala Ser Ile Ile Ile Ser Met Thr Thr Asp Asp Leu Asp Glu Ile
 210 215 220

aac cac ggt gat cat gcc gat gcc agt cta ctt aac aac ctg tac ccc 720
 Asn His Gly Asp His Gly Asp Gly Ser Leu Leu Asn Asn Leu Tyr Pro
 225 230 235 240

acg aac acg ggt tac tca ttg aac ttg gcc gag atc atg aac ctc atc 768
 Thr Asn Thr Gly Tyr Ser Leu Asn Leu Ala Glu Ile Met Asn Leu Ile
 245 250 255

gct gcc aaa tac gac ttc gct gtg ctc ctc gat ggt gag acg ggg cag 816
 Ala Ala Lys Tyr Asp Phe Ala Val Leu Leu Asp Gly Glu Thr Gly Gln
 260 265 270

ccg ttg aac gtc aat agg atg cag gcc tca gcc aac ctg act caa gcc 864
 Pro Leu Asn Val Asn Arg Met Gln Arg Ser Ala Asn Leu Thr Gln Arg
 275 280 285

atc gcc ttg ttt gct tct gag ttg gtg tgc tcg gca ccc aat tgt gac 912
 Ile Ala Leu Phe Ala Ser Glu Leu Val Cys Ser Ala Pro Asn Cys Asp
 290 295 300

agg ccg cag tta gag tgc gag gtt cat cat tta gat ccc tgg atg aga 960
 Arg Pro Gln Leu Glu Cys Glu Val His His Leu Asp Pro Trp Met Arg
 305 310 315 320

ggt ggg ctg acc aac ctg gtc aat ctc acg cat cag tgc ttt aat cac 1008
 Gly Gly Leu Thr Asn Leu Val Asn Leu Thr His Gln Cys Phe Asn His
 325 330 335

cac cca gcc aac gat gat tcc agg agt ggg gtc aat ggt aaa ggg ttt 1056
 His Pro Arg Asn Asp Asp Ser Arg Ser Gly Val Asn Gly Lys Gly Phe
 340 345 350

atg gac gcc gat ccc gtc act gcc aga gta ggt cac tac tca gca agt 1104
 Met Asp Arg Asp Pro Val Thr Gly Arg Val Gly His Tyr Ser Ala Ser
 355 360 365

ggt gag ggg ccg gtg ttt aac cgg tcg gct gct gct gat cgt tcc ggt 1152
 Gly Glu Gly Pro Val Phe Asn Arg Ser Ala Ala Asp Arg Ser Gly
 370 375 380

ggt gca tagtccagac gtaagcatta tgg 1181
 Gly Ala
 385

<210> 1466
 <211> 386
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1466
 His Ser Leu Tyr Pro Ile Pro Lys Pro Asn Ser Gly Ser Gly Asn Gly
 1 5 10 15
 Gly Asn Gly Gly Asn Pro Asp Gly Gly Pro Asp Gly Gly Asp Ser Gly
 20 25 30

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Asp Asp Asp Ser Gly Asp Asp Asp Pro Asp Pro Glu Pro Asp Lys Pro
   35                               40                               45

Glu Asp Gly Lys Pro Asp Ser Asp Lys Pro Arg Arg Pro Arg Ile Ser
   50                               55                               60

Ala Glu Lys His Ala Ile Ile Thr Asp Glu Leu Ala Arg Leu Asn Pro
   65                               70                               75                               80

Asn Thr Thr Pro Ser Ala Glu Glu Leu Arg Thr Gln Ala Leu Ser Gln
   85                               90                               95

Ala Ile Trp Arg Thr Pro Glu Asp Leu Arg Thr Trp Leu Arg His Gln
  100                               105                               110

Val Thr Thr Ala Asn Lys Asn Asn Pro Asn Pro Ile Thr Ala Met Lys
  115                               120                               125

Arg Arg Tyr Leu Ser Val Gly Lys Pro Asp Ala Asp Asn Met Val Arg
  130                               135                               140

Ile Ser Gly Leu Val Pro Ala Ala Thr Ala Ala Leu Ile Thr Ala Asn
  145                               150                               155                               160

Thr Ala Pro Leu Thr Lys Arg Gly Asn Leu Val Asp Leu Pro Ala Ala
  165                               170                               175

Glu Asp Met Arg Thr Arg Gly Gln Arg His Ala Asp Ala Leu His His
  180                               185                               190

Ile Met Glu Ile Tyr Asn His Gly Ile Val Thr Pro Ala Arg Gly Gly
  195                               200                               205

Thr Ala Ser Ile Ile Ile Ser Met Thr Thr Asp Asp Leu Asp Glu Ile
  210                               215                               220

Asn His Gly Asp His Gly Asp Gly Ser Leu Leu Asn Asn Leu Tyr Pro
  225                               230                               235                               240

Thr Asn Thr Gly Tyr Ser Leu Asn Leu Ala Glu Ile Met Asn Leu Ile
  245                               250                               255

Ala Ala Lys Tyr Asp Phe Ala Val Leu Leu Asp Gly Glu Thr Gly Gln
  260                               265                               270

Pro Leu Asn Val Asn Arg Met Gln Arg Ser Ala Asn Leu Thr Gln Arg
  275                               280                               285

Ile Ala Leu Phe Ala Ser Glu Leu Val Cys Ser Ala Pro Asn Cys Asp
  290                               295                               300

Arg Pro Gln Leu Glu Cys Glu Val His His Leu Asp Pro Trp Met Arg
  305                               310                               315                               320

Gly Gly Leu Thr Asn Leu Val Asn Leu Thr His Gln Cys Phe Asn His
  325                               330                               335

His Pro Arg Asn Asp Asp Ser Arg Ser Gly Val Asn Gly Lys Gly Phe
  340                               345                               350

Met Asp Arg Asp Pro Val Thr Gly Arg Val Gly His Tyr Ser Ala Ser

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355

360

365

Gly Glu Gly Pro Val Phe Asn Arg Ser Ala Ala Ala Asp Arg Ser Gly
 370 375 380

Gly Ala
 385

<210> 1467

<211> 1575

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1552)

<223> FRXA00071

<400> 1467

gcttttctat ttcgaaaaat agccttggat tcgaaaaatt gatcgggtat ggtggttgg 60

akwrksrswg gkaacwamac ggggaaagg ggaagacacc atg agc atc acc aca 115
 Met Ser Ile Thr Thr 5

cac gtc caa gca ctc acc aca gca ctc aac gcc atc gac aac cat ttg 163
 His Val Gln Ala Leu Thr Thr Ala Leu Asn Ala Ile Asp Asn His Leu 10 15 20

gcc agc atg cty gac cat ggt gtc acc cca gac caa tac aag gcc atc 211
 Ala Ser Met Xaa Asp His Gly Val Thr Pro Asp Gln Tyr Lys Ala Ile 25 30 35

gag ccc gac ctc atc gcc cta gaa cac acc atc aac cac cac gcc acc 259
 Glu Pro Asp Leu Ile Ala Leu Glu His Thr Ile Asn His His Ala Thr 40 45 50

atc gcc gcc caa acc acm gcc ctc gcc gaa cgc acc aay gcy gcs cas 307
 Ile Ala Ala Gln Thr Xaa Ala Leu Ala Glu Arg Thr Xaa Xaa Xaa Xaa 55 60 65

wcs att ggc tcc acc cac ctc atc gac tac ctc acc acc acc ttc ggc 355
 Xaa Ile Gly Ser Thr His Leu Ile Asp Tyr Leu Thr Thr Thr Phe Gly 70 75 80 85

cta tct aaa gca cgc gcc cac cac cgc atc aat ctc gcc cac tcc ctc 403
 Leu Ser Lys Ala Arg Ala His His Arg Ile Asn Leu Ala His Ser Leu 90 95 100

tac ccc ata ccg aag cca aac tct gga tct ggc aac ggc ggt aat ggt 451
 Tyr Pro Ile Pro Lys Pro Asn Ser Gly Ser Gly Asn Gly Gly Asn Gly 105 110 115

ggc aat ccc gac gcc ggt cct gat ggt ggc gac tcg ggt gat gac gac 499
 Gly Asn Pro Asp Gly Gly Pro Asp Gly Gly Asp Ser Gly Asp Asp Asp 120 125 130

tcc ggc gat gat gac ccc gac ccc gaa ccg gac aag cct gaa gac gcc 547
 Ser Gly Asp Asp Asp Pro Asp Pro Glu Pro Asp Lys Lys Pro Glu Asp Gly 135 140 145

aaa cct gat agt gat aag ccc cgt agg cca cgg atc agc gcg gaa aaa	595
Lys Pro Asp Ser Asp Lys Pro Arg Arg Pro Arg Ile Ser Ala Glu Lys	
150 155 160 165	
cac gcc atc atc acc gac gaa ctc gcc cgc ctc aac ccg aat acc aca	643
His Ala Ile Ile Thr Asp Glu Leu Ala Arg Leu Asn Pro Asn Thr Thr	
170 175 180	
ccc agc gcc gag gaa ctr cgc amc caa gcc ctg agt car gcg atc tgg	691
Pro Ser Ala Glu Glu Xaa Arg Xaa Gln Ala Leu Ser Xaa Ala Ile Trp	
185 190 195	
cgc acc cca gaa gac ctc cgc acg tgg cta cgc cac cag gtc acc acc	739
Arg Thr Pro Glu Asp Leu Arg Thr Trp Leu Arg His Gln Val Thr Thr	
200 205 210	
gcg aac aaa aac aac ccc aac ccc atc acc gcc atg aaa agg cgc tac	787
Ala Asn Lys Asn Asn Pro Asn Pro Ile Thr Ala Met Lys Arg Arg Tyr	
215 220 225	
ctc tca gta ggt aaa ccc gat gcc gac aac atg gtc cgc atc agc ggc	835
Leu Ser Val Gly Lys Pro Asp Ala Asp Asn Met Val Arg Ile Ser Gly	
230 235 240 245	
ctc gtg ccc gca gcc acc gca gca ctg atc acc gcg aac acc gca ccg	883
Leu Val Pro Ala Ala Thr Ala Ala Leu Ile Thr Ala Asn Thr Ala Pro	
250 255 260	
tta acc aaa cgt gcc aac ctc gtg gat cta cca gca gca gaa gat atg	931
Leu Thr Lys Arg Gly Asn Leu Val Asp Leu Pro Ala Ala Glu Asp Met	
265 270 275	
cgc acc cgc ggg caa cgc cat gcg gat gcg ttg cat cac atc atg gag	979
Arg Thr Arg Gly Gln Arg His Ala Asp Ala Leu His His Ile Met Glu	
280 285 290	
atc tac aac cac ggt att gtc acc cca gct cgt ggt gga aca gcc agc	1027
Ile Tyr Asn His Gly Ile Val Thr Pro Ala Arg Gly Gly Thr Ala Ser	
295 300 305	
atc atc atc tcc atg acc acc gat gat ctt gac gag atc aac cac ggt	1075
Ile Ile Ile Ser Met Thr Thr Asp Asp Leu Asp Glu Ile Asn His Gly	
310 315 320 325	
gat cat gcc gat gcc agt cta ctt aac aac ctg tac ccc acg aac acg	1123
Asp His Gly Asp Gly Ser Leu Leu Asn Asn Leu Tyr Pro Thr Asn Thr	
330 335 340	
ggt tac tca ttg aac ttg gcg gag atc atg aac ctc atc gct gcg aaa	1171
Gly Tyr Ser Leu Asn Leu Ala Glu Ile Met Asn Leu Ile Ala Ala Lys	
345 350 355	
tac gac ttc gct gtg ctc ctc gat ggt gag acg ggg cag ccg ttg aac	1219
Tyr Asp Phe Ala Val Leu Leu Asp Gly Glu Thr Gly Gln Pro Leu Asn	
360 365 370	
gtc aat agg atg cag cgc tca gcg aac ctg act caa cgc atc gcg ttg	1267
Val Asn Arg Met Gln Arg Ser Ala Asn Leu Thr Gln Arg Ile Ala Leu	
375 380 385	

ttt gct tct gag ttg gtg tgc tcg gca ccc aat tgt gac agg ccg cag 1315
 Phe Ala Ser Glu Leu Val Cys Ser Ala Pro Asn Cys Asp Arg Pro Gln
 390 395 400 405

tta gag tgc gag gtt cat cat tta gat ccc tgg atg aga ggt ggg ctg 1363
 Leu Glu Cys Glu Val His His Leu Asp Pro Trp Met Arg Gly Gly Leu
 410 415 420

acc aac ctg gtc aat ctc acg cat cag tgc ttt aat cac cac cca cgc 1411
 Thr Asn Leu Val Asn Leu Thr His Gln Cys Phe Asn His His Pro Arg
 425 430 435

aac gat gat tcc agg agt ggg gtc aat ggt aaa ggg ttt atg gac cgc 1459
 Asn Asp Asp Ser Arg Ser Gly Val Asn Gly Lys Gly Phe Met Asp Arg
 440 445 450

gat ccc gtc act ggc aga gta ggt cac tac tca gca agt ggt gag ggg 1507
 Asp Pro Val Thr Gly Arg Val Gly His Tyr Ser Ala Ser Gly Glu Gly
 455 460 465

ccg gtg ttt aac cgg tcg gct gct gct gat cgt tcc ggt ggt gca 1552
 Pro Val Phe Asn Arg Ser Ala Ala Ala Asp Arg Ser Gly Gly Ala
 470 475 480

tagtccagac gtaagcatta tgg 1575

<210> 1468

<211> 484

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1468

Met Ser Ile Thr Thr His Val Gln Ala Leu Thr Thr Ala Leu Asn Ala
 1 5 10 15

Ile Asp Asn His Leu Ala Ser Met Xaa Asp His Gly Val Thr Pro Asp
 20 25 30

Gln Tyr Lys Ala Ile Glu Pro Asp Leu Ile Ala Leu Glu His Thr Ile
 35 40 45

Asn His His Ala Thr Ile Ala Ala Gln Thr Xaa Ala Leu Ala Glu Arg
 50 55 60

Thr Xaa Xaa Xaa Xaa Xaa Ile Gly Ser Thr His Leu Ile Asp Tyr Leu
 65 70 75 80

Thr Thr Thr Phe Gly Leu Ser Lys Ala Arg Ala His His Arg Ile Asn
 85 90 95

Leu Ala His Ser Leu Tyr Pro Ile Pro Lys Pro Asn Ser Gly Ser Gly
 100 105 110

Asn Gly Gly Asn Gly Gly Asn Pro Asp Gly Gly Pro Asp Gly Gly Asp
 115 120 125

Ser Gly Asp Asp Asp Ser Gly Asp Asp Asp Pro Asp Pro Glu Pro Asp
 130 135 140

Lys Pro Glu Asp Gly Lys Pro Asp Ser Asp Lys Pro Arg Arg Pro Arg

145		150		155		160
Ile Ser Ala Glu Lys	His Ala Ile Ile Thr Asp Glu Leu Ala Arg Leu					
	165			170		175
Asn Pro Asn Thr Thr	Pro Ser Ala Glu Glu Xaa Arg Xaa Gln Ala Leu					
	180		185			190
Ser Xaa Ala Ile Trp Arg Thr	Pro Glu Asp Leu Arg Thr Trp Leu Arg					
	195		200		205	
His Gln Val Thr Thr Ala	Asn Lys Asn Asn Pro Asn Pro Ile Thr Ala					
	210		215		220	
Met Lys Arg Arg Tyr Leu Ser Val Gly Lys	Pro Asp Ala Asp Asn Met					
	225		230		235	240
Val Arg Ile Ser Gly Leu Val Pro Ala Ala Thr	Ala Ala Leu Ile Thr					
	245		250		255	
Ala Asn Thr Ala Pro Leu Thr Lys Arg Gly Asn Leu Val Asp Leu Pro						
	260		265		270	
Ala Ala Glu Asp Met Arg Thr Arg Gly Gln Arg His Ala Asp Ala Leu						
	275		280		285	
His His Ile Met Glu Ile Tyr Asn His Gly Ile Val Thr Pro Ala Arg						
	290		295		300	
Gly Gly Thr Ala Ser Ile Ile Ile Ser Met Thr Thr Asp Asp Leu Asp						
	305		310		315	320
Glu Ile Asn His Gly Asp His Gly Asp Gly Ser Leu Leu Asn Asn Leu						
	325		330		335	
Tyr Pro Thr Asn Thr Gly Tyr Ser Leu Asn Leu Ala Glu Ile Met Asn						
	340		345		350	
Leu Ile Ala Ala Lys Tyr Asp Phe Ala Val Leu Leu Asp Gly Glu Thr						
	355		360		365	
Gly Gln Pro Leu Asn Val Asn Arg Met Gln Arg Ser Ala Asn Leu Thr						
	370		375		380	
Gln Arg Ile Ala Leu Phe Ala Ser Glu Leu Val Cys Ser Ala Pro Asn						
	385		390		395	400
Cys Asp Arg Pro Gln Leu Glu Cys Glu Val His His Leu Asp Pro Trp						
	405		410		415	
Met Arg Gly Gly Leu Thr Asn Leu Val Asn Leu Thr His Gln Cys Phe						
	420		425		430	
Asn His His Pro Arg Asn Asp Asp Ser Arg Ser Gly Val Asn Gly Lys						
	435		440		445	
Gly Phe Met Asp Arg Asp Pro Val Thr Gly Arg Val Gly His Tyr Ser						
	450		455		460	
Ala Ser Gly Glu Gly Pro Val Phe Asn Arg Ser Ala Ala Ala Asp Arg						
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<210> 1469
<211> 747
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS
<222> (101)..(724)
<223> RXN03098
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tccgcgcacc accctcttcg agggcgaggc ctaaacaccc atg ccc acc acg gac 115																
Met Pro Thr Thr Asp 1 5																
gtc ttc aac cgc gtc cgg ttg gca ttg gaa cct cta gct gat ccc gca 163																
Val Phe Asn Arg Val Arg Leu Ala Leu Glu Pro Leu Ala Asp Pro Ala 10 15 20																
cgt gcc acc gga atg gca agc tac atg cgg gat cag ttt tct ttt ctc 211																
Arg Ala Thr Gly Met Ala Ser Tyr Met Arg Asp Gln Phe Ser Phe Leu 25 30 35																
ggc atc cca tcc acc ccc aga aaa gaa gcc tgc aaa ccc gtg ctg tcc 259																
Gly Ile Pro Ser Thr Pro Arg Lys Glu Ala Cys Lys Pro Val Leu Ser 40 45 50																
gcg cta aaa gag ttg gac act gac ttt gtc tca gac tgc ttt ggc gca 307																
Ala Leu Lys Glu Leu Asp Thr Asp Phe Val Ser Asp Cys Phe Gly Ala 55 60 65																
gct gaa cgg gaa tac cag tat gtc gcc tgc gat cac atc aat cgc gtc 355																
Ala Glu Arg Glu Tyr Gln Tyr Val Ala Cys Asp His Ile Asn Arg Val 70 75 80 85																
ggc atc acc gat tta ggt ttt gcc aaa gca tta gtg cag acc aaa tcc 403																
Gly Ile Thr Asp Leu Gly Phe Ala Lys Ala Leu Val Gln Thr Lys Ser 90 95 100																
tgg tgg gac acc gtc gat tcc cta gca aaa ccg atc ggc gcc aaa cac 451																
Trp Trp Asp Thr Val Asp Ser Leu Ala Lys Pro Ile Gly Ala Lys His 105 110 115																
gat gat gat ctg atg aaa acg tgg gcg ctt gat gag gac ttc tgg gtg 499																
Asp Asp Asp Leu Met Lys Thr Trp Arg Leu Asp Glu Asp Phe Thr Val 120 125 130																
cgc cgc atc gcg atc atc cac caa ctg gcc cgc aag aaa aac acc gac 547																
Arg Arg Ile Ala Ile Ile His Gln Leu Gly Arg Lys Lys Asn Thr Asp 135 140 145																
gct gcc ctg ctg gcc tgg atc atc gag cag aac ctc gcc tcc agc gag 595																
Ala Ala Leu Leu Ala Trp Ile Ile Glu Gln Asn Leu Gly Ser Ser Glu 150 155 160 165																

ttc ttc atc aac aaa gcg atc ggc tgg gca ctg cgg gat ttc gcc cgc 643
 Phe Phe Ile Asn Lys Ala Ile Gly Trp Ala Leu Arg Asp Phe Ala Arg
 170 175 180

cac gac ccc agc tgg gtc cgg gct ttt gtc gac gcc acg gac ctt tcc 691
 His Asp Pro Ser Trp Val Arg Ala Phe Val Asp Ala Thr Asp Leu Ser
 185 190 195

cca ctg agc cgg cga gaa gcc ctg aag aat att tagccctcag gcacatcatctg 744
 Pro Leu Ser Arg Arg Glu Ala Leu Lys Asn Ile
 200 205

agc 747

<210> 1470

<211> 208

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1470

Met Pro Thr Thr Asp Val Phe Asn Arg Val Arg Leu Ala Leu Glu Pro
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Leu Ala Asp Pro Ala Arg Ala Thr Gly Met Ala Ser Tyr Met Arg Asp
 20 25 30

Gln Phe Ser Phe Leu Gly Ile Pro Ser Thr Pro Arg Lys Glu Ala Cys
 35 40 45

Lys Pro Val Leu Ser Ala Leu Lys Glu Leu Asp Thr Asp Phe Val Ser
 50 55 60

Asp Cys Phe Gly Ala Ala Glu Arg Glu Tyr Gln Tyr Val Ala Cys Asp
 65 70 75 80

His Ile Asn Arg Val Gly Ile Thr Asp Leu Gly Phe Ala Lys Ala Leu
 85 90 95

Val Gln Thr Lys Ser Trp Trp Asp Thr Val Asp Ser Leu Ala Lys Pro
 100 105 110

Ile Gly Ala Lys His Asp Asp Asp Leu Met Lys Thr Trp Ala Leu Asp
 115 120 125

Glu Asp Phe Trp Val Arg Arg Ile Ala Ile Ile His Gln Leu Gly Arg
 130 135 140

Lys Lys Asn Thr Asp Ala Ala Leu Leu Ala Trp Ile Ile Glu Gln Asn
 145 150 155 160

Leu Gly Ser Ser Glu Phe Phe Ile Asn Lys Ala Ile Gly Trp Ala Leu
 165 170 175

Arg Asp Phe Ala Arg His Asp Pro Ser Trp Val Arg Ala Phe Val Asp
 180 185 190

Ala Thr Asp Leu Ser Pro Leu Ser Arg Arg Glu Ala Leu Lys Asn Ile
 195 200 205

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<210> 1471
 <211> 798
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(775)
 <223> RXN03099

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 atgtgcggga aacgatctga tcattctgcgg tgatgtcggt gtg gtt gat gcc gta 115
 Val Val Asp Ala Val
 1 5
 cac gat gtt ctt cag atc gcc ctt gcc cgg cgc ggt gag tac aac ctt 163
 His Asp Val Leu Gln Ile Ala Leu Ala Arg Arg Gly Glu Tyr Asn Leu
 10 15 20
 ggc aac gcc ctt gga ctt gag gtg ctg gga cag gcc ttc gcg gtc acg 211
 Gly Asn Ala Leu Gly Leu Glu Val Leu Gly Gln Ala Phe Ala Val Thr
 25 30 35
 cca gcg gcc ggt gtt gtc tac cac gac gcc gtc att gat gcc gta ttc 259
 Pro Ala Ala Gly Val Val Tyr His Asp Gly Val Ile Asp Ala Val Phe
 40 45 50
 ggt gta atc aat ggt ggc tgg gtc att gga gta gat gac ctt gat tgg 307
 Gly Val Ile Asn Gly Gly Trp Val Ile Gly Val Asp Asp Leu Asp Trp
 55 60 65
 ggt gcc gtt ggc cca gat gat gtt gtt gtc ata atc ggt ggt gat ggt 355
 Gly Ala Val Gly Pro Asp Asp Val Val Val Ile Ile Gly Gly Asp Gly
 70 75 80 85
 gcc atc gaa tcc acc gtg gac aga atc acg acg cag caa gga tgc gcg 403
 Ala Ile Glu Ser Thr Val Asp Arg Ile Thr Thr Gln Gln Gly Cys Ala
 90 95 100
 ctt gac cag gtc ttc ttc acc att ttt gcg gac cac gat gcc gcg cag 451
 Leu Asp Gln Val Phe Phe Thr Ile Phe Ala Asp His Asp Gly Ala Gln
 105 110 115
 acg agc acc gtc ata cag tgc ctc gcg gga aac cag gat gcg gcc cag 499
 Thr Ser Thr Val Ile Gln Cys Leu Ala Gly Asn Gln Asp Ala Gly Gln
 120 125 130
 cag gcg acc gat gcg gcc gaa acc gta cag cac gat atc agt tgg gtt 547
 Gln Ala Thr Asp Ala Ala Glu Thr Val Gln His Asp Ile Ser Trp Val
 135 140 145
 gat gtc ggt ttc cgc acc aat gac cgg cgc gag agc gtc ctc cag gaa 595
 Asp Val Gly Phe Arg Thr Asn Asp Arg Arg Glu Ser Val Leu Gln Glu
 150 155 160 165

ggc acg cag gtc ggt gct ttc gga ttc ttc gaa gct gta ggc cag ctg 643
 Gly Thr Gln Val Gly Ala Phe Gly Phe Phe Glu Ala Val Gly Gln Leu
 170 175 180
 tcc cag gtc gat cga tgc ggt acc aag gtt cat atc tac cag ttc gcg 691
 Ser Gln Val Asp Arg Cys Gly Thr Lys Val His Ile Tyr Gln Phe Ala
 185 190 195
 caa aat atc caa gga gct ttc cag tgg aag ttc ctt gga tat gat gtg 739
 Gln Asn Ile Gln Gly Ala Phe Gln Trp Lys Phe Leu Gly Tyr Asp Val
 200 205 210
 gcg ggc gta gcg gtg aga ctt gat gat atc gat gtc tgagacattc 785
 Ala Gly Val Ala Val Arg Leu Asp Asp Ile Asp Val
 215 220 225
 acaaggagac gac 798

<210> 1472
 <211> 225
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1472
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 Gly Glu Tyr Asn Leu Gly Asn Ala Leu Gly Leu Glu Val Leu Gly Gln
 20 25 30
 Ala Phe Ala Val Thr Pro Ala Ala Gly Val Val Tyr His Asp Gly Val
 35 40 45
 Ile Asp Ala Val Phe Gly Val Ile Asn Gly Gly Trp Val Ile Gly Val
 50 55 60
 Asp Asp Leu Asp Trp Gly Ala Val Gly Pro Asp Asp Val Val Val Ile
 65 70 75 80
 Ile Gly Gly Asp Gly Ala Ile Glu Ser Thr Val Asp Arg Ile Thr Thr
 85 90 95
 Gln Gln Gly Cys Ala Leu Asp Gln Val Phe Phe Thr Ile Phe Ala Asp
 100 105 110
 His Asp Gly Ala Gln Thr Ser Thr Val Ile Gln Cys Leu Ala Gly Asn
 115 120 125
 Gln Asp Ala Gly Gln Gln Ala Thr Asp Ala Ala Glu Thr Val Gln His
 130 135 140
 Asp Ile Ser Trp Val Asp Val Gly Phe Arg Thr Asn Asp Arg Arg Glu
 145 150 155 160
 Ser Val Leu Gln Glu Gly Thr Gln Val Gly Ala Phe Gly Phe Phe Glu
 165 170 175
 Ala Val Gly Gln Leu Ser Gln Val Asp Arg Cys Gly Thr Lys Val His
 180 185 190

Ile Tyr Gln Phe Ala Gln Asn Ile Gln Gly Ala Phe Gln Trp Lys Phe
195 200 205

Leu Gly Tyr Asp Val Ala Gly Val Ala Val Arg Leu Asp Asp Ile Asp
210 215 220

Val
225

<210> 1473
<211> 300
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> {101}..(277)
<223> RXN03104

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gggacagtgc ctcaacacag gaagagtagg tgctgtatc ttg gag ctg aac gcc 115
Leu Glu Leu Asn Ala
1 5

tgg gag gac atc ctt gac ctt ctg agc tgg agt gga tcc gga aac gga 163
Trp Glu Asp Ile Leu Asp Leu Leu Ser Trp Ser Gly Ser Gly Asn Ala Gly
10 15 20

gca cag gat caa acc gtt atc caa gtc ctc gag ggt ttc aat gcg atc 211
Ala Gln Asp Gln Thr Val Ile Gln Val Leu Glu Gly Phe Asn Ala Ile
25 30 35

gtc atc ttg gcg aac aag cag agc ctg gtg ggt aag cag gta tgg gcc 259
Val Ile Leu Ala Asn Lys Gln Ser Leu Val Gly Lys Gln Val Trp Ala
40 45 50

acc gaa gtt gac gga ctc tgaacggcca gcgttgatgg agt 300
Thr Glu Val Asp Gly Leu
55

<210> 1474
<211> 59
<212> PRT
<213> Corynebacterium glutamicum

<400> 1474
Leu Glu Leu Asn Ala Trp Glu Asp Ile Leu Asp Leu Leu Ser Trp Ser
1 5 10 15

Gly Ser Gly Asn Gly Ala Gln Asp Gln Thr Val Ile Gln Val Leu Glu
20 25 30

Gly Phe Asn Ala Ile Val Ile Leu Ala Asn Lys Gln Ser Leu Val Gly
35 40 45

Lys Gln Val Trp Ala Thr Glu Val Asp Gly Leu
50 55

<210> 1475
 <211> 292
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(292)
 <223> RXN03106

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 aggcacotca cagggtgcaat tattacacaa cccacacagcg atg tcc gca tcc ttt 115
 Met Ser Ala Ser Phe
 1 5
 gat gac ccc aac ctc atc tcg ctt gct gga ctg gtt cca acc atg cac 163
 Asp Asp Pro Asn Leu Ile Ser Leu Ala Gly Leu Val Pro Thr Met His
 10 15 20
 tta gcc gat gct gcc agc ctg tcc acc ttg gcc cag gac cgg ttg agc 211
 Leu Ala Asp Ala Ala Ser Leu Ser Thr Leu Ala Gln Asp Arg Leu Ser
 25 30 35
 atc acc ggt gat aaa ggt gcc aat gct ggt gcg aag atc gcc tcc cta 259
 Ile Thr Gly Asp Lys Gly Ala Asn Ala Gly Ala Lys Ile Ala Ser Leu
 40 45 50
 gtc gcg gcc atg gtc gcc ggt gct gat tcc atc 292
 Val Ala Gly Met Val Ala Gly Ala Asp Ser Ile
 55 60

<210> 1476
 <211> 64
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 1476
 Met Ser Ala Ser Phe Asp Asp Pro Asn Leu Ile Ser Leu Ala Gly Leu
 1 5 10 15
 Val Pro Thr Met His Leu Ala Asp Ala Ala Ser Leu Ser Thr Leu Ala
 20 25 30
 Gln Asp Arg Leu Ser Ile Thr Gly Asp Lys Gly Ala Asn Ala Gly Ala
 35 40 45
 Lys Ile Ala Ser Leu Val Ala Gly Met Val Ala Gly Ala Asp Ser Ile
 50 55 60

<210> 1477
 <211> 324
 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(301)

<223> RXN03107

<400> 1477

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atcacaaata cctcaactag aagtaggaga tgagcaccac atg agc gat ttt tcc 115
Met Ser Asp Phe Ser
1 5

aac aag gca gag gac ctc aca ggt aag gct aaa gaa gga ttc ggc gag 163
Asn Lys Ala Glu Asp Leu Thr Gly Lys Ala Lys Glu Gly Phe Gly Glu
10 15 20

gca act gat aac gag tcc ctc gct gat gag ggc cgt gcg gat cag gct 211
Ala Thr Asp Asn Glu Ser Leu Ala Asp Glu Gly Arg Ala Asp Gln Ala
25 30 35

aag gca gac atc aag gat gct gtc gaa aac gcc ggt gaa aag gta aag 259
Lys Ala Asp Ile Lys Asp Ala Val Glu Asn Ala Gly Glu Lys Val Lys
40 45 50

gac gca gct aac aag gtt ctg ggt gcg ttc aag aag gac gac 301
Asp Ala Ala Asn Lys Val Leu Gly Ala Phe Lys Lys Asp Asp
55 60 65

taatcccgta ctgttcagg att 324

<210> 1478

<211> 67

<212> PRT

<213> Corynebacterium glutamicum

<400> 1478

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Glu Gly Phe Gly Glu Ala Thr Asp Asn Glu Ser Leu Ala Asp Glu Gly
20 25 30

Arg Ala Asp Gln Ala Lys Ala Asp Ile Lys Asp Ala Val Glu Asn Ala
35 40 45

Gly Glu Lys Val Lys Asp Ala Ala Asn Lys Val Leu Gly Ala Phe Lys
50 55 60

Lys Asp Asp
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<210> 1479

<211> 1722

<212> DNA

<213> Corynebacterium glutamicum

<220>

<400> 1479

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Val Leu Asp Phe Leu
1 5

gct gcg aac ccg ctg att gcg ctg gtg gtt att ttg gcc gtt ggt tta 163
Ala Ala Asn Pro Leu Ile Ala Leu Val Val Ile Leu Ala Val Gly Leu
10 15 20

gca att ggt cag att agg gtc ttt ggc ctt tct tta ggt gcc gcc gcg 211
Ala Ile Gly Gln Ile Arg Val Phe Gly Leu Ser Leu Gly Ala Ala Ala
25 30 35

gtg ctg ttt gtg gcc ctg gtg gtt tca act gca aat acc gac atc gtc 259
Val Leu Phe Val Ala Leu Val Val Ser Thr Ala Asn Thr Asp Ile Val
40 45 50

atc ccc atg att gtt tat cag ctg ggc ttg gcg atg ttc gtt tat gtc 307
Ile Pro Met Ile Val Tyr Gln Leu Gly Leu Ala Met Phe Val Tyr Val
55 60 65

atc ggt ttg tcc gcc gga cca gca ttt ttc agt gag ttc gct aaa aag 355
Ile Gly Leu Ser Ala Gly Pro Ala Phe Phe Ser Glu Phe Ala Lys Lys
70 75 80 85

ggc tgg aag ctc acc atc ttt atg ctc ctg ctg ctg gca aca ctg att 403
Gly Trp Lys Leu Thr Ile Phe Met Leu Leu Leu Leu Ala Thr Leu Ile
90 95 100

ggt ttg gcg tgg gtg ctt att aag tca ctg ggg ctt gat gca gcg atc 451
Gly Leu Ala Trp Val Leu Ile Lys Ser Leu Gly Leu Asp Ala Ala Ile
105 110 115

ggt acc ggt atg ttc acc ggc gcg ctg acc tcg act ccc ggt atg gca 499
Gly Thr Gly Met Phe Thr Gly Ala Leu Thr Ser Thr Pro Gly Met Ala
120 125 130

gcg gtc gtg gaa ttg att gaa gga atc gat cca agc ctt gcc agt gaa 547
Ala Val Val Glu Leu Ile Glu Gly Ile Asp Pro Ser Leu Ala Ser Glu
135 140 145

cct gtt att ggt tat tcc ttg gca tat ccg gga gcc gtg ctg gga tcc 595
Pro Val Ile Gly Tyr Ser Leu Ala Tyr Pro Gly Ala Val Leu Gly Ser
150 155 160 165

att gtg gtg gcc gcg gtt gga gcg aaa ctg ctc aaa gta aat cac cgg 643
Ile Val Val Ala Ala Val Gly Ala Lys Leu Leu Lys Val Asn His Arg
170 175 180

gaa gat gct cga aaa gaa ggc atg atc acc gca ccg ctg gtg tgg aag 691
Glu Asp Ala Arg Lys Glu Gly Met Ile Thr Ala Pro Leu Val Trp Lys
185 190 195

ggt gtg cag ctc aaa cct gga atc aca ggc agg gtg gga gat ctt cca 739
Gly Val Gln Leu Lys Pro Gly Ile Thr Gly Arg Val Gly Asp Leu Pro

200	205	210	
cgc ctt gca ggt gaa agt atc atc gca acc cgc att gtg gat gat cca Arg Leu Ala Gly Glu Ser Ile Ile Ala Thr Arg Ile Val Asp Asp Pro 215 220 225			787
cat aca cac cgc ctc gcg gat cca gat ctg ccg att act gaa ggc atg His Thr His Arg Leu Ala Asp Pro Asp Leu Pro Ile Thr Glu Gly Met 230 235 240 245			835
gaa ctg ttg atc aac gcg act gaa gaa gcc gtg gat ccg gca att aag Glu Leu Leu Ile Asn Gly Thr Glu Glu Ala Val Asp Arg Ala Ile Lys 250 255 260			883
gcg ttg ggt gaa gaa cgc gaa acc aaa att gag gac aca gag ctg atc Ala Leu Gly Glu Glu Arg Glu Thr Lys Ile Glu Asp Thr Glu Leu Ile 265 270 275			931
tac acc cgc ctg acg gta tct agc cct gag gtt gca ggt aga acc gtt Tyr Thr Arg Leu Thr Val Ser Ser Pro Glu Val Ala Arg Thr Val 280 285 290			979
gct gag ctt gat act gta gct cac gga ttc atg att gcc cgt atc cgc Ala Glu Leu Asp Thr Val Ala His Gly Phe Met Ile Ala Arg Ile Arg 295 300 305			1027
cag gcc gat tct gag gta gtg cct aaa cct gac acc gtg atc aac tac Gln Gly Asp Ser Glu Val Val Pro Lys Pro Asp Thr Val Ile Asn Tyr 310 315 320 325			1075
tct gac cgc atc cgc gtg gtg gtt gct cct ggt cgt gtg gct gaa gtg Ser Asp Arg Ile Arg Val Val Val Ala Pro Gly Arg Val Ala Glu Val 330 335 340			1123
cga cga ttc tta ggg gac tct gaa aag tcc ctt gct gat gtt aat ctg Arg Arg Phe Leu Gly Asp Ser Glu Lys Ser Leu Ala Asp Val Asn Leu 345 350 355			1171
ctg cct tta gcc atc gga tta tct ctt gcc ctg ttg ttg gcc gcg atc Leu Pro Leu Ala Ile Gly Leu Ser Leu Gly Leu Leu Leu Gly Ala Ile 360 365 370			1219
ccg att cct ctt cca gcc gcc acc acg atg tcc ctt gcc ttt ggt gcc Pro Ile Pro Leu Pro Gly Gly Thr Thr Met Ser Leu Gly Phe Gly Gly 375 380 385			1267
ggc ccg att att gcc gcc ctg att ttg gga gca ctc aag cac aca gga Gly Pro Ile Ile Ala Gly Leu Ile Leu Gly Ala Leu Lys His Thr Gly 390 395 400 405			1315
ccg ctg acg tgg cag atg ccg ttc cac gcc aac cgc acg atc tcc acc Pro Leu Thr Trp Gln Met Pro Phe His Ala Asn Arg Thr Ile Ser Thr 410 415 420			1363
ttg gcc ctg gcg ctg ttt ttg gct ggt gtg ggt acc tct gca ggt gca Leu Gly Leu Ala Leu Phe Leu Ala Gly Val Gly Thr Ser Ala Gly Ala 425 430 435			1411
gga ttt aga gct gcg ctt acc gat tcc tcc tcc ttg atc tac atg gcc Gly Phe Arg Ala Ala Leu Thr Asp Ser Ser Ser Leu Ile Tyr Met Ala 440 445 450			1459

ggt ggc ttg gtg atc acc ttg gcc tct gcg ctg ctg tgt gct gtg atc 1507
 Gly Gly Leu Val Ile Thr Leu Ala Ser Ala Leu Leu Cys Ala Val Ile
 455 460 465
 ggc atg tgg gta ctc agg ttg agg tgg gat gaa gcc atg ggt gtt gcc 1555
 Gly Met Trp Val Leu Arg Leu Arg Trp Asp Glu Ala Met Gly Val Ala
 470 475 480 485
 gct ggc acc acc aca aat cct gca att att tcc tat ctg aat ggg caa 1603
 Ala Gly Thr Thr Thr Asn Pro Ala Ile Ile Ser Tyr Leu Asn Gly Gln
 490 495 500
 acc gga acg gat ctt gcc aac agg gga tat gcc act gtg tac ccc acg 1651
 Thr Gly Thr Asp Leu Ala Asn Arg Gly Tyr Ala Thr Val Tyr Pro Thr
 505 510 515
 gcg atg atc ggt aaa atc ctc gcc gcg cag ata ttg ttc ttg ctg ctc 1699
 Ala Met Ile Gly Lys Ile Leu Gly Ala Gln Ile Leu Phe Leu Leu Leu
 520 525 530
 taaggtgatt ttgtggcagt ggt 1722

<210> 1480
 <211> 533
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1480
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 Leu Gly Ala Ala Ala Val Leu Phe Val Ala Leu Val Val Ser Thr Ala
 35 40 45
 Asn Thr Asp Ile Val Ile Pro Met Ile Val Tyr Gln Leu Gly Leu Ala
 50 55 60
 Met Phe Val Tyr Val Ile Gly Leu Ser Ala Gly Pro Ala Phe Phe Ser
 65 70 75 80
 Glu Phe Ala Lys Lys Gly Trp Lys Leu Thr Ile Phe Met Leu Leu Leu
 85 90 95
 Leu Ala Thr Leu Ile Gly Leu Ala Trp Val Leu Ile Lys Ser Leu Gly
 100 105 110
 Leu Asp Ala Ala Ile Gly Thr Gly Met Phe Thr Gly Ala Leu Thr Ser
 115 120 125
 Thr Pro Gly Met Ala Ala Val Val Glu Leu Ile Glu Gly Ile Asp Pro
 130 135 140
 Ser Leu Ala Ser Glu Pro Val Ile Gly Tyr Ser Leu Ala Tyr Pro Gly
 145 150 155 160
 Ala Val Leu Gly Ser Ile Val Val Ala Ala Val Gly Ala Lys Leu Leu

	165		170		175
Lys Val Asn His Arg Glu Asp Ala Arg	180	Lys Glu Gly Met Ile Thr Ala	190		
Pro Leu Val Trp Lys Gly Val Gln Leu Lys Pro Gly Ile Thr Gly Arg	195	200	205		
Val Gly Asp Leu Pro Arg Leu Ala Gly Glu Ser Ile Ile Ala Thr Arg	210	215	220		
Ile Val Asp Asp Pro His Thr His Arg Leu Ala Asp Pro Asp Leu Pro	225	230	235	240	
Ile Thr Glu Gly Met Glu Leu Leu Ile Asn Gly Thr Glu Glu Ala Val	245	250	255		
Asp Arg Ala Ile Lys Ala Leu Gly Glu Glu Arg Glu Thr Lys Ile Glu	260	265	270		
Asp Thr Glu Leu Ile Tyr Thr Arg Leu Thr Val Ser Ser Pro Glu Val	275	280	285		
Ala Gly Arg Thr Val Ala Glu Leu Asp Thr Val Ala His Gly Phe Met	290	295	300		
Ile Ala Arg Ile Arg Gln Gly Asp Ser Glu Val Val Pro Lys Pro Asp	305	310	315	320	
Thr Val Ile Asn Tyr Ser Asp Arg Ile Arg Val Val Val Ala Pro Gly	325	330	335		
Arg Val Ala Glu Val Arg Arg Phe Leu Gly Asp Ser Glu Lys Ser Leu	340	345	350		
Ala Asp Val Asn Leu Leu Pro Leu Ala Ile Gly Leu Ser Leu Gly Leu	355	360	365		
Leu Leu Gly Ala Ile Pro Ile Pro Leu Pro Gly Gly Thr Thr Met Ser	370	375	380		
Leu Gly Phe Gly Gly Gly Pro Ile Ile Ala Gly Leu Ile Leu Gly Ala	385	390	395	400	
Leu Lys His Thr Gly Pro Leu Thr Trp Gln Met Pro Phe His Ala Asn	405	410	415		
Arg Thr Ile Ser Thr Leu Gly Leu Ala Leu Phe Leu Ala Gly Val Gly	420	425	430		
Thr Ser Ala Gly Ala Gly Phe Arg Ala Ala Leu Thr Asp Ser Ser Ser	435	440	445		
Leu Ile Tyr Met Ala Gly Gly Leu Val Ile Thr Leu Ala Ser Ala Leu	450	455	460		
Leu Cys Ala Val Ile Gly Met Trp Val Leu Arg Leu Arg Trp Asp Glu	465	470	475	480	
Ala Met Gly Val Ala Ala Gly Thr Thr Thr Asn Pro Ala Ile Ile Ser	485	490	495		

Tyr Leu Asn Gly Gln Thr Gly Thr Asp Leu Ala Asn Arg Gly Tyr Ala
 500 505 510

Thr Val Tyr Pro Thr Ala Met Ile Gly Lys Ile Leu Gly Ala Gln Ile
 515 520 525

Leu Phe Leu Leu Leu
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<210> 1481

<211> 1441

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1441)

<223> FRXA00506

<400> 1481

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cgggcaagaa acgtccttaa aaaaagggga gtgattgtga gtg ctt gat ttc tta 115
 Val Leu Asp Phe Leu
 1 5

gct gcg aac ccg ctg att gcg ctg gtg gtt att ttg gcc gtt ggt tta 163
 Ala Ala Asn Pro Leu Ile Ala Leu Val Val Ile Leu Ala Val Gly Leu
 10 15 20

gca att ggt cag att agg gtc ttt gcc ctt tct tta ggt gcc gcc gcg 211
 Ala Ile Gly Gln Ile Arg Val Phe Gly Leu Ser Leu Gly Ala Ala Ala
 25 30 35

gtg ctg ttt gtg gcc ctg gtg gtt tca act gca aat acc gac atc gtc 259
 Val Leu Phe Val Ala Leu Val Val Ser Thr Ala Asn Thr Asp Ile Val
 40 45 50

atc ccc atg att gtt tat cag ctg gcc ttg gcg atg ttc gtt tat gtc 307
 Ile Pro Met Ile Val Tyr Gln Leu Gly Leu Ala Met Phe Val Tyr Val
 55 60 65

atc ggt ttg tcc gcc gga cca gca ttt ttc agt gag ttc gct aaa aag 355
 Ile Gly Leu Ser Ala Gly Pro Ala Phe Phe Ser Glu Phe Ala Lys Lys
 70 75 80 85

ggc tgg aag ctc acc atc ttt atg ctc ctg ctg ctg gca aca ctg att 403
 Gly Trp Lys Leu Thr Ile Phe Met Leu Leu Leu Ala Thr Leu Ile
 90 95 100

ggt ttg gcg tgg gtg ctt att aag tca ctg ggg ctt gat gca gcg atc 451
 Gly Leu Ala Trp Val Leu Ile Lys Ser Leu Gly Leu Asp Ala Ala Ile
 105 110 115

ggt acc ggt atg ttc acc gcc gcg ctg acc tgg act ccc ggt atg gca 499
 Gly Thr Gly Met Phe Thr Gly Ala Leu Thr Ser Thr Pro Gly Met Ala
 120 125 130

gcg gtc gtg gaa ttg att gaa gga atc gat cca agc ctt gcc agt gaa 547

Ala Val Val Glu Leu Ile Glu Gly Ile Asp Pro Ser Leu Ala Ser Glu	
135 140 145	
cct gtt att ggt tat tcc ttg gca tat ccg gga gcc gtg ctg gga tcc	595
Pro Val Ile Gly Tyr Ser Leu Ala Tyr Pro Gly Ala Val Leu Gly Ser	
150 155 160 165	
att gtg gtg gcc gcg gtt gga gcg aaa ctg ctc aaa gta aat cac cgg	643
Ile Val Val Ala Val Gly Ala Lys Leu Lys Val Asn His Arg	
170 175 180	
gaa gat gct cga aaa gaa ggc atg atc acc gca ccg ctg gtg tgg aag	691
Glu Asp Ala Arg Lys Glu Gly Met Ile Thr Ala Pro Leu Val Trp Lys	
185 190 195	
ggt gtg cag ctc aaa cct gga atc aca ggc agg gtg gga gat ctt cca	739
Gly Val Gln Leu Lys Pro Gly Ile Thr Gly Arg Val Gly Asp Leu Pro	
200 205 210	
cgc ctt gca ggt gaa agt atc atc gca acc cgc att gtg gat gat cca	787
Arg Leu Ala Gly Glu Ser Ile Ile Ala Thr Arg Ile Val Asp Asp Pro	
215 220 225	
cat aca cac cgc ctc gcg gat ctg ccg att act gaa ggc atg	835
His Thr His Arg Leu Ala Asp Pro Asp Leu Pro Ile Thr Glu Gly Met	
230 235 240 245	
gaa ctg ttg atc aac ggc act gaa gaa gcc gtg gat ccg gca att aag	883
Glu Leu Leu Ile Asn Gly Thr Glu Glu Ala Val Asp Arg Ala Ile Lys	
250 255 260	
gcg ttg ggt gaa gaa cgc gaa acc aaa att gag gac aca gag ctg atc	931
Ala Leu Gly Glu Glu Arg Glu Thr Lys Ile Glu Asp Thr Gly Val Leu Ile	
265 270 275	
tac acc cgc ctg acg gta tct agc cct gag gtt gca ggt aga acc gtt	979
Tyr Thr Arg Leu Thr Val Ser Pro Glu Val Ala Gly Arg Thr Val	
280 285 290	
gct gag ctt gat act gta gct cac gga ttc atg att gcc cgt atc cgc	1027
Ala Glu Leu Asp Thr Val Ala His Gly Phe Met Ile Ala Arg Ile Arg	
295 300 305	
cag ggc gat tct gag gta gtg cct aaa cct gac acc gtg atc aac tac	1075
Gln Gly Asp Ser Glu Val Val Pro Lys Pro Asp Thr Val Ile Asn Tyr	
310 315 320 325	
tct gac cgc atc cgc gtg gtg gtt gct cct ggt cgt gtg gct gaa gtg	1123
Ser Asp Arg Ile Arg Val Val Val Ala Pro Gly Arg Val Ala Glu Val	
330 335 340	
cga cga ttc tta ggg gac tct gaa aag tcc ctt gct gat gtt aat ctg	1171
Arg Arg Phe Leu Gly Asp Ser Glu Lys Ser Leu Ala Asp Val Asn Leu	
345 350 355	
ctg cct tta gcc atc gga tta tct ctt ggc ctg ttg ttg ggc gcg atc	1219
Leu Pro Leu Ala Ile Gly Leu Ser Leu Gly Leu Leu Gly Ala Ile	
360 365 370	
ccg att cct ctt cca ggc ggc acc acg atg tcc ctt ggc ttt ggt ggc	1267
Pro Ile Pro Leu Pro Gly Gly Thr Thr Met Ser Leu Gly Phe Gly Gly	

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375                               380                               385

ggc ccg att att gcc gcc ctg att ttg gga gca ctc aag cac aca gga 1315
Gly Pro Ile Ile Ala Gly Leu Ile Leu Gly Ala Leu Lys His Thr Gly
390                               395                               400                               405

ccg ctg acg tgg cag atg ccg ttc cac gcc aac cgc acg atc tcc acc 1363
Pro Leu Thr Trp Gln Met Pro Phe His Ala Asn Arg Thr Ile Ser Thr
410                               415                               420

ttg gcc ctg gcc ctg ttt ttg gct ggt gtg ggt acc tct gca ggt gca 1411
Leu Gly Leu Ala Leu Phe Leu Ala Gly Val Gly Thr Ser Ala Gly Ala
425                               430                               435

gga ttt aga gct gcg ott acc gat tcc tcc 1441
Gly Phe Arg Ala Ala Leu Thr Asp Ser Ser
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<210> 1482
<211> 447
<212> PRT
<213> Corynebacterium glutamicum

<400> 1482
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20 25 30
Leu Gly Ala Ala Ala Val Leu Phe Val Ala Leu Val Val Ser Thr Ala
35 40 45
Asn Thr Asp Ile Val Ile Pro Met Ile Val Tyr Gln Leu Gly Leu Ala
50 55 60
Met Phe Val Tyr Val Ile Gly Leu Ser Ala Gly Pro Ala Phe Phe Ser
65 70 75 80
Glu Phe Ala Lys Lys Gly Trp Lys Leu Thr Ile Phe Met Leu Leu Leu
85 90 95
Leu Ala Thr Leu Ile Gly Leu Ala Trp Val Leu Ile Lys Ser Leu Gly
100 105 110
Leu Asp Ala Ala Ile Gly Thr Gly Met Phe Thr Gly Ala Leu Thr Ser
115 120 125
Thr Pro Gly Met Ala Ala Val Val Glu Leu Ile Glu Gly Ile Asp Pro
130 135 140
Ser Leu Ala Ser Glu Pro Val Ile Gly Tyr Ser Leu Ala Tyr Pro Gly
145 150 155 160
Ala Val Leu Gly Ser Ile Val Val Ala Ala Val Gly Ala Lys Leu Leu
165 170 175
Lys Val Asn His Arg Glu Asp Ala Arg Lys Glu Gly Met Ile Thr Ala
180 185 190

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Pro Leu Val Trp Lys Gly Val Gln Leu Lys Pro Gly Ile Thr Gly Arg
 195 200
 Val Gly Asp Leu Pro Arg Leu Ala Gly Glu Ser Ile Ile Ala Thr Arg
 210 215
 Ile Val Asp Asp Pro His Thr His Arg Leu Ala Asp Pro Asp Leu Pro
 225 230 235 240
 Ile Thr Glu Gly Met Glu Leu Leu Ile Asn Gly Thr Glu Glu Ala Val
 245 250 255
 Asp Arg Ala Ile Lys Ala Leu Gly Glu Glu Arg Glu Thr Lys Ile Glu
 260 265 270
 Asp Thr Glu Leu Ile Tyr Thr Arg Leu Thr Val Ser Ser Pro Glu Val
 275 280 285
 Ala Gly Arg Thr Val Ala Glu Leu Asp Thr Val Ala His Gly Phe Met
 290 295 300
 Ile Ala Arg Ile Arg Gln Gly Asp Ser Glu Val Val Pro Lys Pro Asp
 305 310 315 320
 Thr Val Ile Asn Tyr Ser Asp Arg Ile Arg Val Val Val Ala Pro Gly
 325 330 335
 Arg Val Ala Glu Val Arg Arg Phe Leu Gly Asp Ser Glu Lys Ser Leu
 340 345 350
 Ala Asp Val Asn Leu Leu Pro Leu Ala Ile Gly Leu Ser Leu Gly Leu
 355 360 365
 Leu Leu Gly Ala Ile Pro Ile Pro Leu Pro Gly Gly Thr Thr Met Ser
 370 375 380
 Leu Gly Phe Gly Gly Gly Pro Ile Ile Ala Gly Leu Ile Leu Gly Ala
 385 390 395 400
 Leu Lys His Thr Gly Pro Leu Thr Trp Gln Met Pro Phe His Ala Asn
 405 410 415
 Arg Thr Ile Ser Thr Leu Gly Leu Ala Leu Phe Leu Ala Gly Val Gly
 420 425 430
 Thr Ser Ala Gly Ala Gly Phe Arg Ala Ala Leu Thr Asp Ser Ser
 435 440 445

<210> 1483

<211> 522

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(499)

<223> RXN03115

<400> 1483

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[illegible]

<211> 133

<213> Cor

Val Glv Ly

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      20              25              30
Glu Asp Gln Glu Ala Glu Ile Ala Glu Met Glu His Met Leu Asn Glu
      35              40              45
Leu

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 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(451)
 <223> RXN03134

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 ccagtttgct gatcagcggg tttgtttcgc gtggggcggtg gtg gct tgg cgc gtc 115
 Val Ala Trp Arg Val
 1 5
 ggc cca ggt tcc cat gag cat gac ata gtt ggg tcc tcc ggc ttt gga 163
 Gly Pro Gly Ser His Glu His Asp Ile Val Gly Ser Ser Gly Phe Gly
 10 15 20
 tcc gag gcc gac gga gga ttt ttt cca gcc tcc gaa gga ttg gcg ttg 211
 Ser Glu Ala Asp Gly Gly Phe Phe Pro Ala Ser Glu Gly Leu Ala Leu
 25 30 35
 gac aat ggc gcc ggt gat gcc gcg gtt gac gta ggc gtt tcc gac atc 259
 Asp Asn Gly Ala Gly Asp Ala Ala Val Asp Val Gly Val Ser Asp Ile
 40 45 50
 gac gtg gtc aag cca ggt gcg gac ttc gtc gcc gtc gag gga ttg gag 307
 Asp Val Val Lys Pro Gly Ala Asp Phe Val Gly Val Glu Gly Leu Glu
 55 60 65
 tcc gcc ggt gag tcc gaa gtc gtt gcc gtt ttg gaa ttc gat gcc ttc 355
 Ser Ala Gly Glu Ser Glu Val Val Ala Val Leu Glu Phe Asp Gly Phe
 70 75 80 85
 att gag gtc ggt gcc ttt cat cag gcc gag gac tgg tcc gaa tac ttc 403
 Ile Glu Val Gly Gly Phe His Gln Ala Glu Asp Trp Ser Glu Tyr Phe
 90 95 100
 tgt gag gtg gaa gaa ggt tcc tgg ttt gac gcc ttc ttt gat gcc ggg 451
 Cys Glu Val Glu Glu Gly Ser Trp Phe Asp Ala Phe Phe Asp Ala Gly
 105 110 115
 tgaccagagt cggcgggtgt cgt 474

<210> 1488
 <211> 117
 <212> PRT
 <213> *Corynebacterium glutamicum*

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Glu Gly	Leu Ala	Leu Asp	Asn Gly	Ala Gly	Asp Ala
	35		40		45
Gly Val	Ser Asp	Ile Asp	Val Val	Lys Pro	Gly Ala
	50		55		60
Val Glu	Gly Leu	Glu Ser	Ala Gly	Glu Ser	Glu Val
	65		70		75
Glu Phe	Asp Gly	Phe Ile	Glu Val	Gly Gly	Phe His
	85		90		95
Trp Ser	Glu Tyr	Phe Cys	Glu Val	Glu Gly	Ser Trp
	100		105		110
Phe Phe	Asp Ala	Gly			
	115				

<210> 1489

<211> 852

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(829)

<223> RXN03135

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cggtctctgc	tgcggtggcg	acggcttttg	tggtccactg	ttg gtt	ttg gat	gag	115
				Leu Val	Leu Asp	Glu	
				1		5	

cgc tgg	gtt ggt	gtc ggg	ctc gtt	gat aaa	tgg gac	gag ggg	ggc gtc	163
Arg Trp	Val Gly	Val Gly	Leu Val	Asp Lys	Trp Asp	Glu Gly	Gly Val	
	10			15		20		

gag aag	cgt ctc	ttt gct	gcg gtc	ttg tgt	gtg gtt	ggg gcc	ggg cgc	211
Glu Lys	Arg Leu	Phe Ala	Ala Val	Leu Cys	Val Val	Gly Ala	Gly Arg	
	25		30			35		

ggg cac	gtc gat	gag cgt	ggc gag	gtc aga	tat gga	ggc gcg	gaa gcg	259
Gly His	Val Asp	Glu Arg	Gly Gly	Val Arg	Tyr Gly	Gly Ala	Glu Ala	
	40		45		50			

gct ctc	ctc tcg	ctt gaa	gga cgg	gtt gtc	ggc gtc	gag gtc	gaa gat	307
Ala Leu	Leu Ser	Leu Glu	Gly Arg	Val Val	Gly Val	Glu Val	Glu Asp	
	55		60		65			

ggc gga	cat gaa	gtt ttc	gct cgc	ggc gtt	ttc ctc	gag gcg	gcg cac	355
Gly Gly	His Glu	Val Phe	Ala Arg	Gly Val	Phe Leu	Glu Ala	Ala His	
	70		75		80		85	

gag gta	aga aat	ggc cac	gtc gaa	ttc ttg	tgg gcg	cac ggc	tgg tac	403
Glu Val	Arg Asn	Gly His	Val Glu	Phe Leu	Trp Ala	His Gly	Trp Tyr	
	90			95		100		

gta aag cag cag ctc acc gac gtc aac gct gac ggc gcg cgc ctg atc 451
Val Lys Gln Gln Leu Thr Asp Val Asn Ala Asp Gly Ala Arg Leu Ile
105 110 115

gga cgc cat gcc ctg cag cat ttc gaa ctc cac acg gtc cgc tac ccc 499
Gly Arg His Ala Leu Gln His Phe Glu Leu His Thr Val Arg Tyr Pro
120 125 130

acg ctc cac aga gag caa atg tgc gaa tgc tat gtc gaa aag gtt gtg 547
Thr Leu His Arg Glu Gln Met Cys Glu Cys Tyr Val Glu Lys Val Val
135 140 145

gcc ggc aac gcc cag gcg cag gcc ctc cat gtt ttc ttt gcg cat cgt 595
Ala Gly Asn Ala Gln Ala Gln Ala Leu His Val Phe Phe Ala His Arg
150 155 160 165

cca ata gag gac gcg ctt gta att ggc atc ggt ggc ttg ttt gga agg 643
Pro Ile Glu Asp Ala Leu Val Ile Gly Ile Gly Gly Leu Phe Gly Arg
170 175 180

ttc tgt ggc aac tgg cca gcc ggt gat ctg cgc gtg gac gtg ctc cat 691
Phe Cys Gly Asn Trp Pro Ala Gly Asp Leu Arg Val Asp Val Leu His
185 190 195

agg caa att agc acc ctt gac cag gcg aac ctt aac gcc cgc ccc gcc 739
Arg Gln Ile Ser Thr Leu Asp Gln Ala Asn Leu Asn Ala Arg Pro Ala
200 205 210

tgt gtt gac gcg ctc gcg gcc gaa ctg cgc caa gtc ctg gat tgc acc 787
Cys Val Asp Ala Leu Ala Ala Glu Leu Arg Gln Val Leu Asp Cys Thr
215 220 225

gag ggc atc ggg aag gta cgc ctg caa cac aat tcc gcc ttc 829
Glu Gly Ile Gly Lys Val Arg Leu Gln His Asn Ser Gly Phe
230 235 240

tagttcatgc agctctggat tgg 852

<210> 1490

<211> 243

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1490

Leu Val Leu Asp Glu Arg Trp Val Gly Val Gly Leu Val Asp Lys Trp
1 5 10 15

Asp Glu Gly Gly Val Glu Lys Arg Leu Phe Ala Ala Val Leu Cys Val
20 25 30

Val Gly Ala Gly Arg Gly His Val Asp Glu Arg Gly Glu Val Arg Tyr
35 40 45

Gly Gly Ala Glu Ala Ala Leu Leu Ser Leu Glu Gly Arg Val Val Gly
50 55 60

Val Glu Val Glu Asp Gly Gly His Glu Val Phe Ala Arg Gly Val Phe
65 70 75 80

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Leu Glu Ala Ala His Glu Val Arg Asn Gly His Val Glu Phe Leu Trp
      85                      90                      95

Ala His Gly Trp Tyr Val Lys Gln Gln Leu Thr Asp Val Asn Ala Asp
      100                      105                      110

Gly Ala Arg Leu Ile Gly Arg His Ala Leu Gln His Phe Glu Leu His
      115                      120                      125

Thr Val Arg Tyr Pro Thr Leu His Arg Glu Gln Met Cys Glu Cys Tyr
      130                      135                      140

Val Glu Lys Val Val Ala Gly Asn Ala Gln Ala Gln Ala Leu His Val
      145                      150                      155                      160

Phe Phe Ala His Arg Pro Ile Glu Asp Ala Leu Val Ile Gly Ile Gly
      165                      170                      175

Gly Leu Phe Gly Arg Phe Cys Gly Asn Trp Pro Ala Gly Asp Leu Arg
      180                      185                      190

Val Asp Val Leu His Arg Gln Ile Ser Thr Leu Asp Gln Ala Asn Leu
      195                      200                      205

Asn Ala Arg Pro Ala Cys Val Asp Ala Leu Ala Ala Glu Leu Arg Gln
      210                      215                      220

Val Leu Asp Cys Thr Glu Gly Ile Gly Lys Val Arg Leu Gln His Asn
      225                      230                      235                      240

Ser Gly Phe

<210> 1491
<211> 852
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(829)
<223> FRXA02285

<400> 1491
ttagctgtgc gacgtccccc tcttccaaca cctcgggtt tgtttgttt tccaaccaac 60

cgggctctgc tgcggtggcg acggcttttg tggcccactg ttg gtt ttg gat gag 115
                                   Leu Val Leu Asp Glu
                                   1 5

cgc tgg gtt ggt gtc ggg ctc gtt gat aaa tgg gac gag ggg ggc gtc 163
Arg Trp Val Gly Val Gly Leu Val Asp Lys Trp Asp Glu Gly Gly Val
      10                      15                      20

gag aag cgt ctc ttt gct gcg gtc ttg tgt gtg gtt ggg gcc ggg cgc 211
Glu Lys Arg Leu Phe Ala Ala Val Leu Cys Val Val Gly Ala Gly Arg
      25                      30                      35

ggg cac gtc gat gag cgt ggc gag gtc aga tat gga ggc gcg gaa gcg 259
Gly His Val Asp Glu Arg Gly Glu Val Arg Tyr Gly Gly Ala Glu Ala

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40	45	50	
gct ctc ctc tcg ctt gaa gga cgg gtt gtc ggc gtc gag gtc gaa gat			307
Ala Leu Leu Ser Leu Glu Gly Arg Val Val Gly Val Glu Val Glu Asp			
55	60	65	
ggc gga cat gaa gtt ttc gct cgc ggc gtt ttc ctc gag gcg gcg cac			355
Gly Gly His Glu Val Phe Ala Arg Gly Val Phe Leu Glu Ala Ala His			
70	75	80	85
gag gta aga aat ggc cac gtc gaa ttc ttg tgg gcg cac ggc tgg tac			403
Glu Val Arg Asn Gly His Val Glu Phe Leu Trp Ala His Gly Trp Tyr			
90	95	100	
gta aag cag cag ctc acc gac gtc aac gct gac ggc gcg cgc ctg atc			451
Val Lys Gln Gln Leu Thr Asp Val Asn Ala Asp Gly Ala Arg Leu Ile			
105	110	115	
gga cgc cat gcc ctg cag cat ttc gaa ctc cac acg gtc cgc tac ccc			499
Gly Arg His Ala Leu Gln His Phe Glu Leu His Thr Val Arg Tyr Pro			
120	125	130	
acg ctc cac aga gag caa atg tgc gaa tgc tat gtc gaa aag gtt gtg			547
Thr Leu His Arg Glu Gln Met Cys Glu Cys Tyr Val Glu Lys Val Val			
135	140	145	
gcc ggc aac gcc cag gcg cag gcc ctc cat gtt ttc ttt gcg cat cgt			595
Ala Gly Asn Ala Gln Ala Gln Ala Leu His Val Phe Phe Ala His Arg			
150	155	160	165
cca ata gag gac gcg ctt gta att ggc atc ggt ggc ttg ttt gga agg			643
Pro Ile Glu Asp Ala Leu Val Ile Gly Ile Gly Gly Leu Phe Gly Arg			
170	175	180	
ttc tgt ggc aac tgg cca gcc ggt gat ctg cgc gtg gac gtg ctc cat			691
Phe Cys Gly Asn Trp Pro Ala Gly Asp Leu Arg Val Asp Val Leu His			
185	190	195	
agg caa att agc acc ctt gac cag gcg aac ctt aac gcc cgc ccc gcc			739
Arg Gln Ile Ser Thr Leu Asp Gln Ala Asn Leu Asn Ala Arg Pro Ala			
200	205	210	
tgt gtt gac gcg ctc gcg gcc gaa ctg cgc caa gtc ctg gat tgc acc			787
Cys Val Asp Ala Leu Ala Ala Glu Leu Arg Gln Val Leu Asp Cys Thr			
215	220	225	
gag ggc atc ggg aag gta cgc ctg caa cac aat tcc gcc ttc			829
Glu Gly Ile Gly Lys Val Arg Leu Gln His Asn Ser Gly Phe			
230	235	240	
tagttcatgc agctctggat tgg			852

<210> 1492

<211> 243

<212> PRT

<213> Corynebacterium glutamicum

<400> 1492

Leu	Val	Leu	Asp	Glu	Arg	Trp	Val	Gly	Val	Gly	Leu	Val	Asp	Lys	Trp
1				5				10					15		

Asp Glu Gly Gly Val Glu Lys Arg Leu Phe Ala Ala Val Leu Cys Val
 20 25 30
 Val Gly Ala Gly Arg Gly His Val Asp Glu Arg Gly Glu Val Arg Tyr
 35 40 45
 Gly Gly Ala Glu Ala Ala Leu Ser Leu Glu Gly Arg Val Val Gly
 50 55 60
 Val Glu Val Glu Asp Gly Gly His Glu Val Phe Ala Arg Gly Val Phe
 65 70 75 80
 Leu Glu Ala Ala His Glu Val Arg Asn Gly His Val Glu Phe Leu Trp
 85 90 95
 Ala His Gly Trp Tyr Val Lys Gln Gln Leu Thr Asp Val Asn Ala Asp
 100 105 110
 Gly Ala Arg Leu Ile Gly Arg His Ala Leu Gln His Phe Glu Leu His
 115 120 125
 Thr Val Arg Tyr Pro Thr Leu His Arg Glu Gln Met Cys Glu Cys Tyr
 130 135 140
 Val Glu Lys Val Val Ala Gly Asn Ala Gln Ala Gln Ala Leu His Val
 145 150 155 160
 Phe Phe Ala His Arg Pro Ile Glu Asp Ala Leu Val Ile Gly Ile Gly
 165 170 175
 Gly Leu Phe Gly Arg Phe Cys Gly Asn Trp Pro Ala Gly Asp Leu Arg
 180 185 190
 Val Asp Val Leu His Arg Gln Ile Ser Thr Leu Asp Gln Ala Asn Leu
 195 200 205
 Asn Ala Arg Pro Ala Cys Val Asp Ala Leu Ala Ala Glu Leu Arg Gln
 210 215 220
 Val Leu Asp Cys Thr Glu Gly Ile Gly Lys Val Arg Leu Gln His Asn
 225 230 235 240
 Ser Gly Phe

<210> 1493

<211> 594

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(571)

<223> RXN03138

<400> 1493

agaatgttcc agtcttggca tccaaccagc cgattccgct ggcccacact gggcggttg 60

cgagggtcttt ggcggtgtac aagttgagga ctaccttgac ttg gat att gtt ccg 115

Leu Asp Ile Val Pro
1 5

aag gat gtc gct gaa agc ttc gcc gta ggt gag gtc gtt ttt ctt cgc 163
Lys Asp Val Ala Glu Ser Phe Ala Val Gly Glu Val Val Phe Leu Arg
10 15 20

gtg ttg ggt gac ggc gtc gtt gat gat gtg ccc gtc cac agc atc gac 211
Val Leu Gly Asp Gly Val Val Asp Asp Val Pro Val His Ser Ile Asp
25 30 35

gga ggc tcc gat ttc ggc ggt tcc gtc tgg gga gaa ggt cac tcc gaa 259
Gly Gly Ser Asp Phe Gly Gly Ser Val Trp Gly Glu Gly His Ser Glu
40 45 50

aga gct gtc gtc ttg ggt acc gcg cga acc ggt ggc tct tgc gtc gtc 307
Arg Ala Val Val Leu Gly Thr Ala Arg Thr Gly Gly Ser Cys Val Val
55 60 65

aag caa atc tct tat ttc ttt tat ctt gcg tcc tat gga cgc cgg gct 355
Lys Gln Ile Ser Tyr Phe Phe Tyr Leu Ala Ser Tyr Gly Arg Arg Ala
70 75 80 85

tgg cag aat ctg gtt ggg gct ggt ggc ggt gag gta ttc ggt gag gat 403
Trp Gln Asn Leu Val Gly Ala Gly Gly Glu Val Phe Gly Glu Asp
90 95 100

tgc gtc ggc gcc ggc gag gtt gtc ggg gtt gat gcc ggc gag ttc gtt 451
Cys Val Gly Ala Gly Glu Val Val Gly Val Asp Ala Gly Glu Phe Val
105 110 115

gct aat ggt gat cag tcg gga gag gtc gag gtg gta cag ctt ttg ttg 499
Ala Asn Gly Asp Gln Ser Gly Glu Val Glu Val Val Gln Leu Leu Leu
120 125 130

cag ggc ttt gag ttc ggg caa gtc ggc gag cgt ggc aaa cgc gat gga 547
Gln Gly Phe Glu Phe Gly Gln Val Gly Glu Arg Gly Lys Arg Asp Gly
135 140 145

tat gcg gga gac ctg cgc ttt tgt tagacctgtg acgatggcga ggc 594
Tyr Ala Gly Asp Leu Arg Phe Cys
150 155

<210> 1494

<211> 157

<212> PRT

<213> Corynebacterium glutamicum

<400> 1494

Leu Asp Ile Val Pro Lys Asp Val Ala Glu Ser Phe Ala Val Gly Glu
1 5 10 15

Val Val Phe Leu Arg Val Leu Gly Asp Gly Val Val Asp Asp Val Pro
20 25 30

Val His Ser Ile Asp Gly Gly Ser Asp Phe Gly Gly Ser Val Trp Gly
35 40 45

Glu Gly His Ser Glu Arg Ala Val Val Leu Gly Thr Ala Arg Thr Gly
50 55 60

Gly Ser Cys Val Val Lys Gln Ile Ser Tyr Phe Phe Tyr Leu Ala Ser
 65 70 75 80
 Tyr Gly Arg Arg Ala Trp Gln Asn Leu Val Gly Ala Gly Gly Gly Glu
 85 90 95
 Val Phe Gly Glu Asp Cys Val Gly Ala Gly Glu Val Val Gly Val Asp
 100 105 110
 Ala Gly Glu Phe Val Ala Asn Gly Asp Gln Ser Gly Glu Val Glu Val
 115 120 125
 Val Gln Leu Leu Leu Gln Gly Phe Glu Phe Gly Gln Val Gly Glu Arg
 130 135 140
 Gly Lys Arg Asp Gly Tyr Ala Gly Asp Leu Arg Phe Cys
 145 150 155

<210> 1495

<211> 372

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(349)

<223> RXN03140

<400> 1495

ctcaagcgat cggtggaaca tocactaacg gggttaccaa aaatcctctcg cggacactcc 60

cgaaggaaca cttcttgcca gaaggaaagg aagaagcact gtg aag ggc att cat 115
 Val Lys Gly Ile His
 1 5

cag gaa att agc cgt atc gag cgt agc cac gat tat ctg tgg agc gtc 163
 Gln Glu Ile Ser Arg Ile Glu Arg Ser His Asp Tyr Leu Trp Ser Val
 10 15 20

cga gaa gac ctg cat gca cga ttc gac aac caa ctg aag gca cac ttt 211
 Arg Glu Asp Leu His Ala Arg Phe Asp Asn Gln Leu Lys Ala His Phe
 25 30 35

gta gac agt gtc ctg gat agc att gca gaa gga tat gaa ggc cga atc 259
 Val Asp Ser Val Leu Asp Ser Ile Ala Glu Gly Tyr Glu Gly Arg Ile
 40 45 50

aac cga ttc cgc aaa atc ttc att gaa atg aaa gcg gtt gaa gag ctg 307
 Asn Arg Phe Arg Lys Ile Phe Ile Glu Met Lys Ala Val Glu Glu Leu
 55 60 65

cgc acc atc gcc gcc acc cgc cca agc cac ctc ttg gct gca 349
 Arg Thr Ile Ala Ala Thr Arg Pro Ser His Leu Leu Ala Ala
 70 75 80

taagacactt aaaagttaaa taa 372

<210> 1496

<211> 83
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1496
 Val Lys Gly Ile His Gln Glu Ile Ser Arg Ile Glu Arg Ser His Asp
 1 5 10 15
 Tyr Leu Trp Ser Val Arg Glu Asp Leu His Ala Arg Phe Asp Asn Gln
 20 25 30
 Leu Lys Ala His Phe Val Asp Ser Val Leu Asp Ser Ile Ala Glu Gly
 35 40 45
 Tyr Glu Gly Arg Ile Asn Arg Phe Arg Lys Ile Phe Ile Glu Met Lys
 50 55 60
 Ala Val Glu Glu Leu Arg Thr Ile Ala Ala Thr Arg Pro Ser His Leu
 65 70 75 80
 Leu Ala Ala

<210> 1497
 <211> 453
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(430)
 <223> RXN03141

<400> 1497
 ggccctgctg cttcatgcgg tgagctgcgc gaccgaaagc gatctgtgag gaagcggtga 60
 aatctgggtt tcggtccagc ttgaggatgt attccacggt gtg gtt gaa gcc acc 115
 Val Val Glu Ala Thr
 1 5
 ggt gtc gcc ggt ggt aat cac gtg gcc acc gtg tgg cat gcc ggt gtg 163
 Gly Val Ala Gly Gly Asn His Val Ala Thr Val Trp His Ala Gly Val
 10 15 20
 ctc gga gtc gaa ggt tgc ttc gtc gat gaa gtt gac ttc gac ttc gta 211
 Leu Gly Val Glu Gly Cys Phe Val Asp Glu Val Asp Phe Asp Phe Val
 25 30 35
 gcc aac gaa gta atc agg cat ggt gcg gat gtc gtt ttc gat gcg ctc 259
 Ala Asn Glu Val Ile Arg His Gly Ala Asp Val Val Phe Asp Ala Leu
 40 45 50
 gtg atc ggc cgc gtc ggc aac cac gaa gca ttg gcg ctt gtg ggt ttg 307
 Val Ile Gly Arg Val Gly Asn His Glu Ala Leu Ala Leu Val Gly Leu
 55 60 65
 ctt tcc ggt aag gtc gcc ggc ttc gcc gcg gcg ggc ctt ttc cag ggc 355
 Leu Ser Gly Lys Val Ala Gly Phe Ala Ala Ala Gly Leu Phe Gln Gly
 70 75 80 85

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gtc ttc gga tgg gag ggt gta ctg gac tgc ctt ttg aac gcc agg gat 403
Val Phe Gly Trp Glu Gly Val Leu Asp Cys Leu Leu Ala Arg Asp
          90                      95          100

gcg tcg caa agc atc gga gtg gcc ctg tgacaaacct gggccccaga 450
Ala Ser Gln Ser Ile Gly Val Ala Leu
          105                      110

agg 453

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<210> 1498
<211> 110
<212> PRT
<213> Corynebacterium glutamicum

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<400> 1498
Val Val Glu Ala Thr Gly Val Ala Gly Gly Asn His Val Ala Thr Val
  1              5              10              15

Trp His Ala Gly Val Leu Gly Val Glu Gly Cys Phe Val Asp Glu Val
          20              25              30

Asp Phe Asp Phe Val Ala Asn Glu Val Ile Arg His Gly Ala Asp Val
          35              40              45

Val Phe Asp Ala Leu Val Ile Gly Arg Val Gly Asn His Glu Ala Leu
          50              55              60

Ala Leu Val Gly Leu Leu Ser Gly Lys Val Ala Gly Phe Ala Ala Ala
  65              70              75              80

Gly Leu Phe Gln Gly Val Phe Gly Trp Glu Gly Val Leu Asp Cys Leu
          85              90              95

Leu Asn Ala Arg Asp Ala Ser Gln Ser Ile Gly Val Ala Leu
          100              105              110

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<210> 1499
<211> 594
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(571)
<223> RXN03146

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<400> 1499
taacgtgggg gtttttaagct tgcgtagaca tatcgttttt cgatagattt acatcttgaa 60

acgatacggc catccacggc gcatgtctga aaggttcccc atg aat ccc cgc atc 115
          Met Asn Pro Arg Ile
          1              5

ctc atg ctg ctt cgc atc att ttc ggc gcg gcc ttc ctc gca ctg ttg 163
Leu Met Leu Leu Arg Ile Ile Phe Gly Ala Ala Phe Leu Ala Leu Leu
          10              15              20

gtg ctg caa gtc ctg ctc gcc atc aaa atc gtg cgc gat gcc ctc aac 211

```

Val Leu Gln Val Leu Leu Ala Ile Lys Ile Val Arg Asp Gly Leu Asn
25 30 35

tcc gcc gag ctc tcc ccc atc ccg ctc acc att ctc gcg agc ttc gtg 259
Ser Gly Glu Leu Ser Pro Ile Pro Leu Thr Ile Leu Ala Ser Phe Val
40 45 50

atc atc ggt ttc ggg ctc gtg cag ttc atc atc gtc tgt ctg ttc gcg 307
Ile Ile Gly Phe Gly Leu Val Gln Phe Ile Ile Val Cys Leu Phe Ala
55 60 65

cta ctg cgt ctc gtg gaa gac gat gaa atc ttc gac gcc cac tcg ctc 355
Leu Leu Arg Leu Val Glu Asp Asp Glu Ile Phe Asp Ala His Ser Leu
70 75 80 85

gcc tgg gtt gat cga att gcc atc acc atc gca gcc gcc ggc gcc gtt tta 403
Ala Trp Val Asp Arg Ile Ala Ile Thr Ile Ala Ala Gly Ala Val Leu
90 95 100

ctc ctc cca atg gcc tac atc gtc gca gaa gtc gac gac gcc ccc gga 451
Leu Leu Pro Met Ala Tyr Ile Val Ala Glu Val Asp Asp Ala Pro Gly
105 110 115

gcc atc gtc ttc ggt ctc atc ctc gcg atg ctc atc acg ggc gta tcc 499
Ala Ile Val Phe Gly Leu Ile Leu Ala Met Leu Ile Thr Gly Val Ser
120 125 130

ctg ctg gta aaa atc atg cgc gca ctc ctg gcc cgc gcc atc gga ttc 547
Leu Leu Val Lys Ile Met Arg Ala Leu Leu Ala Arg Ala Ile Gly Phe
135 140 145

tcc acg gaa ctg gaa tcg gtg atc taaatggcca tcacgtcgca cat 594
Ser Thr Glu Leu Glu Ser Val Ile
150 155

<210> 1500
<211> 157
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 1500
Met Asn Pro Arg Ile Leu Met Leu Leu Arg Ile Ile Phe Gly Ala Ala
1 5 10 15

Phe Leu Ala Leu Leu Val Leu Gln Val Leu Leu Ala Ile Lys Ile Val
20 25 30

Arg Asp Gly Leu Asn Ser Gly Glu Leu Ser Pro Ile Pro Leu Thr Ile
35 40 45

Leu Ala Ser Phe Val Ile Ile Gly Phe Gly Leu Val Gln Phe Ile Ile
50 55 60

Val Cys Leu Phe Ala Leu Leu Arg Leu Val Glu Asp Asp Glu Ile Phe
65 70 75 80

Asp Ala His Ser Leu Ala Trp Val Asp Arg Ile Ala Ile Thr Ile Ala
85 90 95

Ala Gly Ala Val Leu Leu Leu Pro Met Ala Tyr Ile Val Ala Glu Val

	100		105		110
Asp Asp Ala Pro Gly Ala Ile Val Phe Gly Leu Ile Leu Ala Met Leu					
115			120		125
Ile Thr Gly Val Ser Leu Leu Val Lys Ile Met Arg Ala Leu Leu Ala					
130		135		140	
Arg Ala Ile Gly Phe Ser Thr Glu Leu Glu Ser Val Ile					
145		150		155	

<210> 1501
 <211> 375
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(352)
 <223> RXN03147

<400> 1501
 ccctgatccc gaggacgatg accgccaaaag cgatggcgcc tccaatcagg atgtactgca 60
 gtgggattgg gcgggcgatc tcgatggcat cgaatgcagtt ttg gaa atc ctc ttt 115
 Leu Glu Ile Leu Phe
 1 5
 aag agc ggt ttg gga ttc gtt gta atc atc ggt gcg gtc ggc gaa tac 163
 Lys Ser Gly Leu Gly Phe Val Val Ile Ile Gly Ala Val Gly Glu Tyr
 10 15 20
 ttc ggc gcg gat ttc tgc ggt gcg ggt gcc ggt ggt ggc ggc ttg ttg 211
 Phe Gly Ala Asp Phe Cys Gly Ala Gly Ala Gly Gly Gly Leu Leu
 25 30 35
 aag ttg gct gag tac atc gct ggc tgg atc gct gga gaa tcc gct gat 259
 Lys Leu Ala Glu Tyr Ile Ala Gly Trp Ile Ala Gly Glu Ser Ala Asp
 40 45 50
 gat gtc ttt ggc ttc gtc gta tgt gta ctc cgt ttt gaa act ttc ctc 307
 Asp Val Phe Gly Phe Val Val Cys Val Leu Arg Phe Glu Thr Phe Leu
 55 60 65
 ggc gtt ggg gtc tgc cag cgt ggg atc gtc tgg gag gag cat ggc 352
 Gly Val Gly Val Cys Gln Arg Gly Ile Val Trp Glu Glu His Gly
 70 75 80
 taggccttcg ccggattoga tgg 375

<210> 1502
 <211> 84
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1502
 Leu Glu Ile Leu Phe Lys Ser Gly Leu Gly Phe Val Val Ile Ile Gly
 1 5 10 15

<212> PRT

<213> Corynebacterium glutamicum

<400> 1504

Val	Val	Ile	Gly	Glu	Leu	Leu	Pro	Lys	Ser	Tyr	Ser	Ile	Val	Asn	Thr
1				5					10					15	

Glu	Lys	Val	Val	Leu	Phe	Val	Val	Lys	Pro	Leu	His	Tyr	Phe	Tyr	Lys
		20						25					30		

Val	Met	Phe	Pro	Phe	Ile	Trp	Val	Leu	Asn	His	Ser	Ala	Ala	Gly	Leu
		35					40					45			

Gly	Lys	Leu	Leu	Gly	Val	Arg	Leu	Val	Ser	Glu	Gly	Glu	Glu	Thr	Leu
	50					55					60				

Ser	Gln	Glu	Glu	Leu	Thr	Leu	Val	Ala	Leu	Asn	Ser	Tyr	Glu	Lys	Gly
	65				70					75					80

Glu	Leu	Pro	Lys	Lys	Asn	Ile	Ile	Ile
				85				

<210> 1505

<211> 396

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(373)

<223> RXN03152

<400> 1505

gcaaaatattc agctttgacc tgcacatata gttgcacaat ggtgaaagtg cacataaagt 60

aactttcgtat	ttcgaatatt	taaacctaag	gggttttagca	atg	aag	cta	ttt	tct	115
				Met	Lys	Leu	Phe	Ser	
				1				5	

cgt	act	ccc	ctc	gtc	gca	ctc	ggc	aca	gct	gct	gca	atg	gca	gca	acc	163
Arg	Thr	Pro	Leu	Val	Ala	Leu	Gly	Thr	Ala	Ala	Ala	Met	Ala	Ala	Thr	
			10					15					20			

tcc	atc	tcc	gtt	cct	gca	cag	gct	gaa	gaa	gtc	gca	cca	gca	cag	gtt	211
Ser	Ile	Ser	Val	Pro	Ala	Gln	Ala	Glu	Glu	Val	Ala	Pro	Ala	Gln	Val	
			25				30						35			

gtg	tac	gtg	gct	gac	acc	gta	gaa	gaa	gaa	acg	ggc	agc	tcc	aac	gga	259
Val	Tyr	Val	Ala	Asp	Thr	Val	Glu	Glu	Glu	Thr	Gly	Ser	Ser	Asn	Gly	
		40					45					50				

tct	tct	gac	att	gac	tct	gac	acc	att	ttg	gat	tac	gtc	gtc	gtt	att	307
Ser	Ser	Asp	Ile	Asp	Ser	Asp	Thr	Ile	Leu	Asp	Tyr	Val	Val	Val	Ile	
		55				60					65					

act	ggc	atc	gtt	ggc	gtc	ctc	agc	gct	ggc	ttg	acc	ttc	gct	act	gct	355
Thr	Gly	Ile	Val	Gly	Val	Leu	Ser	Ala	Gly	Leu	Thr	Phe	Ala	Thr	Ala	
		70			75					80					85	

ttc	cag	cgt	tca	ttg	cag	taaatttcag	cggttaatcac	caa	396
Phe	Gln	Arg	Ser	Leu	Gln				

90

<210> 1506

<211> 91

<212> PRT

<213> Corynebacterium glutamicum

<400> 1506

Met Lys Leu Phe Ser Arg Thr Pro Leu Val Ala Leu Gly Thr Ala Ala
 1 5 10 15

Ala Met Ala Ala Thr Ser Ile Ser Val Pro Ala Gln Ala Glu Glu Val
 20 25 30

Ala Pro Ala Gln Val Val Tyr Val Ala Asp Thr Val Glu Glu Glu Thr
 35 40 45

Gly Ser Ser Asn Gly Ser Ser Asp Ile Asp Ser Asp Thr Ile Leu Asp
 50 55 60

Tyr Val Val Val Ile Thr Gly Ile Val Gly Val Leu Ser Ala Gly Leu
 65 70 75 80

Thr Phe Ala Thr Ala Phe Gln Arg Ser Leu Gln
 85 90

<210> 1507

<211> 687

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(664)

<223> RXN03153

<400> 1507

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ttcacggccc tcgttacgac tacaaagatc ggggtatatt atg cga cga atc tgg 115
 Met Arg Arg Ile Trp
 1 5

ctg ctc gta tgc ggc atc gca ttg act gtc gcc ggc tgc acg agt gga 163
 Leu Leu Val Cys Gly Ile Ala Leu Thr Val Ala Gly Cys Thr Ser Gly
 10 15 20

tcc acc act ccc aca acc gtc acg gta acc gca acg cca acg tgc gag 211
 Ser Thr Thr Pro Thr Thr Val Thr Val Thr Ala Thr Pro Thr Ser Glu
 25 30 35

gag gct gca tcc acg gag ccg acc aac gac ata ctt gcc agc caa ttt 259
 Glu Ala Ala Ser Thr Glu Pro Thr Asn Asp Ile Leu Ala Ser Gln Phe
 40 45 50

cat ccg tgt gaa gta ctc acg cag gaa cag ttc gaa gaa gtc gga ttg 307
 His Pro Cys Glu Val Leu Thr Gln Glu Gln Phe Glu Glu Val Gly Leu
 55 60 65

gga gtc ttg att gtt gaa gac gct tac ctc ggc tcg aca ggt tta ggt 355
 Gly Val Leu Ile Val Glu Asp Ala Tyr Leu Gly Ser Thr Gly Leu Gly
 70 75 80 85

tgc agt ttc ggg aaa gca gac aga gag gat ttt tca ggt acg tgg ctc 403
 Cys Ser Phe Gly Lys Ala Asp Arg Glu Asp Phe Ser Gly Thr Trp Leu
 90 95 100

att tca act gac caa gca aac cga caa ttt gtt gaa aac caa gat cta 451
 Ile Ser Thr Asp Gln Ala Asn Arg Gln Phe Val Glu Asn Gln Asp Leu
 105 110 115

gag aca ttg gat tgg gga tcc aat gac aat cca gat ctg tat gtg cat 499
 Glu Thr Leu Asp Trp Gly Ser Asn Asp Asn Pro Asp Leu Tyr Val His
 120 125 130

caa atg tcc gag acg ggt cgt caa tgt gag gca gca gtt gac tat gac 547
 Gln Met Ser Glu Thr Gly Arg Gln Cys Glu Ala Val Asp Tyr Asp
 135 140 145

tgg ggc cgg ctt acg gtt gac tat ctc gaa tta ggt gag ggc tgg gag 595
 Trp Gly Arg Leu Thr Val Asp Tyr Leu Glu Gly Glu Gly Trp Glu
 150 155 160 165

cca gaa att ttg tgc tct gat gct gtt gaa att tta gaa aat ctc atc 643
 Pro Glu Ile Leu Cys Ser Asp Ala Val Glu Ile Leu Glu Asn Leu Ile
 170 175 180

aag gaa cta agg gga att cca tgacattgaa aattgatccc tcg 687
 Lys Glu Leu Arg Gly Ile Pro
 185

<210> 1508
 <211> 188
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 1508
 Met Arg Arg Ile Trp Leu Leu Val Cys Gly Ile Ala Leu Thr Val Ala
 1 5 10 15
 Gly Cys Thr Ser Gly Ser Thr Thr Pro Thr Thr Val Thr Val Thr Ala
 20 25 30
 Thr Pro Thr Ser Glu Glu Ala Ala Ser Thr Glu Pro Thr Asn Asp Ile
 35 40 45
 Leu Ala Ser Gln Phe His Pro Cys Glu Val Leu Thr Gln Glu Gln Phe
 50 55 60
 Glu Glu Val Gly Leu Gly Val Leu Ile Val Glu Asp Ala Tyr Leu Gly
 65 70 75 80
 Ser Thr Gly Leu Gly Cys Ser Phe Gly Lys Ala Asp Arg Glu Asp Phe
 85 90 95
 Ser Gly Thr Trp Leu Ile Ser Thr Asp Gln Ala Asn Arg Gln Phe Val
 100 105 110
 Glu Asn Gln Asp Leu Glu Thr Leu Asp Trp Gly Ser Asn Asp Asn Pro

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115              120              125
Asp Leu Tyr Val His Gln Met Ser Glu Thr Gly Arg Gln Cys Glu Ala
130              135              140
Ala Val Asp Tyr Asp Trp Gly Arg Leu Thr Val Asp Tyr Leu Glu Leu
145              150              155              160
Gly Glu Gly Trp Glu Pro Glu Ile Leu Cys Ser Asp Ala Val Glu Ile
165              170              175
Leu Glu Asn Leu Ile Lys Glu Leu Arg Gly Ile Pro
180              185

<210> 1509
<211> 1035
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1012)
<223> RXN03154

<400> 1509
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cattctgaaa attcagtcgc ttaaatgggc gcagcgggaa atg ctg aaa act aca 115
Met Leu Lys Thr Thr
1 5

tta atc acc gat acc cta ggg cac gtg acc tct act gaa ccc acc acc 163
Leu Ile Thr Asp Thr Leu Gly His Val Thr Ser Thr Glu Pro Thr Thr
10 15 20

aca gcc cat gtt cca cta cct gat gga tct tcc act cca gtc caa att 211
Thr Ala His Val Pro Leu Pro Asp Gly Ser Ser Thr Pro Val Gln Ile
25 30 35

tgg gcg tca gat aac aaa gac tcc caa ctg gtg atg ctg tgg cca ggt 259
Trp Ala Ser Asp Asn Lys Asp Ser Gln Leu Val Met Leu Trp Pro Gly
40 45 50

ttc ggc atg ggt ggc tat tac tat cgt ccg ett gcg gca gcg cta aat 307
Phe Gly Met Gly Gly Tyr Tyr Arg Pro Leu Ala Ala Leu Asn
55 60 65

aaa gct gga ttc cat gtg gcg att ggt gaa ctt cgt ggt cag ggg caa 355
Lys Ala Gly Phe His Val Ala Ile Gly Glu Leu Arg Gly Gln Gly Gln
70 75 80 85

agt tcc gcg aag gct tct cgg aaa agt cag tgg gga tac cat gat ctc 403
Ser Ser Ala Lys Ala Ser Arg Lys Ser Gln Trp Gly Tyr His Asp Leu
90 95 100

gca tcg gta gat ttt ccg ctg cag att gcc gct gcg aaa aag gcg ctt 451
Ala Ser Val Asp Phe Pro Leu Gln Ile Ala Ala Lys Lys Ala Leu
105 110 115

gac ctg gag gaa ggc cat ccc atg agg ttt ttg tcg cat tcg atg ggt 499

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Asp Leu Glu Glu Gly His Pro Met Arg Phe Leu Ser His Ser Met Gly
 120 125 130
 ggg cag att tct tgt ctt ttc gca gcg agg ccg gag gct gag aaa tat 547
 Gly Gln Ile Ser Cys Leu Phe Ala Ala Arg Pro Glu Ala Glu Lys Tyr
 135 140 145
 aat ctt cgg gcg att ttc ggg gtg ggt gca ggg tcg ccg ttt agg cct 595
 Asn Leu Arg Ala Ile Phe Gly Val Gly Ala Gly Ser Pro Phe Arg Pro
 150 155 160 165
 acg ttt agt ccg aaa atg ggg aag cgt ttg gga ttg ggt gcg gtg ctg 643
 Thr Phe Ser Pro Lys Met Gly Lys Arg Leu Gly Leu Gly Ala Val Leu
 170 175 180
 ctt ggt ggg att ggt ggc cac att gtg gga ttt tgg ccc ggc aaa gtt 691
 Leu Gly Gly Ile Gly Gly His Ile Val Gly Phe Trp Pro Gly Lys Val
 185 190 195
 tta gga aaa gac ctg gtg ggt tat ggc cga caa tcg gga act cac atg 739
 Leu Gly Lys Asp Leu Val Gly Tyr Gly Arg Gln Ser Gly Thr His Met
 200 205 210
 agg gaa tgg cgt cga ttc cat aag cac aat tct ttg gac gat ctc acc 787
 Arg Glu Trp Arg Arg Phe His Lys His Asn Ser Leu Asp Asp Leu Thr
 215 220 225
 gcg cag gac atc aac tat gtg gag gtg atg aag aag gtg agc att cct 835
 Ala Gln Asp Ile Asn Tyr Val Glu Val Met Lys Lys Val Ser Ile Pro
 230 235 240 245
 att act ttt agt cgt tgt cct gat gat gag gac tgc ccg cag gca tcg 883
 Ile Thr Phe Ser Arg Cys Pro Asp Asp Glu Asp Cys Pro Gln Ala Ser
 250 255 260
 att gat ggg ttg gcg agt ttt gtt ccc gca gcg cag atc aaa atg ata 931
 Ile Asp Gly Leu Ala Ser Phe Val Pro Ala Ala Gln Ile Lys Met Ile
 265 270 275
 gaa att cca gaa gcc ctg gga cat aac cgg tgg gct ccg gaa cct gaa 979
 Glu Ile Pro Glu Ala Leu Gly His Asn Arg Trp Ala Arg Glu Pro Glu
 280 285 290
 tca aca gtg aaa ctc ttc ctg gaa caa gct ctt tagtgaccga tggagcggag 1032
 Ser Thr Val Lys Leu Phe Leu Glu Gln Ala Leu
 295 300
 gta 1035

<210> 1510

<211> 304

<212> PRT

<213> Corynebacterium glutamicum

<400> 1510

Met Leu Lys Thr Thr Leu Ile Thr Asp Thr Leu Gly His Val Thr Ser
 1 5 10 15

Thr Glu Pro Thr Thr Thr Ala His Val Pro Leu Pro Asp Gly Ser Ser
 20 25 30

Thr Pro Val Gln Ile Trp Ala Ser Asp Asn Lys Asp Ser Gln Leu Val
 35 40 45
 Met Leu Trp Pro Gly Phe Gly Met Gly Gly Tyr Tyr Tyr Arg Pro Leu
 50 55 60
 Ala Ala Ala Leu Asn Lys Ala Gly Phe His Val Ala Ile Gly Glu Leu
 65 70 75 80
 Arg Gly Gln Gly Gln Ser Ser Ala Lys Ala Ser Arg Lys Ser Gln Trp
 85 90 95
 Gly Tyr His Asp Leu Ala Ser Val Asp Phe Pro Leu Gln Ile Ala Ala
 100 105 110
 Ala Lys Lys Ala Leu Asp Leu Glu Gly His Pro Met Arg Phe Leu
 115 120 125
 Ser His Ser Met Gly Gly Gln Ile Ser Cys Leu Phe Ala Ala Arg Pro
 130 135 140
 Glu Ala Glu Lys Tyr Asn Leu Arg Ala Ile Phe Gly Val Gly Ala Gly
 145 150 155 160
 Ser Pro Phe Arg Pro Thr Phe Ser Pro Lys Met Gly Lys Arg Leu Gly
 165 170 175
 Leu Gly Ala Val Leu Leu Gly Gly Ile Gly Gly His Ile Val Gly Phe
 180 185 190
 Trp Pro Gly Lys Val Leu Gly Lys Asp Leu Val Gly Tyr Gly Arg Gln
 195 200 205
 Ser Gly Thr His Met Arg Glu Trp Arg Arg Phe His Lys His Asn Ser
 210 215 220
 Leu Asp Asp Leu Thr Ala Gln Asp Ile Asn Tyr Val Glu Val Met Lys
 225 230 235 240
 Lys Val Ser Ile Pro Ile Thr Phe Ser Arg Cys Pro Asp Asp Glu Asp
 245 250 255
 Cys Pro Gln Ala Ser Ile Asp Gly Leu Ala Ser Phe Val Pro Ala Ala
 260 265 270
 Gln Ile Lys Met Ile Glu Ile Pro Glu Ala Leu Gly His Asn Arg Trp
 275 280 285
 Ala Arg Glu Pro Glu Ser Thr Val Lys Leu Phe Leu Glu Gln Ala Leu
 290 295 300

<210> 1511

<211> 303

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> {101}..(280)

<223> RXN03156

<400> 1511

gtatcgacct cgatgatcgc gttgctgcag agatgacct tttaggctgc cctgtgccta 60

aagaaggata accaccacac cagaaaagaa gtacctcatt atg gct cga acc aca 115
 Met Ala Arg Thr Thr
 1 5

cct cca cca gct gat gta ctc gac atc atc att tcc acc gtg aag cag 163
 Pro Pro Pro Ala Asp Val Leu Asp Ile Ile Ile Ser Thr Val Lys Gln
 10 15 20

acc atc ggc att gat ctt gct gaa ctg att cag ggc cgt gca ctc ggc 211
 Thr Ile Gly Ile Asp Leu Ala Glu Leu Ile Gln Gly Arg Ala Leu Gly
 25 30 35

cag gct caa ggt gag gca caa ggc aaa gct agt gca gca gcc ctt gag 259
 Gln Ala Gln Gly Glu Ala Gln Gly Lys Ala Ser Ala Ala Leu Glu
 40 45 50

cag gca cct cat aat gag cag taaataaacac acaccacatg tgc 303
 Gln Ala Pro His Asn Glu Gln
 55 60

<210> 1512

<211> 60

<212> PRT

<213> Corynebacterium glutamicum

<400> 1512

Met Ala Arg Thr Thr Pro Pro Pro Ala Asp Val Leu Asp Ile Ile Ile
 1 5 10 15

Ser Thr Val Lys Gln Thr Ile Gly Ile Asp Leu Ala Glu Leu Gln
 20 25 30

Gly Arg Ala Leu Gly Gln Ala Gln Gly Glu Ala Gln Gly Lys Ala Ser
 35 40 45

Ala Ala Ala Leu Glu Gln Ala Pro His Asn Glu Gln
 50 55 60

<210> 1513

<211> 182

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> {1}..(159)

<223> FRXA00176

<400> 1513

cag ctg atg tac tcg aca tca tca ttt acc acc gtg aag cag acc atc 48
 Gln Leu Met Tyr Ser Thr Ser Ser Phe Thr Thr Val Lys Gln Thr Ile

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      1              5              10              15
ggc att gat ctt gct gaa ctg att cag ggc cgt gca ctc ggc cag gct 96
Gly Ile Asp Leu Ala Glu Leu Ile Gln Gly Arg Ala Leu Gly Gln Ala
      20              25              30

caa ggt gag gca caa ggc aaa gct agt gca gca gcc ctt gag cag gca 144
Gln Gly Glu Ala Gln Gly Lys Ala Ser Ala Ala Ala Leu Glu Gln Ala
      35              40              45

cct cat aat gag cag taaataacac acaccacatg tgc 182
Pro His Asn Glu Gln
      50

<210> 1514
<211> 53
<212> PRT
<213> Corynebacterium glutamicum

<400> 1514
Gln Leu Met Tyr Ser Thr Ser Ser Phe Thr Thr Val Lys Gln Thr Ile
      1              5              10              15
Gly Ile Asp Leu Ala Glu Leu Ile Gln Gly Arg Ala Leu Gly Gln Ala
      20              25              30
Gln Gly Glu Ala Gln Gly Lys Ala Ser Ala Ala Ala Leu Glu Gln Ala
      35              40              45
Pro His Asn Glu Gln
      50

<210> 1515
<211> 519
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(496)
<223> RXN03162

<400> 1515
ggtc aatcag ttcctgccac tgctctggct tgcgtaggt gtacttcgcg ccggagaaca 60
gggttgcgga gaagttgtcg ccgccttctg ctggtctctt gtg cac gac gaa cac 115
Val His Asp Glu His
      1              5
tgg gtg tgg tcc gac gag aag gat gcg gat ttc gcc ttc gac gat gcg 163
Trp Val Trp Ser Asp Glu Lys Asp Ala Asp Phe Ala Phe Asp Asp Ala
      10              15              20
tgg cat gaa acg cat atc aac gag cat gcc gtt gtc gcc gat gat gta 211
Trp His Glu Thr His Ile Asn Glu His Ala Val Val Ala Asp Asp Val
      25              30              35
ctg gtc aca gaa atc cat gaa ctc gcc gag ctt gcg gac ttc agt gtg 259
Leu Val Thr Glu Ile His Glu Leu Ala Glu Leu Ala Asp Phe Ser Val

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40 45 50

gtt gtc gac tgc ttc ggt gca ctt gat ttc agt gtc caa tgg cag tgc 307
 Val Val Asp Cys Phe Gly Ala Leu Asp Phe Ser Val Gln Trp Gln Cys
 55 60 65

ggt gcc tgg ctc gat gga tgc agc cag ttc ctt gtc tac caa ctg gac 355
 Gly Ala Trp Leu Asp Gly Cys Ser Gln Phe Leu Val Tyr Gln Leu Asp
 70 75 80 85

gcg cca aat gcc gga gcc ggt gga gcc acg gtt ttg ctt gag cac gcg 403
 Ala Pro Asn Ala Gly Ala Gly Gly Ala Thr Val Leu Leu Glu His Ala
 90 95 100

ctc acc gaa gga cag gga ggt tgg gaa aac ctt gtg gaa ggt ctc cac 451
 Leu Thr Glu Gly Gln Gly Trp Glu Asn Leu Val Glu Gly Leu His
 105 110 115

gtc gta gta cgc ctc ggt gtc gga tgg cac cag gtc ggt ttg gga 496
 Val Val Val Arg Leu Gly Val Gly Trp His Gln Val Gly Leu Gly
 120 125 130

tagcttgacc agcgcatctt tcg 519

<210> 1516
 <211> 132
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 1516
 Val His Asp Glu His Trp Val Trp Ser Asp Glu Lys Asp Ala Asp Phe
 1 5 10 15
 Ala Phe Asp Asp Ala Trp His Glu Thr His Ile Asn Glu His Ala Val
 20 25 30
 Val Ala Asp Asp Val Leu Val Thr Glu Ile His Glu Leu Ala Glu Leu
 35 40 45
 Ala Asp Phe Ser Val Val Val Asp Cys Phe Gly Ala Leu Asp Phe Ser
 50 55 60
 Val Gln Trp Gln Cys Gly Ala Trp Leu Asp Gly Cys Ser Gln Phe Leu
 65 70 75 80
 Val Tyr Gln Leu Asp Ala Pro Asn Ala Gly Ala Gly Gly Ala Thr Val
 85 90 95
 Leu Leu Glu His Ala Leu Thr Glu Gly Gln Gly Gly Trp Glu Asn Leu
 100 105 110
 Val Glu Gly Leu His Val Val Val Arg Leu Gly Val Gly Trp His Gln
 115 120 125
 Val Gly Leu Gly
 130

<210> 1517

<211> 730

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(730)

<223> RKN03167

<400> 1517

g c g c g c a c t g c g g t g c t t t t g c g c t g t t g c g t a a a a a a t a g t t t t t a t t a a g g g c a t t c 60

c c t g a t t c c c a g g t g g t g c c a c a t t g t t t a t t g g t g g a g a t a t g a a c a c g a a c t t g 115
 Met Asn Thr Asn Leu
 1 5

c c g a a c c t a t a c a c c g c a t t t g a c c t t g a t c g a a g t g a a t c c t c c g a a 163
 Pro Asn Leu Tyr Thr Ala Phe Asp Leu Asp Arg Ser Glu Ser Ser Glu
 10 15 20

g c t t t a g g t g t t t c c c t t t c t g c c c g c g a t c t t c g c t t a g a a c a a a t g 211
 Ala Leu Gly Val Ser Leu Ser Ala Arg Asp Leu Arg Leu Glu Gln Met
 25 30 35

g g a a t t g c c c a g g a c g a t c c t c g a c g t g c c c a a a c c g t c c a a g c t t t c 259
 Gly Ile Ala Gln Asp Asp Pro Arg Arg Ala Gln Thr Val Gln Ala Phe
 40 45 50

g c a g t g c t t g c a g a c c c a g c a a a c g c g c c a c c t a c g a t g c t c a a t t a 307
 Ala Val Leu Ala Asp Pro Ala Lys Arg Ala Thr Tyr Asp Ala Gln Leu
 55 60 65

g a a g c t g g a g t t c c a c t c a c c t g g c g c c a g a t t c a g c a t t t a g g a a a c 355
 Glu Ala Gly Val Pro Leu Thr Trp Ala Gln Ile Gln His Leu Gly Asn
 70 75 80 85

t t c g g c a c c t t g c c t t c c a c c c c t a c t g c g c a g c c g t t t g c g g c a c c t 403
 Phe Gly Thr Leu Pro Ser Thr Pro Thr Ala Gln Pro Phe Ala Ala Pro
 90 95 100

c a g c c g g a g c c g t c g c c g g a a c c g c a a c a g c a g t g g a a t a g c g g a c a a 451
 Gln Pro Glu Pro Ser Pro Glu Pro Gln Gln Gln Trp Asn Ser Gly Gln
 105 110 115

a a c t a t g c g t a t g g c a a t c c g a c c a t g g a t t a c c a a a c t c a g c a g a g c 499
 Asn Tyr Ala Tyr Gly Asn Pro Thr Met Asp Tyr Gln Thr Gln Gln Ser
 120 125 130

t a c a a c c c g a t g c a g g a c c a a a c c c a a g c g t c g a t g t a t g c g c a a c c t 547
 Tyr Asn Pro Met Gln Asp Gln Thr Gln Ala Ser Met Tyr Ala Gln Pro
 135 140 145

t t c g c g a a c a c c c c t g c a c c g a t g t a c a a c a g c a a t c a g g t t t t a a c 595
 Phe Ala Asn Thr Pro Ala Pro Met Tyr Asn Ser Asn Gln Val Phe Asn
 150 155 160 165

a g g c c t a c t g c g g g t a c g c g t t t g g a t g c g c a t c c t c g a c a g t a t t 643
 Arg Pro Thr Ala Gly Thr Arg Leu Trp Met Ala Ile Leu Asp Ser Ile
 170 175 180

t t t g c c g g c a t c g c t g g t g g a a t t g t c t c c g g t a t t t t c g g c t t t g g a 691
 Phe Ala Gly Ile Ala Gly Gly Ile Val Ser Gly Ile Phe Gly Phe Gly

185

190

195

tct gaa ttc ctc acc agt gtc atc atg att ttg gtg ctg
 Ser Glu Phe Leu Thr Ser Val Ile Met Ile Leu Val Leu
 200 205 210

730

<210> 1518

<211> 210

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1518

Met Asn Thr Asn Leu Pro Asn Leu Tyr Thr Ala Phe Asp Leu Asp Arg
 1 5 10 15

Ser Glu Ser Ser Glu Ala Leu Gly Val Ser Leu Ser Ala Arg Asp Leu
 20 25 30

Arg Leu Glu Gln Met Gly Ile Ala Gln Asp Asp Pro Arg Arg Ala Gln
 35 40 45

Thr Val Gln Ala Phe Ala Val Leu Ala Asp Pro Ala Lys Arg Ala Thr
 50 55 60

Tyr Asp Ala Gln Leu Glu Ala Gly Val Pro Leu Thr Trp Ala Gln Ile
 65 70 75 80

Gln His Leu Gly Asn Phe Gly Thr Leu Pro Ser Thr Pro Thr Ala Gln
 85 90 95

Pro Phe Ala Ala Pro Gln Pro Glu Pro Ser Pro Glu Pro Gln Gln Gln
 100 105 110

Trp Asn Ser Gly Gln Asn Tyr Ala Tyr Gly Asn Pro Thr Met Asp Tyr
 115 120 125

Gln Thr Gln Gln Ser Tyr Asn Pro Met Gln Asp Gln Thr Gln Ala Ser
 130 135 140

Met Tyr Ala Gln Pro Phe Ala Asn Thr Pro Ala Pro Met Tyr Asn Ser
 145 150 155 160

Asn Gln Val Phe Asn Arg Pro Thr Ala Gly Thr Arg Leu Trp Met Ala
 165 170 175

Ile Leu Asp Ser Ile Phe Ala Gly Ile Ala Gly Gly Ile Val Ser Gly
 180 185 190

Ile Phe Gly Phe Gly Ser Glu Phe Leu Thr Ser Val Ile Met Ile Leu
 195 200 205

Val Leu
 210

<210> 1519

<211> 736

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(736)

<223> FRXA02862

<400> 1519

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cctgattccc aggtggtgcc acattgttta tgggtggagat atg aac acg aac ttg 115
 Met Asn Thr Asn Leu
 1 5

cgg aac cta tac acc gca ttt gac ctt gat cga agt gaa tcc tcc gaa 163
 Pro Asn Leu Tyr Thr Ala Phe Asp Leu Asp Arg Ser Glu Ser Ser Glu
 10 15 20

gct tta ggt gtt tcc ctt tct gcc cgc gat ctt cgc tta gaa caa atg 211
 Ala Leu Gly Val Ser Leu Ser Ala Arg Asp Leu Arg Leu Glu Gln Met
 25 30 35

gga att gcc cag gac gat cct cga cgt gcc caa acc gtc caa gct ttc 259
 Gly Ile Ala Gln Asp Asp Pro Arg Arg Ala Gln Thr Val Gln Ala Phe
 40 45 50

gca gtg ctt gca gac cca gca aaa cgc gcc acc tac gat gct caa tta 307
 Ala Val Leu Ala Asp Pro Ala Lys Arg Ala Thr Tyr Asp Ala Gln Leu
 55 60 65

gaa gct gga gtt cca ctc acc tgg gcg cag att cag cat tta gga aac 355
 Glu Ala Gly Val Pro Leu Thr Trp Ala Gln Ile Gln His Leu Gly Asn
 70 75 80 85

ttc ggc acc ttg cct tcc acc cct act gcg cag ccg ttt gcg gca cct 403
 Phe Gly Thr Leu Pro Ser Thr Pro Thr Ala Gln Pro Phe Ala Ala Pro
 90 95 100

cag ccg gag ccg tcg ccg gaa ccg caa cag cag tgg aat agc gga caa 451
 Gln Pro Glu Pro Ser Pro Glu Pro Gln Gln Gln Trp Asn Ser Gly Gln
 105 110 115

aac tat gcg tat ggc aat ccg acc atg gat tac caa act cag cag agc 499
 Asn Tyr Ala Tyr Gly Asn Pro Thr Met Asp Tyr Gln Thr Gln Gln Ser
 120 125 130

tac aac ccg atg cag gac caa acc caa gcg tcg atg tat gcg caa cct 547
 Tyr Asn Pro Met Gln Asp Gln Thr Gln Ala Ser Met Tyr Ala Gln Pro
 135 140 145

ttc gcg aac acc cct gca ccg atg tac aac agc aat cag gtt ttt aac 595
 Phe Ala Asn Thr Pro Ala Pro Met Tyr Asn Ser Asn Gln Val Phe Asn
 150 155 160 165

agg cct act gcg ggt acg cgt ttg tgg atg gcg atc ctc gac agt att 643
 Arg Pro Thr Ala Gly Thr Arg Leu Trp Met Ala Ile Leu Asp Ser Ile
 170 175 180

ttt gcc gcc atc gct ggt gga att gtc tcc ggt att ttc gcc ttt gga 691
 Phe Ala Gly Ile Ala Gly Gly Ile Val Ser Gly Ile Phe Gly Phe Gly
 185 190 195

tct gaa ttc ctc acc agt gtc atc atg att ttg gtg ctg atc gtc 736

Ser Glu Phe Leu Thr Ser Val Ile Met Ile Leu Val Leu Ile Val
 200 205 210

<210> 1520

<211> 212

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1520

Met Asn Thr Asn Leu Pro Asn Leu Tyr Thr Ala Phe Asp Leu Asp Arg
 1 5 10 15

Ser Glu Ser Ser Glu Ala Leu Gly Val Ser Leu Ser Ala Arg Asp Leu
 20 25 30

Arg Leu Glu Gln Met Gly Ile Ala Gln Asp Asp Pro Arg Arg Ala Gln
 35 40 45

Thr Val Gln Ala Phe Ala Val Leu Ala Asp Pro Ala Lys Arg Ala Thr
 50 55 60

Tyr Asp Ala Gln Leu Glu Ala Gly Val Pro Leu Thr Trp Ala Gln Ile
 65 70 75 80

Gln His Leu Gly Asn Phe Gly Thr Leu Pro Ser Thr Pro Thr Ala Gln
 85 90 95

Pro Phe Ala Ala Pro Gln Pro Glu Pro Ser Pro Glu Pro Gln Gln Gln
 100 105 110

Trp Asn Ser Gly Gln Asn Tyr Ala Tyr Gly Asn Pro Thr Met Asp Tyr
 115 120 125

Gln Thr Gln Gln Ser Tyr Asn Pro Met Gln Asp Gln Thr Gln Ala Ser
 130 135 140

Met Tyr Ala Gln Pro Phe Ala Asn Thr Pro Ala Pro Met Tyr Asn Ser
 145 150 155 160

Asn Gln Val Phe Asn Arg Pro Thr Ala Gly Thr Arg Leu Trp Met Ala
 165 170 175

Ile Leu Asp Ser Ile Phe Ala Gly Ile Ala Gly Gly Ile Val Ser Gly
 180 185 190

Ile Phe Gly Phe Gly Ser Glu Phe Leu Thr Ser Val Ile Met Ile Leu
 195 200 205

Val Leu Ile Val
 210

<210> 1521

<211> 372

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(349)

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(349)

<223> FRXA02856

<400> 1523

gttaaatcat tgccgccag aagaagaccg cgcggcgcaa tttgggcttg gaggaacca 60

aacggccact tttccagtc aacaaagtat gaggattaat ttg ccc cac gcc aaa 115
 Leu Pro His Ala Lys
 1 5

gag ctc gcc cac gag ctg tgt ttg ttg ccc acc cct gct gtg ccc gcg 163
 Glu Leu Ala His Glu Leu Cys Leu Leu Pro Thr Pro Ala Val Pro Ala
 10 15 20

ctt ccc act gat tct ggc gcg cag ttt gat atc cac cag gca cta tcc 211
 Leu Pro Thr Asp Ser Gly Ala Gln Phe Asp Ile His Gln Ala Leu Ser
 25 30 35

gcc tcc ctt gcc acc tat gcc cgc aac ctc acc ttg ctg tcc cac acc 259
 Ala Ser Leu Ala Thr Tyr Ala Arg Asn Leu Thr Leu Leu Ser His Thr
 40 45 50

gcc gag aat tta gga aac cgc gcg ctg acg ggc ctc gct gaa atc gaa 307
 Ala Glu Asn Leu Gly Asn Arg Ala Leu Thr Gly Leu Ala Glu Ile Glu
 55 60 65

gac acc gac gac caa ctc gca cac gca ttg gag cgc ctg aca 349
 Asp Thr Asp Asp Gln Leu Ala His Ala Leu Glu Arg Leu Thr
 70 75 80

tgatcggtct gatcagcgc ctt 372

<210> 1524

<211> 83

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1524

Leu Pro His Ala Lys Glu Leu Ala His Glu Leu Cys Leu Leu Pro Thr
 1 5 10 15

Pro Ala Val Pro Ala Leu Pro Thr Asp Ser Gly Ala Gln Phe Asp Ile
 20 25 30

His Gln Ala Leu Ser Ala Ser Leu Ala Thr Tyr Ala Arg Asn Leu Thr
 35 40 45

Leu Leu Ser His Thr Ala Glu Asn Leu Gly Asn Arg Ala Leu Thr Gly
 50 55 60

Leu Ala Glu Ile Glu Asp Thr Asp Asp Gln Leu Ala His Ala Leu Glu
 65 70 75 80

Arg Leu Thr

<210> 1525
 <211> 1049
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
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 <222> (1)..(1026)
 <223> RXN03172

<400> 1525
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 Pro Glu Trp Lys Lys Phe Asn Ser Gly Asp Ala Ala Arg Val Val Pro
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 gac gcc aac gca gag ctc gac atc atc ggc gca cca gca ctt ctt gcc 96
 Asp Ala Asn Ala Glu Leu Asp Ile Ile Gly Ala Pro Ala Leu Leu Ala
 20 25 30
 gat cgc ccc tcc tac gca aac gtc aaa acc ctc tcc cgc atc ttc gct 144
 Asp Arg Pro Ser Tyr Ala Asn Val Lys Thr Leu Ser Arg Ile Phe Ala
 35 40 45
 gtc atg cgc agc ctc ggc cac gtc acc gct gcc tcc cca gtc acc gtg 192
 Val Met Arg Ser Leu Gly His Val Thr Ala Ala Ser Pro Val Thr Val
 50 55 60
 ttc ttc tcc tcc cac tcc gtg ctc agc aac gtt gac cgc gga tcc gag 240
 Phe Phe Ser Ser His Ser Val Leu Ser Asn Val Asp Arg Gly Ser Glu
 65 70 75 80
 cac tac tcc gga ccc aac ggc ctg ggc gaa tgg acc tcc gtt ggt cgc 288
 His Tyr Ser Gly Pro Asn Gly Leu Gly Glu Trp Thr Ser Val Gly Arg
 85 90 95
 gca gta gcc acc aac tgg aac ggc gtt gtc gac gcc ctc gac gaa gcc 336
 Ala Val Ala Thr Asn Trp Asn Gly Val Val Asp Ala Leu Asp Glu Ala
 100 105 110
 atc acc gtc aag gaa gta aac agc ctc ttt acc gaa gac gcc gca acc 384
 Ile Thr Val Lys Glu Val Asn Ser Leu Phe Thr Glu Asp Ala Ala Thr
 115 120 125
 cgc att caa gaa gca caa gca gct gtt cag gca gct cgc gag gct gaa 432
 Arg Ile Gln Glu Ala Gln Ala Ala Val Gln Ala Ala Arg Glu Ala Glu
 130 135 140
 gag caa atc gcc aag gaa gaa gcc gaa aag gtc gac cct tac gac aac 480
 Glu Gln Ile Ala Lys Glu Glu Ala Glu Lys Val Asp Pro Tyr Asp Asn
 145 150 155 160
 tcc cca tgg gct gca gca ggc atc gac ccc atc aag gtc tcc atc gac 528
 Ser Pro Trp Ala Ala Ala Gly Ile Asp Pro Ile Lys Val Ser Ile Asp
 165 170 175
 gga cgc acc atc tac acc ctg cgc acc tac ctc ggc gga cag cca gta 576
 Gly Arg Thr Ile Tyr Thr Leu Arg Thr Tyr Leu Gly Gly Gln Pro Val
 180 185 190
 ttc ctc gga aaa ttc ggc gaa atc tcc acc ttc aac agc caa aaa tcc 624
 Phe Leu Gly Lys Phe Gly Glu Ile Ser Thr Phe Asn Ser Gln Lys Ser

195	200	205	
ctc ctg cgc tgg ctc gtc gaa cac gat gac cac gac ctc gcc cgc gcc			672
Leu Leu Arg Trp Leu Val Glu His Asp Asp His Asp Leu Ala Arg Ala			
210	215	220	
tcc acc tgg agc gac ctc atg ctc ggc atc aac gcc ggt gaa acc gaa			720
Ser Thr Trp Ser Asp Leu Met Leu Gly Ile Asn Ala Gly Glu Thr Glu			
225	230	235	240
ctc ctc gtc cac agc gac aac gtc tac tcc ttc aac ggc ctg gtc aaa			768
Leu Leu Val His Ser Asp Asn Val Tyr Ser Phe Asn Gly Leu Val Lys			
245	250	255	
gac atc aac acc tcc gtc gac gcc gta gac acc caa caa atg gcc cgc			816
Asp Ile Asn Thr Ser Val Asp Ala Val Asp Thr Gln Gln Met Ala Arg			
260	265	270	
gcc tac gaa ctc atg gca gac acc gcc gac tgg gcc gac gac gac tcc			864
Ala Tyr Glu Leu Met Ala Asp Thr Ala Asp Trp Ala Asp Asp Asp Ser			
275	280	285	
atg aat tcc tac ttc ctg gcc aac cca cgc atg cag gac tac atc tcc			912
Met Asn Ser Tyr Phe Leu Ala Asn Pro Arg Met Gln Asp Tyr Ile Ser			
290	295	300	
tac atg ctc ggc ggc agc gac acc tcc gga tat gtc cct cac gca cca			960
Tyr Met Leu Gly Gly Ser Asp Thr Ser Gly Tyr Val Pro His Ala Pro			
305	310	315	320
ttc aac gac cac tct gag agc tgg cgc gag ctg gag gag atg ctg atc			1008
Phe Asn Asp His Ser Glu Ser Trp Arg Glu Leu Glu Glu Met Leu Ile			
325	330	335	
aag cga ttc agc aag ttc taggtgcct atttgggggtt cgt			1049
Lys Arg Phe Ser Lys Phe			
340			
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<213> Corynebacterium glutamicum			
<400> 1526			
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Asp Arg Pro Ser Tyr Ala Asn Val Lys Thr Leu Ser Arg Ile Phe Ala			
35	40	45	
Val Met Arg Ser Leu Gly His Val Thr Ala Ala Ser Pro Val Thr Val			
50	55	60	
Phe Phe Ser Ser His Ser Val Leu Ser Asn Val Asp Arg Gly Ser Glu			
65	70	75	80
His Tyr Ser Gly Pro Asn Gly Leu Gly Glu Trp Thr Ser Val Gly Arg			

85										90										95									
Ala	Val	Ala	Thr	Asn	Trp	Asn	Gly	Val	Val	Asp	Ala	Leu	Asp	Glu	Ala														
			100					105					110																
Ile	Thr	Val	Lys	Glu	Val	Asn	Ser	Leu	Phe	Thr	Glu	Asp	Ala	Ala	Thr														
		115					120					125																	
Arg	Ile	Gln	Glu	Ala	Gln	Ala	Ala	Val	Gln	Ala	Ala	Arg	Glu	Ala	Glu														
		130				135						140																	
Glu	Gln	Ile	Ala	Lys	Glu	Glu	Ala	Glu	Lys	Val	Asp	Pro	Tyr	Asp	Asn														
145				150						155					160														
Ser	Pro	Trp	Ala	Ala	Ala	Gly	Ile	Asp	Pro	Ile	Lys	Val	Ser	Ile	Asp														
			165					170						175															
Gly	Arg	Thr	Ile	Tyr	Thr	Leu	Arg	Thr	Tyr	Leu	Gly	Gly	Gln	Pro	Val														
		180						185					190																
Phe	Leu	Gly	Lys	Phe	Gly	Glu	Ile	Ser	Thr	Phe	Asn	Ser	Gln	Lys	Ser														
		195					200					205																	
Leu	Leu	Arg	Trp	Leu	Val	Glu	His	Asp	Asp	His	Asp	Leu	Ala	Arg	Ala														
		210				215					220																		
Ser	Thr	Trp	Ser	Asp	Leu	Met	Leu	Gly	Ile	Asn	Ala	Gly	Glu	Thr	Glu														
225					230					235					240														
Leu	Leu	Val	His	Ser	Asp	Asn	Val	Tyr	Ser	Phe	Asn	Gly	Leu	Val	Lys														
			245					250						255															
Asp	Ile	Asn	Thr	Ser	Val	Asp	Ala	Val	Asp	Thr	Gln	Gln	Met	Ala	Arg														
		260					265						270																
Ala	Tyr	Glu	Leu	Met	Ala	Asp	Thr	Ala	Asp	Trp	Ala	Asp	Asp	Asp	Ser														
		275					280					285																	
Met	Asn	Ser	Tyr	Phe	Leu	Ala	Asn	Pro	Arg	Met	Gln	Asp	Tyr	Ile	Ser														
		290				295					300																		
Tyr	Met	Leu	Gly	Gly	Ser	Asp	Thr	Ser	Gly	Tyr	Val	Pro	His	Ala	Pro														
305					310					315					320														
Phe	Asn	Asp	His	Ser	Glu	Ser	Trp	Arg	Glu	Leu	Glu	Glu	Met	Leu	Ile														
			325						330					335															
Lys	Arg	Phe	Ser	Lys	Phe																								
			340																										

<210> 1527

<211> 1049

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1026)

<223> FRXA02858

<400> 1527

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Pro Glu Trp Lys Lys Phe Asn Ser Gly Asp Ala Ala Arg Val Val Pro	
1 5 10 15	
gac gcc aac gca gag ctc gac atc atc ggc gca cca gca ctt ctt gcc	96
Asp Ala Asn Ala Glu Leu Asp Ile Ile Gly Ala Pro Ala Leu Leu Ala	
20 25 30	
gat cgc ccc tcc tac gca aac gtc aaa acc ctc tcc cgc atc ttc gct	144
Asp Arg Pro Ser Tyr Ala Asn Val Lys Thr Leu Ser Arg Ile Phe Ala	
35 40 45	
gtc atg cgc agc ctc ggc cac gtc acc gct gcc tcc cca gtc acc gtg	192
Val Met Arg Ser Leu Gly His Val Thr Ala Ala Ser Pro Val Thr Val	
50 55 60	
ttc ttc tcc tcc cac tcc gtg ctc agc aac gtt gac cgc gga tcc gag	240
Phe Phe Ser Ser His Ser Val Leu Ser Asn Val Asp Arg Gly Ser Glu	
65 70 75 80	
cac tac tcc gga ccc aac ggc ctg ggc gaa tgg acc tcc gtt ggt cgc	288
His Tyr Ser Gly Pro Asn Gly Leu Gly Glu Trp Thr Ser Val Gly Arg	
85 90 95	
gca gta gcc acc aac tgg aac ggc gtt gtc gac gcc ctc gac gaa gcc	336
Ala Val Ala Thr Asn Trp Asn Gly Val Val Asp Ala Leu Asp Glu Ala	
100 105 110	
atc acc gtc aag gaa gta aac agc ctc ttt acc gaa gac gcc gca acc	384
Ile Thr Val Lys Glu Val Asn Ser Leu Phe Thr Glu Asp Ala Ala Thr	
115 120 125	
cgc att caa gaa gca caa gca gct gtt cag gca gct cgc gag gct gaa	432
Arg Ile Gln Glu Ala Gln Ala Ala Val Gln Ala Arg Glu Ala Glu	
130 135 140	
gag caa atc gcc aag gaa gaa gcc gaa aag gtc gac cct tac gac aac	480
Glu Gln Ile Ala Lys Glu Glu Ala Glu Lys Val Asp Pro Tyr Asp Asn	
145 150 155 160	
tcc cca tgg gct gca gca ggc atc gac ccc atc aag gtc tcc atc gac	528
Ser Pro Trp Ala Ala Ala Gly Ile Asp Pro Ile Lys Val Ser Ile Asp	
165 170 175	
gga cgc acc atc tac acc ctg cgc acc tac ctc ggc gga cag cca gta	576
Gly Arg Thr Ile Tyr Thr Leu Arg Thr Tyr Leu Gly Gly Pro Val	
180 185 190	
ttc ctc gga aaa ttc ggc gaa atc ttc acc ttc aac agc caa aaa tcc	624
Phe Leu Gly Lys Phe Gly Glu Ile Phe Thr Phe Asn Ser Gln Lys Ser	
195 200 205	
ctc ctg cgc tgg ctc gtc gaa cac gat gac cac gac ctc gcc cgc gcc	672
Leu Leu Arg Trp Leu Val Glu His Asp Asp His Asp Leu Ala Arg Ala	
210 215 220	
tcc acc tgg agc gac ctc atg ctc ggc atc aac gcc ggt gaa acc gaa	720
Ser Thr Trp Ser Asp Leu Met Leu Gly Ile Asn Ala Gly Glu Thr Glu	
225 230 235 240	

ctc ctc gtc cac agc gac aac gtc tac tcc ttc aac ggc ctg gtc aaa 768
 Leu Leu Val His Ser Asp Asn Val Tyr Ser Phe Asn Gly Leu Val Lys
 245 250 255

gac atc aac acc tcc gtc gac gcc gta gac acc caa caa atg gcc cgc 816
 Asp Ile Asn Thr Ser Val Asp Ala Val Asp Thr Gln Gln Met Ala Arg
 260 265 270

gcc tac gaa ctc atg gca gac acc gcc gac tgg gcc gac gac gac tcc 864
 Ala Tyr Glu Leu Met Ala Asp Thr Ala Asp Trp Ala Asp Asp Ser
 275 280 285

atg aat tcc tac ttc ctg gcc aac cca cgc atg cag gac tac atc tcc 912
 Met Asn Ser Tyr Phe Leu Ala Asn Pro Arg Met Gln Asp Tyr Ile Ser
 290 295 300

tac atg ctc ggc ggc agc gac acc tcc gga tat gtc cct cac gca cca 960
 Tyr Met Leu Gly Gly Ser Asp Thr Ser Gly Tyr Val Pro His Ala Pro
 305 310 315 320

ttc aac gac cac tct gag agc tgg cgc gag ctg gag gag atg ctg atc 1008
 Phe Asn Asp His Ser Glu Ser Trp Arg Glu Leu Glu Glu Met Leu Ile
 325 330 335

aag cga ttc agc aag ttc taggtgcgct atttgggggtt cgt 1049
 Lys Arg Phe Ser Lys Phe
 340

<210> 1528
 <211> 342
 <212> PRT
 <213> *Corynebacterium glutamicum*

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 20 25 30

Asp Arg Pro Ser Tyr Ala Asn Val Lys Thr Leu Ser Arg Ile Phe Ala
 35 40 45

Val Met Arg Ser Leu Gly His Val Thr Ala Ala Ser Pro Val Thr Val
 50 55 60

Phe Phe Ser Ser His Ser Val Leu Ser Asn Val Asp Arg Gly Ser Glu
 65 70 75 80

His Tyr Ser Gly Pro Asn Gly Leu Gly Glu Trp Thr Ser Val Gly Arg
 85 90 95

Ala Val Ala Thr Asn Trp Asn Gly Val Val Asp Ala Leu Asp Glu Ala
 100 105 110

Ile Thr Val Lys Glu Val Asn Ser Leu Phe Thr Glu Asp Ala Ala Thr
 115 120 125

Arg Ile Gln Glu Ala Gln Ala Ala Val Gln Ala Ala Arg Glu Ala Glu
 130 135 140

Glu Gln Ile Ala Lys Glu Glu Ala Glu Lys Val Asp Pro Tyr Asp Asn
 145 150 155 160
 Ser Pro Trp Ala Ala Ala Gly Ile Asp Pro Ile Lys Val Ser Ile Asp
 165 170 175
 Gly Arg Thr Ile Tyr Thr Leu Arg Thr Tyr Leu Gly Gly Gln Pro Val
 180 185 190
 Phe Leu Gly Lys Phe Gly Glu Ile Phe Thr Phe Asn Ser Gln Lys Ser
 195 200 205
 Leu Leu Arg Trp Leu Val Glu His Asp Asp His Asp Leu Ala Arg Ala
 210 215 220
 Ser Thr Trp Ser Asp Leu Met Leu Gly Ile Asn Ala Gly Glu Thr Glu
 225 230 235 240
 Leu Leu Val His Ser Asp Asn Val Tyr Ser Phe Asn Gly Leu Val Lys
 245 250 255
 Asp Ile Asn Thr Ser Val Asp Ala Val Asp Thr Gln Gln Met Ala Arg
 260 265 270
 Ala Tyr Glu Leu Met Ala Asp Thr Ala Asp Trp Ala Asp Asp Ser
 275 280 285
 Met Asn Ser Tyr Phe Leu Ala Asn Pro Arg Met Gln Asp Tyr Ile Ser
 290 295 300
 Tyr Met Leu Gly Gly Ser Asp Thr Ser Gly Tyr Val Pro His Ala Pro
 305 310 315 320
 Phe Asn Asp His Ser Glu Ser Trp Arg Glu Leu Glu Glu Met Leu Ile
 325 330 335
 Lys Arg Phe Ser Lys Phe
 340

<210> 1529
 <211> 1121
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(1098)
 <223> RXN03173

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 gac gac ttc gac gca gac tcc ttt acc acc gaa gtc atc cgg atc acc 96
 Asp Asp Phe Asp Ala Asp Ser Phe Thr Thr Glu Val Ile Arg Ile Thr
 20 25 30
 ggc tac tcc cgc cac gaa gtc aac aac ggc ctt aac gcc atg gcc gcg 144

Gly	Tyr	Ser	Arg	His	Glu	Val	Asn	Asn	Gly	Leu	Asn	Ala	Met	Ala	Ala	
		35					40					45				
atg	acc	aac	ctc	cca	cac	ctg	cgc	gcc	atc	caa	gaa	cgc	tac	tac	ttc	192
Met	Thr	Asn	Leu	Pro	His	Leu	Arg	Ala	Ile	Gln	Glu	Arg	Tyr	Tyr	Phe	
		50				55					60					
ctg	agc	atc	cgc	tac	ctc	gcc	tcc	atc	atg	atc	gcc	gtg	gcc	aaa	gca	240
Leu	Ser	Ile	Arg	Tyr	Leu	Ala	Ser	Ile	Met	Ile	Ala	Val	Ala	Lys	Ala	
		65				70					75				80	
gac	ccc	acc	ctg	tgg	gaa	gaa	ctc	gac	ctg	cgc	atc	acc	gac	gcc	tta	288
Asp	Pro	Thr	Leu	Trp	Glu	Glu	Leu	Asp	Leu	Arg	Ile	Thr	Asp	Ala	Leu	
				85					90					95		
aca	cca	gtc	acc	gca	ggg	gaa	gtc	atg	atc	caa	tcc	tcc	acc	ctg	tcc	336
Thr	Pro	Val	Thr	Ala	Gly	Glu	Val	Met	Ile	Gln	Ser	Ser	Thr	Leu	Ser	
			100					105						110		
aaa	cgc	atc	gcc	gcc	tgg	atc	aaa	gaa	ctc	gac	ccc	gaa	ccc	aca	cca	384
Lys	Arg	Ile	Ala	Ala	Trp	Ile	Lys	Glu	Leu	Asp	Pro	Glu	Pro	Thr	Pro	
			115				120					125				
gag	ccc	aca	ccg	aaa	gag	gac	tat	gtt	cac	gtc	cac	acc	act	gat	gag	432
Glu	Pro	Thr	Pro	Lys	Glu	Asp	Tyr	Val	His	Val	His	Thr	Thr	Asp	Glu	
			130			135						140				
gcg	acc	tat	gtc	cgc	atc	aaa	atc	agc	ggc	ccc	aac	cgc	ctg	atc	ctc	480
Ala	Thr	Tyr	Val	Arg	Ile	Lys	Ile	Ser	Gly	Pro	Asn	Arg	Leu	Ile	Leu	
			145			150				155					160	
aat	gac	atc	atc	acc	caa	ctc	aaa	gac	aca	gac	acc	gag	gac	agc	ctg	528
Asn	Asp	Ile	Ile	Thr	Gln	Leu	Lys	Asp	Thr	Asp	Thr	Glu	Asp	Ser	Leu	
				165					170					175		
cct	gaa	gcg	ctc	atg	gcg	ttc	ctg	aca	gag	aaa	atc	cag	tta	aag	atc	576
Pro	Glu	Ala	Leu	Met	Ala	Phe	Leu	Thr	Glu	Lys	Ile	Gln	Leu	Lys	Ile	
				180				185					190			
acc	aaa	tac	ctc	ttc	acc	cca	cat	aag	cac	cct	gag	cag	gtg	tgg	tca	624
Thr	Lys	Tyr	Leu	Phe	Thr	Pro	His	Lys	His	Pro	Glu	Gln	Val	Trp	Ser	
			195				200									
ccg	gac	tac	ggt	gac	att	gat	ccc	gaa	gcc	tat	gcc	aac	gcc	acc	ctc	672
Pro	Asp	Tyr	Gly	Asp	Ile	Asp	Pro	Glu	Ala	Tyr	Ala	Asn	Ala	Thr	Leu	
			210			215					220					
gtg	tgc	gcc	aag	gac	tta	gat	gag	ctc	gct	gga	gcc	acg	gag	aag	agc	720
Val	Cys	Ala	Lys	Asp	Leu	Asp	Glu	Leu	Ala	Gly	Ala	Thr	Glu	Lys	Ser	
		225				230				235					240	
tac	acc	ccg	agt	gag	aag	atg	aaa	gcc	ctg	atc	aga	gct	cgg	gat	ggg	768
Tyr	Thr	Pro	Ser	Glu	Lys	Met	Lys	Ala	Leu	Ile	Arg	Ala	Arg	Asp	Gly	
				245					250					255		
cat	tgc	cgc	ttc	cca	ggg	tgt	tgc	gtt	ccg	gcg	agt	aag	tgc	cag	gtc	816
His	Cys	Arg	Phe	Pro	Gly	Cys	Cys	Val	Pro	Ala	Ser	Lys	Cys	Gln	Val	
			260				265						270			
gat	cac	att	atc	ccg	tgg	gcg	gag	ggc	ggc	ccg	aca	gcg	gcg	tgg	aac	864
Asp	His	Ile	Ile	Pro	Trp	Ala	Glu	Gly	Gly	Pro	Thr	Ala	Ala	Trp	Asn	

275	280	285	
ctg cag ttg ttg tgc cag cgg cat cac aat atg aaa acc gat ggt cgc			912
Leu Gln Leu Leu Cys Gln Arg His His Asn Met Lys Thr Asp Gly Arg			
290	295	300	
ttt act gct gat gct aat gga ttg gcg gag att aga tgg att ggg cgc			960
Phe Thr Ala Asp Ala Asn Gly Leu Ala Glu Ile Arg Trp Ile Gly Pro			
305	310	315	320
atg gat gta cca gcg gtg acc agg ccg acg ggt ccg ttg gtg aaa gcg			1008
Met Asp Val Pro Ala Val Thr Arg Pro Thr Gly Pro Leu Val Lys Ala			
325	330	335	
atg ccg cgg ggg att tgg ggt cag gtg ttg agg gat ccg atc cag gct			1056
Met Pro Arg Gly Ile Trp Gly Gln Val Leu Arg Asp Arg Ile Gln Ala			
340	345	350	
agg ttt gag cgg atc cgc gac cgc gcc ctc aac aaa gaa gac			1098
Arg Phe Glu Arg Ile Arg Asp Arg Ala Leu Asn Lys Glu Asp			
355	360	365	
tagaagcgca caggtttttg cat			1121
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Asp Asp Phe Asp Ala Asp Ser Phe Thr Thr Glu Val Ile Arg Ile Thr			
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Gly Tyr Ser Arg His Glu Val Asn Asn Gly Leu Asn Ala Met Ala Ala			
35	40	45	
Met Thr Asn Leu Pro His Leu Arg Ala Ile Gln Glu Arg Tyr Tyr Phe			
50	55	60	
Leu Ser Ile Arg Tyr Leu Ala Ser Ile Met Ile Ala Val Ala Lys Ala			
65	70	75	80
Asp Pro Thr Leu Trp Glu Glu Leu Asp Leu Arg Ile Thr Asp Ala Leu			
85	90	95	
Thr Pro Val Thr Ala Gly Glu Val Met Ile Gln Ser Ser Thr Leu Ser			
100	105	110	
Lys Arg Ile Ala Ala Trp Ile Lys Glu Leu Asp Pro Glu Pro Thr Pro			
115	120	125	
Glu Pro Thr Pro Lys Glu Asp Tyr Val His Val His Thr Thr Asp Glu			
130	135	140	
Ala Thr Tyr Val Arg Ile Lys Ile Ser Gly Pro Asn Arg Leu Ile Leu			
145	150	155	160

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Asn Asp Ile Ile Thr Gln Leu Lys Asp Thr Asp Thr Glu Asp Ser Leu
      165                      170                      175

Pro Glu Ala Leu Met Ala Phe Leu Thr Glu Lys Ile Gln Leu Lys Ile
      180                      185                      190

Thr Lys Tyr Leu Phe Thr Pro His Lys His Pro Glu Gln Val Trp Ser
      195                      200                      205

Pro Asp Tyr Gly Asp Ile Asp Pro Glu Ala Tyr Ala Asn Ala Thr Leu
      210                      215                      220

Val Cys Ala Lys Asp Leu Asp Glu Leu Ala Gly Ala Thr Glu Lys Ser
      225                      230                      235                      240

Tyr Thr Pro Ser Glu Lys Met Lys Ala Leu Ile Arg Ala Arg Asp Gly
      245                      250                      255

His Cys Arg Phe Pro Gly Cys Cys Val Pro Ala Ser Lys Cys Gln Val
      260                      265                      270

Asp His Ile Ile Pro Trp Ala Glu Gly Gly Pro Thr Ala Ala Trp Asn
      275                      280                      285

Leu Gln Leu Leu Cys Gln Arg His His Asn Met Lys Thr Asp Gly Arg
      290                      295                      300

Phe Thr Ala Asp Ala Asn Gly Leu Ala Glu Ile Arg Trp Ile Gly Pro
      305                      310                      315                      320

Met Asp Val Pro Ala Val Thr Arg Pro Thr Gly Pro Leu Val Lys Ala
      325                      330                      335

Met Pro Arg Gly Ile Trp Gly Gln Val Leu Arg Asp Arg Ile Gln Ala
      340                      345                      350

Arg Phe Glu Arg Ile Arg Asp Arg Ala Leu Asn Lys Glu Asp
      355                      360                      365

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<210> 1531

<211> 503

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(480)

<223> FRXA02874

<400> 1531

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gac tcc gac gac ttc gac gca gac tcc ttt acc acc gaa gtc atc cgg      96
Asp Ser Asp Asp Phe Asp Ala Asp Ser Phe Thr Thr Glu Val Ile Arg
      20                      25                      30

atc acc ggc tac tcc cgc cac gaa gtc aac aac ggc ctt aac gcc atg      144
Ile Thr Gly Tyr Ser Arg His Glu Val Asn Asn Gly Leu Asn Ala Met

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35                               40                               45

gcc gcg atg acc aac ctc cca cac ctg cgc gcc atc caa gaa cgc tac 192
Ala Ala Met Thr Asn Leu Pro His Leu Arg Ala Ile Gln Glu Arg Tyr
50                               55                               60

tac ttc ctg agc atc cgc tac ctc gcc tcc atc atg atc gcc gtg gcc 240
Tyr Phe Leu Ser Ile Arg Tyr Leu Ala Ser Ile Met Ile Ala Val Ala
65                               70                               75

aaa gca gac ccc acc ctg tgg gaa gaa ctc gac ctg cgc atc acc gac 288
Lys Ala Asp Pro Thr Leu Trp Glu Glu Leu Asp Leu Arg Ile Thr Asp
85                               90                               95

gcc tta aca cca gtc acc gca ggg gaa gtc atg atc caa tcc tcc acc 336
Ala Leu Thr Pro Val Thr Ala Gly Glu Val Met Ile Gln Ser Ser Thr
100                              105                              110

ctg tcc aaa cng cat cgc cng cct gga tca aag aac tgc acc cgc aac 384
Leu Ser Lys Xaa His Arg Xaa Pro Gly Ser Lys Asn Ser Thr Pro Asn
115                              120                              125

cca cac cag agc cca cac cga aag agg act atg ttc acg tcc aca cca 432
Pro His Gln Ser Pro His Arg Lys Arg Thr Met Phe Thr Ser Thr Pro
130                              135                              140

ctg atg agg cga cct atg tcc gca tca aaa tca gcg gcc cca acc gcc 480
Leu Met Arg Arg Pro Met Ser Ala Ser Lys Ser Ala Ala Pro Thr Ala
145                              150                              155

tgatcctcaa tgacatcacc acc 503

<210> 1532
<211> 160
<212> PRT
<213> Corynebacterium glutamicum

<400> 1532
Thr Glu Leu Asn Arg Asp Thr His His Leu Trp Val Val Leu Thr Thr
1 5 10 15
Asp Ser Asp Asp Phe Asp Ala Asp Ser Phe Thr Thr Glu Val Ile Arg
20 25 30
Ile Thr Gly Tyr Ser Arg His Glu Val Asn Asn Gly Leu Asn Ala Met
35 40 45
Ala Ala Met Thr Asn Leu Pro His Leu Arg Ala Ile Gln Glu Arg Tyr
50 55 60
Tyr Phe Leu Ser Ile Arg Tyr Leu Ala Ser Ile Met Ile Ala Val Ala
65 70 75
Lys Ala Asp Pro Thr Leu Trp Glu Glu Leu Asp Leu Arg Ile Thr Asp
85 90 95
Ala Leu Thr Pro Val Thr Ala Gly Glu Val Met Ile Gln Ser Ser Thr
100 105 110
Leu Ser Lys Xaa His Arg Xaa Pro Gly Ser Lys Asn Ser Thr Pro Asn

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<210> 1533
<211> 556
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(556)
<223> EXN03174
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400> 1533	gcgatgctcg aacgcgcaga acgctcctgg gtagacaaag ccgctgcata cgatttgcgc	60
tggtcagatc atccaccact gaacgtgata tactoctaaa	atg ctg ctg aca att Met Leu Leu Thr Ile	115
cta tgg gcc atc ggc atc acc gcc gaa ggc atg aca ggc gcg ctg gcc	1 20	163
Leu Trp Ala Ile Gly Ile Thr Ala Glu Gly Met Thr Gly Ala Leu Ala	10 15 20	
gca ggc cga caa aaa atg gat ctc ttc gga gta tcc gtc atc gca tgc	25 30 35	211
Ala Gly Arg Gln Lys Met Asp Leu Phe Gly Val Ser Val Ile Ala Cys		
gtt acc gcg atc ggc ggc gga tcc atc cgc gac atg ctg ctg gga cat	40 45 50	259
Val Thr Ala Ile Gly Gly Ser Ile Arg Asp Met Leu Leu Gly His		
tac ccg ctg gtg tgg gtg gaa aag cca ctg tat cta ctg ctg atc att	55 60 65	307
Tyr Pro Leu Val Trp Val Glu Lys Pro Leu Tyr Leu Leu Ile Ile		
ggc gca gcc att ttg aca gtg tcc att tcc ctg atg gag cac ttc	70 75 80 85	355
Gly Ala Ala Ile Leu Thr Val Ser Ile Ser Phe Leu Met Glu His Phe		
cgt gtg ttg ttc ctc gtg ctc gac gcc gtg ggt ctt tct gca ttc gct	90 95 100	403
Arg Val Leu Phe Leu Val Leu Asp Ala Val Gly Leu Ser Ala Phe Ala		
gtg atc ggc aca caa atc gca ctg gaa atg ggc tac gga ttc atc atc	105 110 115	451
Val Ile Gly Thr Gln Ile Ala Leu Glu Met Gly Tyr Gly Phe Ile Ile		
gca gta gtg gca tca gtg ctc aca ggt gta ttc ggc ggc gtc atg cgt	120 125	499
Ala Val Val Ala Ser Val Leu Thr Gly Val Phe Gly Gly Val Met Arg		

gac ctt ttg tgt gac cgc atc cca ctg gta ttt caa aaa gag ctc tac 547
 Asp Leu Leu Cys Asp Arg Ile Pro Leu Val Phe Gln Lys Glu Leu Tyr
 135 140 145

gca tca atc 556
 Ala Ser Ile
 150

<210> 1534

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 1534

Met Leu Leu Thr Ile Leu Trp Ala Ile Gly Ile Thr Ala Glu Gly Met
 1 5 10 15

Thr Gly Ala Leu Ala Ala Gly Arg Gln Lys Met Asp Leu Phe Gly Val
 20 25 30

Ser Val Ile Ala Cys Val Thr Ala Ile Gly Gly Gly Ser Ile Arg Asp
 35 40 45

Met Leu Leu Gly His Tyr Pro Leu Val Trp Val Glu Lys Pro Leu Tyr
 50 55 60

Leu Leu Leu Ile Ile Gly Ala Ala Ile Leu Thr Val Ser Ile Ser Phe
 65 70 75 80

Leu Met Glu His Phe Arg Val Leu Phe Leu Val Leu Asp Ala Val Gly
 85 90 95

Leu Ser Ala Phe Ala Val Ile Gly Thr Gln Ile Ala Leu Glu Met Gly
 100 105 110

Tyr Gly Phe Ile Ile Ala Val Val Ala Ser Val Leu Thr Gly Val Phe
 115 120 125

Gly Gly Val Met Arg Asp Leu Leu Cys Asp Arg Ile Pro Leu Val Phe
 130 135 140

Gln Lys Glu Leu Tyr Ala Ser Ile
 145 150

<210> 1535

<211> 562

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(562)

<223> FRXA02884

<400> 1535

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tggtcagatc actcaccact gaacgtgatc tactoctaaa atg ctg ctg aca att 115
 Met Leu Leu Thr Ile

1

5

cta tgg gcc atc ggc atc acc gcc gaa ggc atg aca ggc gcg ctg gcc 163
 Leu Trp Ala Ile Gly Ile Thr Ala Glu Gly Met Thr Gly Ala Leu Ala
 10 15 20

gca ggc cga caa aaa atg gat ctc ttc gga gta tcc gtc atc gca tgc 211
 Ala Gly Arg Gln Lys Met Asp Leu Phe Gly Val Ser Val Ile Ala Cys
 25 30 35

gtt acc gcg atc ggc ggc gga tcc atc cgc gac atg ctg ctg gga cat 259
 Val Thr Ala Ile Gly Gly Gly Ser Ile Arg Asp Met Leu Leu Gly His
 40 45 50

tac ccg ctg gtg tgg gtg gaa aag cca ctg tat cta ctg ctg atc att 307
 Tyr Pro Leu Val Trp Val Glu Lys Pro Leu Tyr Leu Leu Ile Ile
 55 60 65

ggc gca gcc att ttg aca gtg tcc att tcc ttc ctg atg gag cac ttc 355
 Gly Ala Ala Ile Leu Thr Val Ser Ile Ser Phe Leu Met Glu His Phe
 70 75 80 85

cgt gtg ttg ttc ctc gtg ctc gac gcc gtg ggt ctt tct gca ttc gct 403
 Arg Val Leu Phe Leu Val Leu Asp Ala Val Gly Leu Ser Ala Phe Ala
 90 95 100

gtg atc ggc aca caa atc gca ctg gaa atg ggc tac gga ttc atc atc 451
 Val Ile Gly Thr Gln Ile Ala Leu Glu Met Gly Tyr Gly Phe Ile Ile
 105 110 115

gca gta gtg gca tca gtg ctc aca ggt gta ttc ggc ggc gtc atg cgt 499
 Ala Val Val Ala Ser Val Leu Thr Gly Val Phe Gly Gly Val Met Arg
 120 125 130

gac ctt ttg tgt gac cgc atc cca ctg gta ttt caa aaa gag ctc tac 547
 Asp Leu Leu Cys Asp Arg Ile Pro Leu Val Phe Gln Lys Glu Leu Tyr
 135 140 145

gca tca atc gca ttc 562
 Ala Ser Ile Ala Phe
 150

<210> 1536

<211> 154

<212> PRT

<213> Corynebacterium glutamicum

<400> 1536

Met Leu Leu Thr Ile Leu Trp Ala Ile Gly Ile Thr Ala Glu Gly Met
 1 5 10 15

Thr Gly Ala Leu Ala Ala Gly Arg Gln Lys Met Asp Leu Phe Gly Val
 20 25 30

Ser Val Ile Ala Cys Val Thr Ala Ile Gly Gly Gly Ser Ile Arg Asp
 35 40 45

Met Leu Leu Gly His Tyr Pro Leu Val Trp Val Glu Lys Pro Leu Tyr
 50 55 60

```

Leu Leu Leu Ile Ile Gly Ala Ala Ile Leu Thr Val Ser Ile Ser Phe
 65          70          75          80

Leu Met Glu His Phe Arg Val Leu Phe Leu Val Leu Asp Ala Val Gly
          85          90          95

Leu Ser Ala Phe Ala Val Ile Gly Thr Gln Ile Ala Leu Glu Met Gly
          100          105          110

Tyr Gly Phe Ile Ile Ala Val Val Ala Ser Val Leu Thr Gly Val Phe
          115          120          125

Gly Gly Val Met Arg Asp Leu Leu Cys Asp Arg Ile Pro Leu Val Phe
          130          135          140

Gln Lys Glu Leu Tyr Ala Ser Ile Ala Phe
145          150

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<210> 1537

<211> 781

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (93)..(758)

<223> RXN03177

<400> 1537

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tatgggctga acaattctaa ggagaattat ccgtg aaa aag aag ctt atg ttg    113
                        Val Lys Lys Lys Leu Met Leu
                        1                      5

```

```

cct ttg att gtt gca gct ttg ggg tta agt gcc tgc agc tcc gaa cct    161
Pro Leu Ile Val Ala Ala Leu Gly Leu Ser Ala Cys Ser Ser Glu Pro
          10          15          20

```

```

gca gca gcc cca ctc gaa gca gag cca tta cat aac ctg ctc att gat    209
Ala Ala Ala Pro Leu Glu Ala Glu Pro Leu His Asn Leu Leu Ile Asp
          25          30          35

```

```

ggc tca gag tcc ggc ttg gac aat gcc act gaa gga aac gac acc tca    257
Gly Ser Glu Ser Gly Leu Asp Asn Ala Thr Glu Gly Asn Asp Thr Ser
          40          45          50          55

```

```

tta agt ggc caa ccc atc aat ctt aca gtg gtc aac ggt gcc tta gat    305
Leu Ser Gly Gln Pro Ile Asn Leu Thr Val Val Asn Gly Ala Leu Asp
          60          65          70

```

```

atc gat ggc tcc tgc gga aaa gcc ctc caa gct gta gag gac gtc aat    353
Ile Asp Gly Ser Cys Gly Lys Ala Leu Gln Ala Val Glu Asp Val Asn
          75          80          85

```

```

ctg gac agc gta gct agc gca tcc agg gca ctg gca tcc ggc gac aaa    401
Leu Asp Ser Val Ala Ser Ala Ser Arg Ala Leu Ala Ser Gly Asp Lys
          90          95          100

```

```

caa gta ggc atc gcc atg tac tca acc gcc gaa gac aac gac atc tca    449

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Gln Val Gly Ile Ala Met Tyr Ser Thr Ala Glu Asp Asn Asp Ile Ser
105                      110                      115

cca atg gac ctc tac gca gac atc gcg aat gct tgc gaa gac ccc gtc 497
Pro Met Asp Leu Tyr Ala Asp Ile Ala Asn Ala Cys Glu Asp Pro Val
120                      125                      130                      135

gtc gat tct tcc gac acc acc tac acc ttc ggc aaa ctc gat gat gct 545
Val Asp Ser Ser Asp Thr Thr Tyr Thr Phe Gly Lys Leu Asp Asp Ala
140                      145                      150

ccc gac ggc gcc gtt gga ttc acc ctc gac att gaa gtc acc cct gac 593
Pro Asp Gly Ala Val Gly Phe Thr Leu Asp Ile Glu Val Thr Pro Asp
155                      160                      165

aat caa ggc tcc acc gtg atg atg atc caa gaa tta gga aac cac cac 641
Asn Gln Gly Ser Thr Val Met Met Ile Gln Glu Leu Gly Asn His His
170                      175                      180

atc atc gtc gca gga ctt gaa acc acc cca gaa gaa acc gcc act gtc 689
Ile Ile Val Ala Gly Leu Glu Thr Thr Pro Glu Glu Thr Ala Thr Val
185                      190                      195

ttc gaa gca caa cgc acc aaa ctc gaa gaa ggc ttg cag ctt aaa cag 737
Phe Glu Ala Gln Arg Thr Lys Leu Glu Gly Leu Glu Lys Gln
200                      205                      210                      215

aat tgg cag ctt ggg tgg gtt taaatgcgcc caacctaaga aaa 781
Asn Trp Gln Leu Gly Trp Val
220

<210> 1538
<211> 222
<212> PRT
<213> Corynebacterium glutamicum

<400> 1538
Val Lys Lys Lys Leu Met Leu Pro Leu Ile Val Ala Ala Leu Gly Leu
1 5 10 15

Ser Ala Cys Ser Ser Glu Pro Ala Ala Ala Pro Leu Glu Ala Glu Pro
20 25 30

Leu His Asn Leu Leu Ile Asp Gly Ser Glu Ser Gly Leu Asp Asn Ala
35 40 45

Thr Glu Gly Asn Asp Thr Ser Leu Ser Gly Gln Pro Ile Asn Leu Thr
50 55 60

Val Val Asn Gly Ala Leu Asp Ile Asp Gly Ser Cys Gly Lys Ala Leu
65 70 75 80

Gln Ala Val Glu Asp Val Asn Leu Asp Ser Val Ala Ser Ala Ser Arg
85 90 95

Ala Leu Ala Ser Gly Asp Lys Gln Val Gly Ile Ala Met Tyr Ser Thr
100 105 110

Ala Glu Asp Asn Asp Ile Ser Pro Met Asp Leu Tyr Ala Asp Ile Ala
115 120 125

```

ctg gac agc gta gct agc gca tcc agg gca ctg gca tcc ggc gac aaa 402
Leu Asp Ser Val Ala Ser Ala Ser Arg Ala Leu Ala Ser Gly Asp Lys
90 95 100

```

caa gta ggc atc gcc atg tac tca acc gcc gaa gac aac gac atc tca 450
Gln Val Gly Ile Ala Met Tyr Ser Thr Ala Glu Asp Asn Asp Ile Ser
105 110 115

cca atg gac ctc tac gca gac atc gcg aat gct tgc gaa gac ccc gtc 498
Pro Met Asp Leu Tyr Ala Asp Ile Ala Asn Ala Cys Glu Asp Pro Val
120 125 130 135

gtc gat tct tcc gac acc acc tac acc ttc ggc aaa ctc gat gat gct 546
Val Asp Ser Ser Asp Thr Thr Tyr Thr Phe Gly Lys Leu Asp Asp Ala
140 145 150

ccc gac ggc gcc gtt gga ttc acc ctc gac att gaa gtc acc cct gac 594
Pro Asp Gly Ala Val Gly Phe Thr Leu Asp Ile Glu Val Thr Pro Asp
155 160 165

aat caa ggc tcc acc gtg atg atg atc caa gaa tta gga aac cac cac 642
Asn Gln Gly Ser Thr Val Met Met Ile Gln Glu Leu Gly Asn His His
170 175 180

atc atc gtc gca gga ctt gaa acc acc cca gaa gaa acc gcc act gtc 690
Ile Ile Val Ala Gly Leu Glu Thr Thr Pro Glu Glu Thr Ala Thr Val
185 190 195

ttc gaa gca caa cgc acc aaa ctc gaa gaa ggc ttg cag ctt aaa cag 738
Phe Glu Ala Gln Arg Thr Lys Leu Glu Glu Gly Leu Gln Leu Lys Gln
200 205 210 215

aat tgg cag ctt ggg tgg gtt taaatgcgcc caacctaaga aaa 782
Asn Trp Gln Leu Gly Trp Val
220

<210> 1540
<211> 222
<212> PRT
<213> Corynebacterium glutamicum

<400> 1540
Val Lys Lys Lys Leu Met Leu Pro Leu Ile Val Ala Ala Leu Gly Leu
1 5 10 15

Ser Ala Cys Ser Ser Glu Pro Ala Ala Ala Pro Leu Glu Ala Glu Pro
20 25 30

Leu His Asn Leu Leu Ile Asp Gly Ser Glu Ser Gly Leu Asp Asn Ala
35 40 45

Thr Glu Gly Asn Asp Thr Ser Leu Ser Gly Gln Pro Ile Asn Leu Thr
50 55 60

Val Val Asn Gly Ala Leu Asp Ile Asp Gly Ser Cys Gly Lys Ala Leu
65 70 75 80

Gln Ala Val Glu Asp Val Asn Leu Asp Ser Val Ala Ser Ala Ser Arg
85 90 95

Ala Leu Ala Ser Gly Asp Lys Gln Val Gly Ile Ala Met Tyr Ser Thr
100 105 110

Ala Glu Asp Asn Asp Ile Ser Pro Met Asp Leu Tyr Ala Asp Ile Ala

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115	120	125
Asn Ala Cys Glu Asp Pro Val Val Asp Ser Ser Asp Thr Thr Tyr Thr		
130	135	140
Phe Gly Lys Leu Asp Asp Ala Pro Asp Gly Ala Val Gly Phe Thr Leu		
145	150	155
Asp Ile Glu Val Thr Pro Asp Asn Gln Gly Ser Thr Val Met Met Ile		
	165	170
Gln Glu Leu Gly Asn His His Ile Ile Val Ala Gly Leu Glu Thr Thr		
	180	185
Pro Glu Glu Thr Ala Thr Val Phe Glu Ala Gln Arg Thr Lys Leu Glu		
	195	200
Glu Gly Leu Gln Leu Lys Gln Asn Trp Gln Leu Gly Trp Val		
	210	215
		220

<210> 1541

<211> 373

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(373)

<223> RXN03182

<400> 1541

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tgtatccgta gcccgcttcc gcaagaggga tgggtgcctaa atg acc ctg caa cta	115
Met Thr Leu Gln Leu	
1	5

ttc acc gac atc gtg tct ctg gtg ttc att ctc agc ggc gca ttc ttg	163
Phe Thr Asp Ile Val Ser Leu Val Phe Ile Leu Ser Gly Ala Phe Leu	
10	15
	20

tca ttc tcc gca tcc atc ggc ctc ata cga ttc aaa gac acc atg tcc	211
Ser Phe Ser Ala Ser Ile Gly Leu Ile Arg Phe Lys Asp Thr Met Ser	
25	30
	35

aga gtc cac gcc atg acc aaa ccc caa aca acc ggc ctt atc etc acc	259
Arg Val His Ala Met Thr Lys Pro Gln Thr Thr Gly Leu Ile Leu Thr	
40	45
	50

gtt gta ggc gca atc atc cgc atc tta ggc cac gaa cac ttc gat caa	307
Val Val Gly Ala Ile Ile Arg Ile Leu Gly His Glu His Phe Asp Gln	
55	60
	65

tca caa cgc agt gac ctc gga gtc ctt gtt ctc ctc gta ctg ttt gca	355
Ser Gln Arg Ser Asp Leu Gly Val Leu Val Leu Leu Val Leu Phe Ala	
70	75
	80
	85

ctg ctc acc agc cca gtg	373
Leu Leu Thr Ser Pro Val	
90	

<210> 1542

<211> 91

<212> PRT

<213> Corynebacterium glutamicum

<400> 1542

Met Thr Leu Gln Leu Phe Thr Asp Ile Val Ser Leu Val Phe Ile Leu

1

5

10

15

Ser Gly Ala Phe Leu Ser Phe Ser Ala Ser Ile Gly Leu Ile Arg Phe

20

25

30

Lys Asp Thr Met Ser Arg Val His Ala Met Thr Lys Pro Gln Thr Thr

35

40

45

Gly Leu Ile Leu Thr Val Val Gly Ala Ile Ile Arg Ile Leu Gly His

50

55

60

Glu His Phe Asp Gln Ser Gln Arg Ser Asp Leu Gly Val Leu Val Leu

65

70

75

80

Leu Val Leu Phe Ala Leu Leu Thr Ser Pro Val

85

90

<210> 1543

<211> 603

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (87)..(584)

<223> RXN03184

<400> 1543

gcacaacgtc gctgggtcagt gccattagtc acgcaagaaa tggggcgggtc cgggtggaaga 60

ctggcctgct gtttgggtgcc gcgggcatg gtt ggc gcg ttt ggc ggt ggc gtt 113

Met Val Gly Ala Phe Gly Gly Gly Val

1

5

ctc ggg ggc tac att cct ggc acg att ttg atg atc gcg ttt gcg ctc 161

Leu Gly Gly Tyr Ile Pro Gly Thr Ile Leu Met Ile Ala Phe Ala Leu

10

15

20

25

atg atg atc gcc acg tcg act gcg atg ttg cgg ggg cgt aag cag aag 209

Met Met Ile Ala Thr Ser Thr Ala Met Leu Arg Gly Arg Lys Gln Lys

30

35

40

aag ggg gcg tcg aaa agc tct ctt tgg cgc gtc ctt gtt gat ggc ctg 257

Lys Gly Ala Ser Lys Ser Ser Leu Trp Arg Val Leu Val Asp Gly Leu

45

50

55

gtg gtc ggc gcg gtg acc ggg ctt gtt ggt gcg ggc ggc ggc ttt ttg 305

Val Val Gly Ala Val Thr Gly Leu Val Gly Ala Gly Gly Phe Leu

60

65

70

gtg gtg ccg gcg ctg gcg ctg ctc ggc ggg ctg tcg atg ccg gtg gct 353

Val Val Pro Ala Leu Ala Leu Leu Gly Gly Leu Ser Met Pro Val Ala
 75 80 85
 gtg ggc acg tgc ttg gtg gtg atc acg atg aag tgc ttt gcg ggg ctt 401
 Val Gly Thr Ser Leu Val Val Ile Thr Met Lys Ser Phe Ala Gly Leu
 90 95 100 105
 gcc ggg tat ctg acc agc gtg cag ctg gat tgg ggg ctg gtg ctg atg 449
 Ala Gly Tyr Leu Thr Ser Val Gln Leu Asp Trp Gly Leu Val Leu Met
 110 115 120
 gtg act gcg gcc gcc atc gtc ggt tgc ctt gcc ggt tgc cgc ctt gcg 497
 Val Thr Ala Ala Ala Ile Val Gly Ser Leu Ala Gly Ser Arg Leu Leu Ala
 125 130 135
 ggg cgc gtg cct gag act ttg ctc cgc aaa ggg ttc ggg gtg ttc gtg 545
 Gly Arg Val Pro Glu Thr Leu Leu Arg Lys Gly Phe Gly Val Phe Val
 140 145 150
 ctg gtc atg ggc gtg ttc gtg ctc ggc ttg gag ctt tta taagcttttc 594
 Leu Val Met Gly Val Phe Val Leu Gly Leu Glu Leu Leu
 155 160 165
 gacgtctcc 603
 <210> 1544
 <211> 166
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 1544
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 1 5 10 15
 Thr Ile Leu Met Ile Ala Phe Ala Leu Met Met Ile Ala Thr Ser Thr
 20 25 30
 Ala Met Leu Arg Gly Arg Lys Gln Lys Lys Gly Ala Ser Lys Ser Ser
 35 40 45
 Leu Trp Arg Val Leu Val Asp Gly Leu Val Val Gly Ala Val Thr Gly
 50 55 60
 Leu Val Gly Ala Gly Gly Gly Phe Leu Val Val Pro Ala Leu Ala Leu
 65 70 75 80
 Leu Gly Gly Leu Ser Met Pro Val Ala Val Gly Thr Ser Leu Val Val
 85 90 95
 Ile Thr Met Lys Ser Phe Ala Gly Leu Ala Gly Tyr Leu Thr Ser Val
 100 105 110
 Gln Leu Asp Trp Gly Leu Val Leu Met Val Thr Ala Ala Ala Ile Val
 115 120 125
 Gly Ser Leu Ala Gly Ser Arg Leu Ala Gly Arg Val Pro Glu Thr Leu
 130 135 140
 Leu Arg Lys Gly Phe Gly Val Phe Val Leu Val Met Gly Val Phe Val
 145 150 155 160

Leu Gly Leu Glu Leu Leu
165

<210> 1545
<211> 295
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (84)..(272)
<223> RXN03185

<400> 1545
agcgccaac cggtcagacc agcggtttct ctgaggatgc aaagtccatg atgggtnagg 60
tcaactgagct gtccgaaacc accatg aat gat ctt gca gct gaa ggt gaa aac 113
Met Asn Asp Leu Ala Glu Gly Glu Asn
1 5 10

gat cct tac cgc atg gtt cag cag ctg cgc cgc aag ctc tct cgc ttc 161
Asp Pro Tyr Arg Met Val Gln Gln Leu Arg Arg Lys Leu Ser Arg Phe
15 20 25

gtc gag cag aag tgg aag cgc cag ccg gtc atc atg cca acc gtc att 209
Val Glu Gln Lys Trp Lys Arg Gln Pro Val Ile Met Pro Thr Val Ile
30 35 40

ccg atg act gcg gaa acc acg cac atc ggt gac gat gag gtt cgc gct 257
Pro Met Thr Ala Glu Thr Thr His Ile Gly Asp Asp Glu Val Arg Ala
45 50 55

tca cgc gag tcc ctg taaaagcatt tcgcttttcg acg 295
Ser Arg Glu Ser Leu
60

<210> 1546
<211> 63
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 1546
Met Asn Asp Leu Ala Ala Glu Gly Glu Asn Asp Pro Tyr Arg Met Val
1 5 10 15
Gln Gln Leu Arg Arg Lys Leu Ser Arg Phe Val Glu Gln Lys Trp Lys
20 25 30
Arg Gln Pro Val Ile Met Pro Thr Val Ile Pro Met Thr Ala Glu Thr
35 40 45
Thr His Ile Gly Asp Asp Glu Val Arg Ala Ser Arg Glu Ser Leu
50 55 60

<210> 1547
<211> 864
<212> DNA

gaa gct aca ggc gtg aag act ctt caa gac ctc cga agc cac tcc tgg 691
Glu Ala Thr Gly Val Lys Thr Leu Gln Asp Leu Arg Ser His Ser Trp
185 190 195

cgt gcg acg ctg cac ggt gtg tac gcg gac gtg atg gac cca gct aca 739
 Arg Ala Thr Leu His Gly Val Tyr Ala Asp Val Met Asp Pro Ala Thr
 200 205 210
 cgc gcc gcc att ttc ggc cac acc gag cag gta gct gag gag tac tac 787
 Arg Ala Ala Ile Phe Gly His Thr Glu Gln Val Ala Glu Glu Tyr Tyr
 215 220 225
 aac gac cgc caa aat att gaa tca ctc atg aga caa gtc aag cgc gcc 835
 Asn Asp Arg Gln Asn Ile Glu Ser Leu Met Arg Gln Val Lys Arg Ala
 230 235 240 245
 tac gcg taactacgct taagactacg cgt 864
 Tyr Ala

<210> 1548

<211> 247

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1548

Val Gln Val Arg Ile Leu Ser Ser Glu Leu Val Cys Ser Leu Ser Gly
 1 5 10 15
 Ala Ile Arg Gly Val Asn Leu Asp Ile Ala Ala Pro Lys Pro Lys Lys
 20 25 30
 Ser Gly Arg Arg Thr Leu Thr Lys Pro Glu Trp Asp Ala Val Ile Lys
 35 40 45
 His Leu Leu Thr Arg Asp Thr Glu Pro Leu Leu Thr Pro Thr Lys His
 50 55 60
 Lys Asn Ile Arg Gln Ser Thr Lys Asn Ile His Ala Arg Ile Val Arg
 65 70 75 80
 Leu Thr Leu Leu Gln Ala Val Ser Gly Leu Arg Ile Ala Glu Ala Asn
 85 90 95
 Gln Leu Gln Trp Lys His Ile Ile Asp Gly Asp Asp Gly Met Leu Ile
 100 105 110
 Asn Ala Ser Ala Asp Ile Val Lys Gly Arg Lys Gly Lys Glu Arg Gly
 115 120 125
 Arg Tyr Ile Pro Ile Leu Arg Ala Asp Val Ala Glu Tyr Leu Arg Thr
 130 135 140
 His Arg Glu Asp Asp Glu His Phe Ile Val Gly Ser Pro Thr Thr Thr
 145 150 155 160
 Ala Arg Pro Trp Asp Ala Thr Asn Ala Asp Asp Lys Val Pro Glu Leu
 165 170 175
 Tyr Arg Gln Ile Ala Glu Ala Thr Gly Val Lys Thr Leu Gln Asp Leu
 180 185 190
 Arg Ser His Ser Trp Arg Ala Thr Leu His Gly Val Tyr Ala Asp Val

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195                200                205
Met Asp Pro Ala Thr Arg Ala Ala Ile Phe Gly His Thr Glu Gln Val
210                215                220
Ala Glu Glu Tyr Tyr Asn Asp Arg Gln Asn Ile Glu Ser Leu Met Arg
225                230                235                240
Gln Val Lys Arg Ala Tyr Ala
245

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<210> 1549
<211> 615
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(592)
<223> RXA00008

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<400> 1549
cattggcgtg gtgatgcgcg gcattatcgc acaactcacc ctgcgcttct acgtgaggaa 60
ataagactat tgaactcctt gccgtagact tagaaagact atg gcc aag aag aaa 115
Met Ala Lys Lys Lys
1 5
aag aaa gtc gac gaa aac aac tca gtt ctc gcg acc aat cgc aag gcc 163
Lys Lys Val Asp Glu Asn Asn Ser Val Leu Ala Thr Asn Arg Lys Ala
10 15 20
cgc cat gac tac cac atc att gat acg tgg gag gcg gcc gtg gtg ctc 211
Arg His Asp Tyr His Ile Ile Asp Thr Trp Glu Ala Gly Val Val Leu
25 30 35
tta gcc acc gaa atc aaa tca ctg cgc gaa ggt aag gta tcc ctc gtg 259
Leu Gly Thr Glu Ile Lys Ser Leu Arg Glu Gly Lys Val Ser Leu Val
40 45 50
gat tcc ttt gcc acc att gat aac gga gaa atc tgg ctt cag cat ctc 307
Asp Ser Phe Ala Thr Ile Asp Asn Gly Glu Ile Trp Leu Gln His Leu
55 60 65
cac atc ccg cag tat tcc atg ggc tcc tgg aca aac cac acg ccc aag 355
His Ile Pro Gln Tyr Ser Met Gly Ser Trp Thr Asn His Thr Pro Lys
70 75 80 85
cgc acc cgc aaa ctt ttg ctg cac cgc aac gag att gat tcc ctg atg 403
Arg Thr Arg Lys Leu Leu Leu His Arg Asn Glu Ile Asp Ser Leu Met
90 95 100
ggt aaa gtc cgc gac gcc aac cgc acg ttg gtt ccg ctc aag ctt tac 451
Gly Lys Val Arg Asp Gly Asn Arg Thr Leu Val Pro Leu Lys Leu Tyr
105 110 115
ctc aaa aac ggt cgc gtc aaa ctc gaa ctc gga ctc gca caa ggt aag 499
Leu Lys Asn Gly Arg Val Lys Leu Glu Leu Gly Leu Ala Gln Gly Lys
120 125 130

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cag gat tac gac aag cgc caa gat atc aag cgt cgc acc gaa gaa cgc 547
 Gln Asp Tyr Asp Lys Arg Gln Asp Ile Lys Arg Arg Thr Glu Glu Arg
 135 140 145

gaa gtc acc cgt gag ctc ggc cgt cgc att aag gga atc aac gcg 592
 Glu Val Thr Arg Glu Leu Gly Arg Arg Ile Lys Gly Ile Asn Ala
 150 155 160

taaatgagta ttcatcgcg cgc aaa 615

<210> 1550

<211> 164

<212> PRT

<213> Corynebacterium glutamicum

<400> 1550

Met Ala Lys Lys Lys Lys Val Asp Glu Asn Asn Ser Val Leu Ala
 1 5 10 15

Thr Asn Arg Lys Ala Arg His Asp Tyr His Ile Ile Asp Thr Trp Glu
 20 25 30

Ala Gly Val Val Leu Leu Gly Thr Glu Ile Lys Ser Leu Arg Glu Gly
 35 40 45

Lys Val Ser Leu Val Asp Ser Phe Ala Thr Ile Asp Asn Gly Glu Ile
 50 55 60

Trp Leu Gln His Leu His Ile Pro Gln Tyr Ser Met Gly Ser Trp Thr
 65 70 75 80

Asn His Thr Pro Lys Arg Thr Arg Lys Leu Leu Leu His Arg Asn Glu
 85 90 95

Ile Asp Ser Leu Met Gly Lys Val Arg Asp Gly Asn Arg Thr Leu Val
 100 105 110

Pro Leu Lys Leu Tyr Leu Lys Asn Gly Arg Val Lys Leu Glu Leu Gly
 115 120 125

Leu Ala Gln Gly Lys Gln Asp Tyr Asp Lys Arg Gln Asp Ile Lys Arg
 130 135 140

Arg Thr Glu Glu Arg Glu Val Thr Arg Glu Leu Gly Arg Arg Ile Lys
 145 150 155 160

Gly Ile Asn Ala

<210> 1551

<211> 432

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(409)

<223> RXA00015

<400> 1551
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acagcaaccg acgacactca acgagcgcga cctccaagac atg att gat atg tgc 115
Met Ile Asp Met Cys
1 5
acc act cct cga caa gag atc atg atc cgc gag caa ttt aag gag atc 163
Thr Thr Pro Arg Gln Glu Ile Met Ile Arg Glu Gln Phe Lys Glu Ile
10 15 20
aac aac ggt agg gtt gta cct cat tac gat cag ctt gaa cag ctc gca 211
Asn Asn Gly Arg Val Val Pro His Tyr Asp Gln Leu Glu Gln Leu Ala
25 30 35
gag att ttt tca act aaa gac tca atc gac atg gtc aac gag ata ctc 259
Glu Ile Phe Ser Thr Lys Asp Ser Ile Asp Met Val Asn Glu Ile Leu
40 45 50
aat cgc gat acg gat ttt ctc agt aat gaa ggc aca att ttt atg gaa 307
Asn Arg Asp Thr Asp Phe Leu Ser Asn Glu Gly Thr Ile Phe Met Glu
55 60 65
tac att ttc aac ggt gga ttc cat acg gac aac ggc tat caa cgg ttg 355
Tyr Ile Phe Asn Gly Gly Phe His Thr Asp Asn Gly Tyr Gln Pro Leu
70 75 80 85
tcc tat gca tat gtt gaa cga ggc tta gcg atc cgc cct cca cgc ata 403
Ser Tyr Ala Tyr Val Glu Arg Gly Leu Ala Ile Arg Pro Pro Arg Ile
90 95 100
gtg ctc tagatatgac acaaatcggt att 432
Val Leu

<210> 1552
<211> 103
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 1552
Met Ile Asp Met Cys Thr Thr Pro Arg Gln Glu Ile Met Ile Arg Glu
1 5 10 15
Gln Phe Lys Glu Ile Asn Asn Gly Arg Val Val Pro His Tyr Asp Gln
20 25 30
Leu Glu Gln Leu Ala Glu Ile Phe Ser Thr Lys Asp Ser Ile Asp Met
35 40 45
Val Asn Glu Ile Leu Asn Arg Asp Thr Asp Phe Leu Ser Asn Glu Gly
50 55 60
Thr Ile Phe Met Glu Tyr Ile Phe Asn Gly Gly Phe His Thr Asp Asn
65 70 75 80
Gly Tyr Gln Pro Leu Ser Tyr Ala Tyr Val Glu Arg Gly Leu Ala Ile
85 90 95
Arg Pro Pro Arg Ile Val Leu

100

<210> 1553
 <211> 1422
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1399)
 <223> RXA00018

<400> 1553
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 ttttaatgac ttacaaatat caagaaagaa tctatttcctt atg tcc gca tta tct 115
 Met Ser Ala Leu Ser
 1 5
 aga ccg cac aag atc gcc acc ggc gtt gct gtc gca act ctt acc ctc 163
 Arg Pro His Lys Ile Ala Thr Gly Val Ala Val Ala Thr Leu Thr Leu
 10 15 20
 acc ttg tgt acc tct gct gcc ggc gtt gtc cat gca gcg caa caa tcc 211
 Thr Leu Cys Thr Ser Ala Ala Gly Val Val His Ala Ala Gln Gln Ser
 25 30 35
 atc agc ggt cca gaa tcc tcc tgt gct ttt aat caa cag cgt tgg gat 259
 Ile Ser Gly Pro Glu Ser Ser Cys Ala Phe Asn Gln Gln Arg Trp Asp
 40 45 50
 gac agc aaa gtt aag ctt gac gac acc atc gct acg gcc aaa aac tca 307
 Asp Ser Lys Val Lys Leu Asp Asp Thr Ile Ala Thr Ala Lys Asn Ser
 55 60 65
 ttg gta caa aca ggc gaa ctg cac cgc aac gaa cag gat cta ctt act 355
 Leu Val Gln Thr Gly Glu Leu His Arg Asn Glu Gln Asp Leu Leu Thr
 70 75 80 85
 ggc tat ctt ttc cag caa ccg cac agc agc aat tac ctt gca ctc aac 403
 Gly Tyr Leu Phe Gln Gln Pro His Ser Ser Asn Tyr Leu Ala Leu Asn
 90 95 100
 aac gct tat gcc gat gcc gta gca atc aaa gac agc ttt gtc cgc cca 451
 Asn Ala Tyr Ala Asp Ala Val Ala Ile Lys Asp Ser Phe Val Arg Pro
 105 110 115
 aca tgt gac ggt tct aaa gag tcc aag att gcc agc gaa cac gcc gtg 499
 Thr Cys Asp Gly Ser Lys Glu Ser Lys Ile Ala Ser Glu His Ala Val
 120 125 130
 tct gag gtt gtg ggt gca gtg aat gta ctc gcc cga gca caa aaa gcg 547
 Ser Glu Val Val Gly Ala Val Asn Val Leu Ala Arg Ala Gln Lys Ala
 135 140 145
 ctg cag att aac tcc gac acc tac gaa cag caa cgt cgt tgt gat gcc 595
 Leu Gln Ile Asn Ser Asp Thr Tyr Glu Gln Gln Arg Arg Cys Asp Ala
 150 155 160 165
 ctt cgt cta gca agc cga gat gaa tca gat gtt ctt atg cgc att gat 643

Leu Arg Leu Ala Ser Arg Asp Glu Ser Asp Val Leu Met Arg Ile Asp	
170 175 180	
cgc acc atg ctg cag ctt cgt cgc aca cta gct gac att gac cag gcg	691
Arg Thr Met Leu Gln Leu Arg Arg Thr Leu Ala Asp Ile Asp Gln Ala	
185 190 195	
tcc aca gac att cgc gat att cgg gct caa aca aca agc ttt gaa cgt	739
Ser Thr Asp Ile Arg Asp Ile Arg Ala Gln Thr Thr Phe Glu Arg	
200 205 210	
gat ctt gcc cgc gag caa aaa gag gcc gac gca gca gca cgt gct caa	787
Asp Leu Ala Arg Glu Gln Lys Glu Ala Asp Ala Ala Arg Ala Gln	
215 220 225	
gct gta gac act tcg acc aca cca aca tca agc aca gaa gat cgt gtc	835
Ala Val Asp Thr Ser Thr Thr Pro Thr Ser Ser Thr Glu Asp Arg Val	
230 235 240 245	
aac gac att ctt aaa gag tcc cgt acc gat cac agt ggc gac agt tac	883
Asn Asp Ile Leu Lys Glu Ser Arg Thr Asp His Ser Gly Asp Ser Tyr	
250 255 260	
acg cgc tca acg aca acg agc gca caa agc act gag ccg gat tct gca	931
Thr Arg Ser Thr Thr Thr Ser Ala Gln Ser Thr Glu Pro Asp Ser Ala	
265 270 275	
acc aac acc tca tat ctg tca cgt cgt ctc gac agc ctg gaa cgc agt	979
Thr Asn Thr Ser Tyr Leu Ser Arg Arg Leu Asp Ser Leu Glu Arg Ser	
280 285 290	
gcg cag cat att gat ctc aat acc cag tgc gac aac ctc gat gat ctt	1027
Ala Gln His Ile Asp Leu Asn Thr Gln Cys Asp Asn Leu Asp Asp Leu	
295 300 305	
cgt gaa ctc acc aac aat gac acg cgt gat cac acc ggc tcc gtc att	1075
Arg Glu Leu Thr Asn Asn Asp Thr Arg Asp His Thr Gly Ser Val Ile	
310 315 320 325	
tcc att gcc gat caa ctc aca gac atc acc aat gaa atc aat gaa tta	1123
Ser Ile Ala Asp Gln Leu Thr Asp Ile Thr Asn Glu Ile Asn Glu Leu	
330 335 340	
cgc gat agc act ttt gcc acc aga gac agt gcc caa caa gca cag gat	1171
Arg Asp Ser Thr Phe Ala Thr Arg Asp Ser Ala Gln Gln Ala Gln Asp	
345 350 355	
cag gta att gct caa cgt gaa gaa ctg caa cga gca aag gaa gca cga	1219
Gln Val Ile Ala Gln Arg Glu Glu Leu Gln Arg Ala Lys Glu Ala Tyr	
360 365 370	
cta gaa gaa cag cga ctc gcc aaa gaa gca gaa gag ggc gct cgc aac	1267
Leu Glu Glu Gln Arg Leu Ala Lys Glu Ala Glu Glu Gly Ala Arg Asn	
375 380 385	
gca gca att cag gaa cgt gac gcg gcc gaa gca gca ctg cgt gaa gca	1315
Ala Ala Ile Gln Glu Arg Asp Ala Ala Glu Ala Ala Leu Arg Glu Ala	
390 395 400 405	
caa gac ctc ctc agt cgc ctc gat gac aca ggc aac gca acc agt gat	1363
Gln Asp Leu Leu Ser Arg Leu Asp Asp Thr Gly Asn Ala Thr Ser Asp	

410 415 420
 gac aca gca gcg cta gta gac ggt ctt ctc aat aac taacaatcag 1409
 Asp Thr Ala Ala Leu Val Asp Gly Leu Leu Asn Asn
 425 430
 caacaccgct cac 1422

 <210> 1554
 <211> 433
 <212> PRT
 <213> *Corynebacterium glutamicum*

 <400> 1554
 Met Ser Ala Leu Ser Arg Pro His Lys Ile Ala Thr Gly Val Ala Val
 1 5 10 15
 Ala Thr Leu Thr Leu Thr Leu Cys Thr Ser Ala Ala Gly Val Val His
 20 25 30
 Ala Ala Gln Gln Ser Ile Ser Gly Pro Glu Ser Ser Cys Ala Phe Asn
 35 40 45
 Gln Gln Arg Trp Asp Asp Ser Lys Val Lys Leu Asp Asp Thr Ile Ala
 50 55 60
 Thr Ala Lys Asn Ser Leu Val Gln Thr Gly Glu Leu His Arg Asn Glu
 65 70 75 80
 Gln Asp Leu Leu Thr Gly Tyr Leu Phe Gln Gln Pro His Ser Ser Asn
 85 90 95
 Tyr Leu Ala Leu Asn Asn Ala Tyr Ala Asp Ala Val Ala Ile Lys Asp
 100 105 110
 Ser Phe Val Arg Pro Thr Cys Asp Gly Ser Lys Glu Ser Lys Ile Ala
 115 120 125
 Ser Glu His Ala Val Ser Glu Val Val Gly Ala Val Asn Val Leu Ala
 130 135 140
 Arg Ala Gln Lys Ala Leu Gln Ile Asn Ser Asp Thr Tyr Glu Gln Gln
 145 150 155 160
 Arg Arg Cys Asp Ala Leu Arg Leu Ala Ser Arg Asp Glu Ser Asp Val
 165 170 175
 Leu Met Arg Ile Asp Arg Thr Met Leu Gln Leu Arg Arg Thr Leu Ala
 180 185 190
 Asp Ile Asp Gln Ala Ser Thr Asp Ile Arg Asp Ile Arg Ala Gln Thr
 195 200 205
 Thr Ser Phe Glu Arg Asp Leu Ala Arg Glu Gln Lys Glu Ala Asp Ala
 210 215 220
 Ala Ala Arg Ala Gln Ala Val Asp Thr Ser Thr Thr Pro Thr Ser Ser
 225 230 235 240
 Thr Glu Asp Arg Val Asn Asp Ile Leu Lys Glu Ser Arg Thr Asp His

$$\begin{aligned} \text{Gen}^2 &= \mathcal{H}^1(\text{Gen}^1, \text{Gen}^2, \text{Gen}^3, \dots, \text{Gen}^n) \\ \text{Gen}^3 &= \mathcal{H}^2(\text{Gen}^1, \text{Gen}^2, \text{Gen}^3, \dots, \text{Gen}^n) \\ \vdots & \\ \text{Gen}^n &= \mathcal{H}^{n-1}(\text{Gen}^1, \text{Gen}^2, \text{Gen}^3, \dots, \text{Gen}^n) \end{aligned}$$

[illegible]

<210> 1556
 <211> 260
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1556
 Met Thr Val Thr Thr Ala Gln Arg Ile Ala Asp Glu Phe Gln Arg Gly
 1 5 10 15
 Ile Ser Ile Gly Pro Trp Asp Leu Cys Glu Val Pro Ala Gly Asp Asp
 20 25 30
 Tyr Leu Glu His Thr Thr Lys Val Arg Arg Arg His Ser Thr Ala Val
 35 40 45
 Glu Ile His Thr Asp Ser Leu Ile Ile Cys Ala Pro Glu Gly Ser Thr
 50 55 60
 Tyr Ser His Asn Arg Thr Lys Ala Gly Leu Ala Ser Thr Gly Thr Val
 65 70 75 80
 Thr Val Pro Val Lys Gly Leu Ser Glu Pro Val Lys Leu Ser Leu Asn
 85 90 95
 Leu Leu Ala Asp Tyr Gly Asn Ser Phe Asp Thr Val His Asp Asp Leu
 100 105 110
 Trp Gln Arg Glu Leu Arg Glu Gln Thr Arg Gly Gln Leu Leu Thr Leu
 115 120 125
 Asn Ala Val Ser Gly Leu Gly Asp Asp Ser Val Ala Ile Met Gly Thr
 130 135 140
 Pro Trp Gly Asp Gly Leu Thr Gly Glu Ala Asn Thr Ile Lys Gly Arg
 145 150 155 160
 Glu His Phe Val Met Trp Ala Ala Gly Cys Arg Phe Glu Asp Gly Tyr
 165 170 175
 Gly Arg His Ala Leu Arg Glu Asp Arg His Val Arg His Gln Ala Arg
 180 185 190
 Ala Gly Glu Asp Ser Thr Ala His His Gly Trp Leu Leu Lys Gly Thr
 195 200 205
 Val Phe Gly Lys Glu Leu Thr Gly Asp Ala Val Thr Ala Ala Met Thr
 210 215 220
 Val Phe Ser Asp Val Val Val Thr Val Asp Glu Gly Arg Ile Pro Gly
 225 230 235 240
 Met Lys Ser Gly Gln Pro Phe Ser Met Ala Thr Arg Leu Arg Ala Ser
 245 250 255
 Ser Ala Pro Val
 260

<210> 1557
 <211> 1896

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1873)

<223> RXA00021

<400> 1557

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caccgcacaa tcgaaaataa aagtaaagga tgttcacctt atg tct gac acc aca 115
Met Ser Asp Thr Thr 5
1
gac agc cac gac cca gca acc tcc cct aca gtc gat tca gcc gca tcc 163
Asp Ser His Asp Pro Ala Thr Ser Pro Thr Val Asp Ser Ala Ala Ser
10 15 20
ggt act tct gac ccc aac cag caa ccc aag aag aaa ttc acc atc att 211
Gly Thr Ser Asp Pro Asn Gln Gln Pro Lys Lys Lys Phe Thr Ile Ile
25 30 35
aag cag gtg aac atg att gcg cgt act gcc att gat gac tgc att aat 259
Lys Gln Val Asn Met Ile Ala Arg Thr Ala Ile Asp Asp Cys Ile Asn
40 45 50
cga cta ggc cca gat gtt gtc acc atg tcc agc gaa gac att gct gat 307
Arg Leu Gly Pro Asp Val Val Thr Met Ser Ser Ser Glu Asp Ile Ala Asp
55 60 65
caa gtg gtc aac tcc att aac gtt gct att gcc aga gaa aac aca cgt 355
Gln Val Val Asn Ser Ile Asn Val Ala Ile Ala Arg Glu Asn Thr Arg
70 75 80 85
gcc caa gat gcc aat gct gcg gtg cgt tac aca cct atc ttt aag ctc 403
Ala Gln Asp Ala Asn Ala Ala Val Arg Tyr Thr Pro Ile Phe Lys Leu
90 95 100
gat ttc tcc cat gtc gct gtc ctt atg cgc aga ctg cat gtg att atc 451
Asp Phe Ser His Val Ala Val Leu Met Arg Arg Leu His Val Ile Ile
105 110 115
aac atc gcg cca tcg cat aac tct gat cct gac agc gat atg ttg gct 499
Asn Ile Ala Pro Ser His Asn Ser Asp Pro Asp Ser Asp Met Leu Ala
120 125 130
att tac gac ccc aac cca cgc agc gag cat tac ggg atc tat cgc acc 547
Ile Tyr Asp Pro Asn Pro Arg Ser Glu His Tyr Gly Ile Tyr Arg Thr
135 140 145
tca gag gct gaa ata cgc cgc gta gcc cgt gaa tac tgc cct gac ctc 595
Ser Glu Ala Glu Ile Arg Arg Val Ala Arg Glu Tyr Cys Pro Asp Leu
150 155 160 165
acc tca gcg cag ttt aga gaa ctg cag atg gca ctc tca gat gct gca 643
Thr Ser Ala Gln Phe Arg Glu Leu Gln Met Ala Leu Ser Asp Ala Ala
170 175 180
cct cgt aaa gtc cgc cac aag cag cgt gac ttg att ccc gtg aaa aac 691
Pro Arg Lys Val Arg His Lys Gln Arg Asp Leu Ile Pro Val Lys Asn

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185	190	195	
ggc atc ttt aat tac tcg act	aaa caa cta gaa ccg ttt tct caa gag	739	
Gly Ile Phe Asn Tyr Ser Thr	Lys Gln Leu Glu Pro Phe Ser Gln Glu		
200	205	210	
ttt gtc ttt ctt gct aaa tct	gca gtg aac tac aac cca aat gca caa	787	
Phe Val Phe Leu Ala Lys Ser	Ala Val Asn Tyr Asn Pro Asn Ala Gln		
215	220	225	
aac cct gtc atc act cat ccc	cag gat ggc tct gtc tgg gat gtt gaa	835	
Asn Pro Val Ile Thr His Pro	Gln Asp Gly Ser Val Trp Asp Val Glu		
230	235	240	245
tca tgg atg aac gat ctc tcc	gat gac cct gaa gtc gtt aac ctg ctg	883	
Ser Trp Met Asn Asp Leu Ser	Asp Asp Pro Glu Val Val Asn Trp Asn Leu Leu		
250	255	260	265
tgg gag att atc ggc gct atc	gtg cgc ccc tat gtg tcc tgg aac aag	931	
Trp Glu Ile Ile Gly Ala Ile	Val Arg Pro Tyr Val Ser Trp Asn Lys		
265	270	275	
tct gcc tgg ttc tac tca gag	gcc ggc aac aac ggt aaa ggc acg ctc	979	
Ser Ala Trp Phe Tyr Ser Glu	Ala Gly Asn Asn Gly Lys Gly Thr Leu		
280	285	290	
gtt gag ctc atg cgc aac atc	ttg ggc gca gag gcc tat acc agt atc	1027	
Val Glu Leu Met Arg Asn Ile	Leu Gly Ala Glu Ala Tyr Thr Ser Ile		
295	300	305	
cag ctc tcg gac ttc tct aaa	gag ttc cac ctt gaa tca ctg act cgt	1075	
Gln Leu Ser Asp Phe Ser Lys	Glu Phe His Leu Glu Ser Leu Thr Arg		
310	315	320	325
gca caa gca atc ctt gtt gat	gag aac gat gtc ggc gcc ttc tta gaa	1123	
Ala Gln Ala Ile Leu Val Asp	Glu Asn Asp Val Gly Ala Phe Leu Glu		
330	335	340	345
aag tca gca aac ctt aaa gcg	att gtc acc aat gac gtc atc tcc att	1171	
Lys Ser Ala Asn Leu Lys Ala	Ile Val Thr Asn Asp Val Ile Ser Ile		
345	350	355	
aac cgc aag cac aaa acc atg	ctc agc tat cag ttt tat ggc ttt atg	1219	
Asn Arg Lys His Lys Thr Met	Leu Ser Tyr Gln Phe Tyr Gly Phe Met		
360	365	370	
gtg cag tgt att aac ggc ttc	ccc aag gtc aaa gac cag tcg gag tca	1267	
Val Gln Cys Ile Asn Gly Phe	Pro Lys Val Lys Asp Gln Ser Glu Ser		
375	380	385	
ttt ttc agg cgc caa ctc ttt	gtg ccg ttt gag aaa agc ttc acc ggt	1315	
Phe Phe Arg Arg Gln Leu Phe	Val Pro Phe Glu Lys Ser Phe Thr Gly		
390	395	400	405
gcc gag cgc aag tac atc aaa	gac gac tac atg tcg cgc act gat gtc	1363	
Ala Glu Arg Lys Tyr Ile Lys	Asp Asp Tyr Met Ser Arg Thr Asp Val		
410	415	420	425
ctc gaa tat gta ctg cac cgc	gta ctg cat atg aac tac gac aat ctc	1411	
Leu Glu Tyr Val Leu His Arg	Val Leu His Met Asn Tyr Asp Asn Leu		
425	430	435	

tcc acc cct gct gca gct ctc gct gtg ctg gat gaa tac aaa gag ttt 1459
 Ser Thr Pro Ala Ala Ala Leu Ala Val Leu Asp Glu Tyr Lys Glu Phe
 440 445 450
 gtc gat cct gtg cgc gca ttc tgg aat gaa ttc agc gat caa ttt gtc 1507
 Val Asp Pro Val Arg Ala Phe Trp Asn Glu Phe Ser Asp Gln Phe Val
 455 460 465
 tgg gat ctt ctt ccc ctg caa ttc ctc tac gag ttt tat cgc aag tgg 1555
 Trp Asp Leu Leu Pro Leu Gln Phe Leu Tyr Glu Phe Tyr Arg Lys Trp
 470 475 480 485
 ttt gac cgt gac agc cca tcc ggg tct gtg ctc ggc aaa cgc agc ttc 1603
 Phe Asp Arg Asp Ser Pro Ser Gly Ser Val Leu Gly Lys Arg Ser Phe
 490 495 500
 att caa aaa atc acc acc atc gcc gtt gat agc ggt cag tgg gag tat 1651
 Ile Gln Lys Ile Thr Thr Ile Ala Val Asp Ser Gly Gln Trp Glu Tyr
 505 510 515
 ccg ctg aca gca cag cgt ccc ggt ggc gat atg gcc gtt cct gag cca 1699
 Pro Leu Thr Ala Gln Arg Pro Gly Gly Asp Met Ala Val Pro Glu Pro
 520 525 530
 tta gtc att gat tat gac ctc acc gag tgg caa aac gcc act gta cct 1747
 Leu Val Ile Asp Tyr Asp Leu Thr Glu Trp Gln Asn Ala Thr Val Pro
 535 540 545
 aaa ggt cac gtc aac aag ggg ctc cct cta cca ctc aag gct aat tat 1795
 Lys Gly His Val Asn Lys Gly Leu Pro Leu Leu Lys Ala Asn Tyr
 550 555 560 565
 cga gga ctg ctc cgc aaa cct cta aca aca cct gct act ccc cct gca 1843
 Arg Gly Leu Leu Arg Lys Pro Leu Thr Thr Pro Ala Thr Pro Pro Ala
 570 575 580
 gcg ccg gtc aac ccc aca cca ccc acc cct taacaaccac aagaagatt 1893
 Ala Pro Val Asn Pro Thr Pro Pro Pro
 585 590
 tat 1896

<210> 1558

<211> 591

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1558

Met Ser Asp Thr Thr Asp Ser His Asp Pro Ala Thr Ser Pro Thr Val
 1 5 10 15

Asp Ser Ala Ala Ser Gly Thr Ser Asp Pro Asn Gln Gln Pro Lys Lys
 20 25 30

Lys Phe Thr Ile Ile Lys Gln Val Asn Met Ile Ala Arg Thr Ala Ile
 35 40 45

Asp Asp Cys Ile Asn Arg Leu Gly Pro Asp Val Val Thr Met Ser Ser
 50 55 60

Glu Asp Ile Ala Asp Gln Val Val Asn Ser Ile Asn Val Ala Ile Ala
 65 70 75 80
 Arg Glu Asn Thr Arg Ala Gln Asp Ala Asn Ala Ala Val Arg Tyr Thr
 85 90 95
 Pro Ile Phe Lys Leu Asp Phe Ser His Val Ala Val Leu Met Arg Arg
 100 105 110
 Leu His Val Ile Ile Asn Ile Ala Pro Ser His Asn Ser Asp Pro Asp
 115 120 125
 Ser Asp Met Leu Ala Ile Tyr Asp Pro Asn Pro Arg Ser Glu His Tyr
 130 135 140
 Gly Ile Tyr Arg Thr Ser Glu Ala Glu Ile Arg Arg Val Ala Arg Glu
 145 150 155 160
 Tyr Cys Pro Asp Leu Thr Ser Ala Gln Phe Arg Glu Leu Gln Met Ala
 165 170 175
 Leu Ser Asp Ala Ala Pro Arg Lys Val Arg His Lys Gln Arg Asp Leu
 180 185 190
 Ile Pro Val Lys Asn Gly Ile Phe Asn Tyr Ser Thr Lys Gln Leu Glu
 195 200 205
 Pro Phe Ser Gln Glu Phe Val Phe Leu Ala Lys Ser Ala Val Asn Tyr
 210 215 220
 Asn Pro Asn Ala Gln Asn Pro Val Ile Thr His Pro Gln Asp Gly Ser
 225 230 235 240
 Val Trp Asp Val Glu Ser Trp Met Asn Asp Leu Ser Asp Asp Pro Glu
 245 250 255
 Val Val Asn Leu Leu Trp Glu Ile Ile Gly Ala Ile Val Arg Pro Tyr
 260 265 270
 Val Ser Trp Asn Lys Ser Ala Trp Phe Tyr Ser Glu Ala Gly Asn Asn
 275 280 285
 Gly Lys Gly Thr Leu Val Glu Leu Met Arg Asn Ile Leu Gly Ala Glu
 290 295 300
 Ala Tyr Thr Ser Ile Gln Leu Ser Asp Phe Ser Lys Glu Phe His Leu
 305 310 315 320
 Glu Ser Leu Thr Arg Ala Gln Ala Ile Leu Val Asp Glu Asn Asp Val
 325 330 335
 Gly Ala Phe Leu Glu Lys Ser Ala Asn Leu Lys Ala Ile Val Thr Asn
 340 345 350
 Asp Val Ile Ser Ile Asn Arg Lys His Lys Thr Met Leu Ser Tyr Gln
 355 360 365
 Phe Tyr Gly Phe Met Val Gln Cys Ile Asn Gly Phe Pro Lys Val Lys
 370 375 380

Asp Gln Ser Glu Ser Phe Phe Arg Arg Gln Leu Phe Val Pro Phe Glu
 385 390 395 400
 Lys Ser Phe Thr Gly Ala Glu Arg Lys Tyr Ile Lys Asp Asp Tyr Met
 405 410 415
 Ser Arg Thr Asp Val Leu Glu Tyr Val Leu His Arg Val Leu His Met
 420 425 430
 Asn Tyr Asp Asn Leu Ser Thr Pro Ala Ala Ala Leu Ala Val Leu Asp
 435 440 445
 Glu Tyr Lys Glu Phe Val Asp Pro Val Arg Ala Phe Trp Asn Glu Phe
 450 455 460
 Ser Asp Gln Phe Val Trp Asp Leu Leu Pro Leu Gln Phe Leu Tyr Glu
 465 470 475 480
 Phe Tyr Arg Lys Trp Phe Asp Arg Asp Ser Pro Ser Gly Ser Val Leu
 485 490 495
 Gly Lys Arg Ser Phe Ile Gln Lys Ile Thr Thr Ile Ala Val Asp Ser
 500 505 510
 Gly Gln Trp Glu Tyr Pro Leu Thr Ala Gln Arg Pro Gly Gly Asp Met
 515 520 525
 Ala Val Pro Glu Pro Leu Val Ile Asp Tyr Asp Leu Thr Glu Trp Gln
 530 535 540
 Asn Ala Thr Val Pro Lys Gly His Val Asn Lys Gly Leu Pro Leu Pro
 545 550 555 560
 Leu Lys Ala Asn Tyr Arg Gly Leu Leu Arg Lys Pro Leu Thr Thr Pro
 565 570 575
 Ala Thr Pro Pro Ala Ala Pro Val Asn Pro Thr Pro Pro Thr Pro
 580 585 590

<210> 1559

<211> 1560

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1537)

<223> RXA00025

<400> 1559

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 cttgatactt ttctgatca cggcgctggc ttcacgata atg gcg tgg atg aac 115
 Met Ala Trp Met Asn
 1 5

 gta tcc gtg att gtt cca ggc tct gat gag gaa cta ttt gta aaa ggc 163
 Val Ser Val Ile Val Pro Gly Ser Asp Glu Glu Leu Phe Val Lys Gly
 10 15 20

ctg ttc acc ggt gaa ggc cta acc tgg ttg act acg aat ctc ggg gca Leu Phe Thr Gly Glu Gly Leu Thr Trp Leu Thr Thr Asn Leu Gly Ala 25 30 35	211
aac tac atc ggg ttc ccg ccg ttg ctc acc gtg ttg cca att ctg ttg Asn Tyr Ile Gly Phe Pro Pro Leu Leu Thr Val Leu Pro Ile Leu Leu 40 45 50	259
gca gtg ggt gtt gct gaa cgt tcc ggc atg ttg gct gcg ctg att agg Ala Val Gly Val Ala Glu Arg Ser Gly Met Leu Ala Ala Leu Ile Arg 55 60 65	307
aaa ctt ttt ggt tcg gcg aaa aag atc gtt ttg cca tat gca gtc ggt Lys Leu Phe Gly Ser Ala Lys Lys Ile Val Leu Pro Tyr Ala Val Gly 70 75 80 85	355
gtg att ggc gtg acc gcg tcg atc atg gcg gac gct gcc ttc gtg gtg Val Ile Gly Val Thr Ala Ser Ile Met Ala Asp Ala Ala Phe Val Val 90 95 100	403
gtg cca cct ttg gcc gcg atg gtg ttt aaa gct gct ggt cgg cac cct Val Pro Pro Leu Ala Ala Met Val Phe Lys Ala Ala Gly Arg His Pro 105 110 115	451
gtg gct ggg cta ttg ggt tcg ttt gca gct gtg ggt gca gga tat tcc Val Ala Gly Leu Leu Gly Ser Phe Ala Ala Val Gly Ala Gly Tyr Ser 120 125 130	499
aca gcg att gtg ccc acc agc ctt gat gca ctt ttt gcg gga att acc Thr Ala Ile Val Pro Thr Ser Leu Asp Ala Leu Phe Ala Gly Ile Thr 135 140 145	547
aac gcc gtg atg gag aca ctt cca gcc att gcg aca act gaa gtc aat Asn Ala Val Met Glu Thr Leu Pro Gly Ile Ala Thr Thr Glu Val Asn 150 155 160 165	595
ccg gtt tct aac tat tac ttc aat att gca tcc tcg att gtg ttg ggt Pro Val Ser Asn Tyr Tyr Phe Asn Ile Ala Ser Ser Ile Val Leu Gly 170 175 180	643
ctg tta tgt ggt ttc ctc att gat aag gtg ctg gaa cct cgg atg ttg Leu Leu Cys Gly Phe Leu Ile Asp Lys Val Leu Glu Pro Arg Met Trp 185 190 195	691
cgt cag aaa atc gct acg gag tat gca gaa agc att gaa ccc acc agc Arg Gln Lys Ile Ala Thr Glu Tyr Ala Glu Ser Ile Glu Pro Thr Ser 200 205 210	739
gca gca gat gat gag gaa atc tct gca acc cta acc gca cag gaa aac Ala Ala Asp Asp Glu Glu Ile Ser Ala Thr Leu Thr Ala Gln Glu Asn 215 220 225	787
cgc gcg ctg aca att tcc atg tgg acc acc ctg gcg acg gcc atc atc Arg Ala Leu Thr Ile Ser Met Trp Thr Thr Leu Ala Thr Ala Ile Ile 230 235 240 245	835
gtg ctg gtt gtg gtg ctg att ccg gga tcc cca tgg aga aat gag gat Val Leu Val Val Val Leu Ile Pro Gly Ser Pro Trp Arg Asn Glu Asp 250 255 260	883
ggg gga ttc ttg cct acc tcg cca ctg ctg agc tct gtg gtg ttt att	931

Gly	Gly	Phe	Leu	Pro	Thr	Ser	Pro	Leu	Leu	Ser	Ser	Val	Val	Phe	Ile		
			265					270					275				
gta	ttt	ttg	ttt	ttc	atg	gtg	atg	ggc	ctg	gcc	tac	ggc	atg	gtg	gtg	979	
Val	Phe	Leu	Phe	Phe	Met	Val	Met	Gly	Leu	Ala	Tyr	Gly	Met	Val	Val		
		280					285				290						
ggc	acg	atc	aag	aac	atg	gat	gat	gtc	gtg	aac	atg	atg	ggc	gaa	gca	1027	
Gly	Thr	Ile	Lys	Asn	Met	Asp	Asp	Val	Val	Asn	Met	Met	Gly	Glu	Ala		
		295				300					305						
atc	aag	gac	atg	att	ggc	ttc	ttg	gtt	ttg	gcc	ttc	att	ttg	gga	cag	1075	
Ile	Lys	Asp	Met	Ile	Gly	Phe	Leu	Val	Leu	Ala	Phe	Ile	Leu	Gly	Gln		
310					315					320				325			
ttt	gtg	gcg	ctg	ttt	aac	tgg	acg	ggc	atc	ggc	acc	tgg	act	gct	gtt	1123	
Phe	Val	Ala	Leu	Phe	Asn	Trp	Thr	Gly	Ile	Gly	Thr	Trp	Thr	Ala	Val		
			330					335						340			
cag	ggc	gct	gcg	gga	ttg	gaa	gcg	atc	ggc	ctt	acc	gga	ttc	cct	gcg	1171	
Gln	Gly	Ala	Ala	Gly	Leu	Glu	Ala	Ile	Gly	Leu	Thr	Gly	Phe	Pro	Ala		
			345					350					355				
atc	att	gca	ttt	att	att	ttg	gcg	tca	tgt	ttg	aac	ctg	ctg	att	att	1219	
Ile	Ile	Ala	Phe	Ile	Ile	Leu	Ala	Ser	Cys	Leu	Asn	Leu	Leu	Ile	Ile		
		360					365					370					
tcc	ggc	tct	gcg	atg	tgg	acg	ctg	atg	gct	gcg	gtg	ttc	gtc	ccg	atg	1267	
Ser	Gly	Ser	Ala	Met	Trp	Thr	Leu	Met	Ala	Ala	Val	Phe	Val	Pro	Met		
		375				380					385						
ttc	gct	ctg	ctt	ggc	tat	gaa	cca	tca	ttc	att	cag	gca	gca	ttc	cgc	1315	
Phe	Ala	Leu	Leu	Gly	Tyr	Glu	Pro	Ser	Phe	Ile	Gln	Ala	Ala	Phe	Arg		
390					395					400				405			
gtg	ggc	gac	tcg	gca	act	cag	gtg	atc	aca	ccg	ctg	aat	ccg	tac	atg	1363	
Val	Gly	Asp	Ser	Ala	Thr	Gln	Val	Ile	Thr	Pro	Leu	Asn	Pro	Tyr	Met		
			410					415						420			
att	gtg	atc	ctc	ggc	ttg	ctc	cgt	cga	tac	gaa	ccg	gat	gca	ggc	tta	1411	
Ile	Val	Ile	Leu	Gly	Leu	Leu	Arg	Arg	Tyr	Glu	Pro	Asp	Ala	Gly	Leu		
		425					430						435				
ggc	acc	ttg	atg	tca	agg	ctt	atc	cca	ttt	gtg	atc	cct	ttc	tgg	cta	1459	
Gly	Thr	Leu	Met	Ser	Arg	Leu	Ile	Pro	Phe	Val	Ile	Pro	Phe	Trp	Leu		
		440				445						450					
gcc	tgg	gct	aca	ttg	ttg	gca	att	tgg	ttc	tac	gcc	gat	ttg	ccg	ctt	1507	
Ala	Trp	Ala	Thr	Leu	Leu	Ala	Ile	Trp	Phe	Tyr	Ala	Asp	Leu	Pro	Leu		
		455				460					465						
gga	cct	ggc	tct	gcg	atc	ttc	ctc	gaa	gga	taagttttca	tgagtactga					1557	
Gly	Pro	Gly	Ser	Ala	Ile	Phe	Leu	Glu	Gly								
470					475												
caa																1560	

<210> 1560

<211> 479

<212> PRT

<213> Corynebacterium glutamicum

<400> 1560

Met Ala Trp Met Asn Val Ser Val Ile Val Pro Gly Ser Asp Glu Glu
 1 5 10 15

Leu Phe Val Lys Gly Leu Phe Thr Gly Glu Gly Leu Thr Trp Leu Thr
 20 25 30

Thr Asn Leu Gly Ala Asn Tyr Ile Gly Phe Pro Pro Leu Leu Thr Val
 35 40 45

Leu Pro Ile Leu Leu Ala Val Gly Val Ala Glu Arg Ser Gly Met Leu
 50 55 60

Ala Ala Leu Ile Arg Lys Leu Phe Gly Ser Ala Lys Lys Ile Val Leu
 65 70 75 80

Pro Tyr Ala Val Gly Val Ile Gly Val Thr Ala Ser Ile Met Ala Asp
 85 90 95

Ala Ala Phe Val Val Val Pro Pro Leu Ala Ala Met Val Phe Lys Ala
 100 105 110

Ala Gly Arg His Pro Val Ala Gly Leu Leu Gly Ser Phe Ala Ala Val
 115 120 125

Gly Ala Gly Tyr Ser Thr Ala Ile Val Pro Thr Ser Leu Asp Ala Leu
 130 135 140

Phe Ala Gly Ile Thr Asn Ala Val Met Glu Thr Leu Pro Gly Ile Ala
 145 150 155 160

Thr Thr Glu Val Asn Pro Val Ser Asn Tyr Tyr Phe Asn Ile Ala Ser
 165 170 175

Ser Ile Val Leu Gly Leu Leu Cys Gly Phe Leu Ile Asp Lys Val Leu
 180 185 190

Glu Pro Arg Met Trp Arg Gln Lys Ile Ala Thr Glu Tyr Ala Glu Ser
 195 200 205

Ile Glu Pro Thr Ser Ala Ala Asp Asp Glu Glu Ile Ser Ala Thr Leu
 210 215 220

Thr Ala Gln Glu Asn Arg Ala Leu Thr Ile Ser Met Trp Thr Thr Leu
 225 230 235 240

Ala Thr Ala Ile Ile Val Leu Val Val Val Leu Ile Pro Gly Ser Pro
 245 250 255

Trp Arg Asn Glu Asp Gly Gly Phe Leu Pro Thr Ser Pro Leu Leu Ser
 260 265 270

Ser Val Val Phe Ile Val Phe Leu Phe Phe Met Val Met Gly Leu Ala
 275 280 285

Tyr Gly Met Val Val Gly Thr Ile Lys Asn Met Asp Asp Val Val Asn
 290 295 300

Met Met Gly Glu Ala Ile Lys Asp Met Ile Gly Phe Leu Val Leu Ala

[illegible][illegible]

65


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tct gaa ttt aaa cat tta ata aca ggg ctc cca gat gta gtt ggt acc 307
Ser Glu Phe Lys His Leu Ile Thr Gly Leu Pro Asp Val Val Gly Thr
55 60 65

gcc cta etc atc ggg cac tgg cca ggc gtg gaa gaa cta gcc cat tat 355
Ala Leu Leu Ile Gly His Trp Pro Gly Val Glu Glu Leu Ala His Tyr
70 75 80 85

ttt ggc atc cgc gat gaa cat ccc ggt tgg gat cag atg gaa gaa aag 403
Phe Gly Ile Arg Asp Glu His Pro Gly Trp Asp Gln Met Glu Glu Lys
90 95 100

ttt ccc acc agc gcc att gcg gtg ttg gaa ttt aac acc cct tgg tca 451
Phe Pro Thr Ser Ala Ile Ala Val Leu Glu Phe Asn Thr Pro Trp Ser
105 110 115

aaa ctt gag aga aac tct gct cgg ttg aca gat ttt gtc att cca cgg 499
Lys Leu Glu Arg Asn Ser Ala Arg Leu Thr Asp Phe Val Ile Pro Arg
120 125 130

ggg tagttctgct tcaattgaac aat 525
Gly

<210> 1562
<211> 134
<212> PRT
<213> Corynebacterium glutamicum

<400> 1562
Val Ala Ala Gly Gln Trp Leu Ala Gly Asn Ile Gly Glu Ile Asp His
1 5 10 15

Val Leu Cys Ser Asp Ala Thr Arg Thr Gln Leu Thr Trp Glu Arg Val
20 25 30

Gln Leu Gly Gly Ala Thr Ala Lys Gly Ser Ser Phe His Asn Asp Ile
35 40 45

Tyr Glu Asn Gln Val Ser Glu Phe Lys His Leu Ile Thr Gly Leu Pro
50 55 60

Asp Val Val Gly Thr Ala Leu Leu Ile Gly His Trp Pro Gly Val Glu
65 70 75 80

Glu Leu Ala His Tyr Phe Gly Ile Arg Asp Glu His Pro Gly Trp Asp
85 90 95

Gln Met Glu Glu Lys Phe Pro Thr Ser Ala Ile Ala Val Leu Glu Phe
100 105 110

Asn Thr Pro Trp Ser Lys Leu Glu Arg Asn Ser Ala Arg Leu Thr Asp
115 120 125

Phe Val Ile Pro Arg Gly
130

<210> 1563

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<220>
<221> CDS
<222> (101)..(787)
<223> RXA00049
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Met Pro Thr Pro Ser
1 5

ggc cgc cgt gca caa aaa cgc gaa caa acc cgc gcg cgc ctg atc act 211
Gly Arg Arg Ala Gln Lys Arg Glu Gln Thr Arg Ala Arg Leu Ile Thr
25 30 35

tcc gct cgc aca ctc atg gca gaa cgg ggt gtc gac aat gta gga ata 259
Ser Ala Arg Thr Leu Met Ala Glu Arg Gly Val Asp Asn Val Gly Ile
40 45 50

gct gaa atc acc gaa ggc gca aac atc gga acg gga acc ttc tac aac 307
Ala Glu Ile Thr Glu Gly Ala Asn Ile Gly Thr Gly Thr Phe Tyr Asn
55 60 65

tac ttc cca gac cgt gaa caa cta ctc caa gct gtc gca gaa gat gcc 355
Tyr Phe Pro Asp Arg Glu Gln Leu Leu Gln Ala Val Ala Glu Asp Ala
70 75 80 85

ttt gaa tcc gtg gga att gcc ctc gac cag gtg cta acc aaa tta gac 403
Phe Glu Ser Val Gly Ile Ala Leu Asp Gln Val Leu Thr Lys Leu Asp
90 95 100

gat ccg gct gaa gta ttt gca ggg tgc ctt cga cat cta gta cgg cac 451
Asp Pro Ala Glu Val Phe Ala Gly Ser Leu Arg His Leu Val Arg His
105 110 115

tcg tta gaa gat cgg att tgg ggc gga ttt ttc ata caa atg ggt gct 49
Ser Leu Glu Asp Arg Ile Trp Gly Gly Phe Phe Ile Gln Met Gly Ala
120 125 130

gct cat ccc gta ctc atg cgc atc cta gga ccc cgc gca cgc cga gat 54
Ala His Pro Val Leu Met Arg Ile Leu Gly Pro Arg Ala Arg Arg Asp
135 140 145

cta ctt cat ggt tta gaa act ggc cga ttc acc atc gaa gat ctg gac 59
Leu Leu His Gly Leu Glu Thr Gly Arg Phe Thr Ile Glu Asp Leu Asp
150 155 160 165

cta gca acc aca tgc act ttt ggt tca ctc atc gca gcg atc caa atg 64
Leu Ala Thr Thr Cys Thr Phe Gly Ser Leu Ile Ala Ala Ile Gln Met
170 175 180

gcg ctt tct gca gat caa gat tcc aac gat gac aaa gat cag att ttc 69

Ala Leu Ser Ala Asp Gln Asp Ser Asn Asp Asp Lys Asp Gln Ile Phe
 185 190 195
 gca gcc gcg atg ctc cgg atg gtg ggt gtt caa gca gca gaa gcc cgg 739
 Ala Ala Ala Met Leu Arg Met Val Gly Val Gln Ala Ala Glu Ala Arg
 200 205 210
 gag atc gct tcg cgt cca ctc ccc gaa ata tcc cca gtc aaa ccg cag 787
 Glu Ile Ala Ser Arg Pro Leu Pro Glu Ile Ser Pro Val Lys Pro Gln
 215 220 225
 tagtgatcgg gcctcaaata aac 810

<210> 1564

<211> 229

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1564

Met Pro Thr Pro Ser Gln His Lys Asp Ala Ser Thr Ala Gln Thr Asp
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 Asn Gln Val Pro Thr Gly Arg Arg Ala Gln Lys Arg Glu Gln Thr Arg
 20 25 30
 Ala Arg Leu Ile Thr Ser Ala Arg Thr Leu Met Ala Glu Arg Gly Val
 35 40 45
 Asp Asn Val Gly Ile Ala Glu Ile Thr Glu Gly Ala Asn Ile Gly Thr
 50 55 60
 Gly Thr Phe Tyr Asn Tyr Phe Pro Asp Arg Glu Gln Leu Leu Gln Ala
 65 70 75 80
 Val Ala Glu Asp Ala Phe Glu Ser Val Gly Ile Ala Leu Asp Gln Val
 85 90 95
 Leu Thr Lys Leu Asp Asp Pro Ala Glu Val Phe Ala Gly Ser Leu Arg
 100 105 110
 His Leu Val Arg His Ser Leu Glu Asp Arg Ile Trp Gly Gly Phe Phe
 115 120 125
 Ile Gln Met Gly Ala Ala His Pro Val Leu Met Arg Ile Leu Gly Pro
 130 135 140
 Arg Ala Arg Arg Asp Leu Leu His Gly Leu Glu Thr Gly Arg Phe Thr
 145 150 155 160
 Ile Glu Asp Leu Asp Leu Ala Thr Thr Cys Thr Phe Gly Ser Leu Ile
 165 170 175
 Ala Ala Ile Gln Met Ala Leu Ser Ala Asp Gln Asp Ser Asn Asp Asp
 180 185 190
 Lys Asp Gln Ile Phe Ala Ala Ala Met Leu Arg Met Val Gly Val Gln
 195 200 205
 Ala Ala Glu Ala Arg Glu Ile Ala Ser Arg Pro Leu Pro Glu Ile Ser
 210 215 220

Pro Val Lys Pro Gln
225

<210> 1565
<211> 834
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (101)..(811)
<223> RXA00052

<400> 1565
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gtccacaagc ttaattggca tactggctgt tgttggccta gtg gcg ttt atc ctt 115
Val Ala Phe Ile Leu
1 5

ttc aac ttc gtg aaa aca aac gac gaa aca tcg aat gtc tct cag agc 163
Phe Asn Phe Val Lys Thr Asn Asp Glu Thr Ser Asn Val Ser Gln Ser
10 15 20

gag tca act gca gag aca gtc agc gaa aca aat ggc gtg ctc tcc gac 211
Glu Ser Thr Ala Glu Thr Val Ser Glu Thr Asn Gly Val Leu Ser Asp
25 30 35

ggc gca gaa aac atc gct tct caa tct gat gag agt aaa tcg ggt gta 259
Gly Ala Glu Asn Ile Ala Ser Gln Ser Asp Glu Ser Lys Ser Gly Val
40 45 50

gag att att gat tct gga ttt ggg cag agc tca aat tcg gcg atg gca 307
Glu Ile Ile Asp Ser Gly Phe Gly Gln Ser Ser Asn Ser Ala Met Ala
55 60 65

att gtt att gcc aaa act tct ggt gga agc ctc gca ggg gaa ttt gtt 355
Ile Val Ile Ala Lys Thr Ser Gly Gly Ser Leu Ala Gly Glu Phe Val
70 75 80 85

acg gcg acg gtg aat ttc ctc gat gaa agt ggc gcc gtt gta gcg act 403
Thr Ala Thr Val Asn Phe Leu Asp Glu Ser Gly Ala Val Val Ala Thr
90 95 100

gaa gat caa gta gaa aca ctc agt tgg gaa gac cag gaa ttg gta ttg 451
Glu Asp Gln Val Glu Thr Leu Ser Trp Glu Asp Gln Glu Leu Val Leu
105 110 115

cca gta tct cac tac aag gag gat tca agc cgc cca gaa att aca agc 499
Pro Val Ser His Tyr Lys Glu Asp Ser Ser Arg Pro Glu Ile Thr Ser
120 125 130

att gag gct ttt ctt tca gta acg gat tac ggt tca gga caa cca gat 547
Ile Glu Ala Phe Leu Ser Val Thr Asp Tyr Gly Ser Gly Gln Pro Asp
135 140 145

gaa act gca ttg ccg gtg ttg gaa acc acc gat att tcc aac cca tac 595
Glu Thr Ala Leu Pro Val Leu Glu Thr Thr Asp Ile Ser Asn Pro Tyr
150 155 160 165

gct ggt agt tac aat gcc tca ttt gcg ttg aaa aat gac tcc tca gat 643
 Ala Gly Ser Tyr Asn Ala Ser Phe Ala Leu Lys Asn Asp Ser Ser Asp
 170 175 180

gat ttt aag aac ctg aga gtt ggt att gtt tgc tac aac gag caa act 691
 Asp Phe Lys Asn Leu Arg Val Gly Ile Val Cys Tyr Asn Glu Gln Thr
 185 190 195

gac atc att ggt ggt ggt ttc aaa ttt ccg aac ctg gtt cca gcg ggt 739
 Asp Ile Ile Gly Gly Gly Phe Lys Phe Pro Asn Leu Val Pro Ala Gly
 200 205 210

ggg agt att cga atg gac gct agt gtg acg gtc tcc gaa atg cca gct 787
 Gly Ser Ile Arg Met Asp Ala Ser Val Thr Val Ser Glu Met Pro Ala
 215 220 225

tct tgt aag gca tat tta aat cac taatagattc ttaaaaggca gca 834
 Ser Cys Lys Ala Tyr Leu Asn His
 230 235

<210> 1566
 <211> 237
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1566
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 Asn Val Ser Gln Ser Glu Ser Thr Ala Glu Thr Val Ser Glu Thr Asn
 20 25 30
 Gly Val Leu Ser Asp Gly Ala Glu Asn Ile Ala Ser Gln Ser Asp Glu
 35 40 45
 Ser Lys Ser Gly Val Glu Ile Ile Asp Ser Gly Phe Gly Gln Ser Ser
 50 55 60
 Asn Ser Ala Met Ala Ile Val Ile Ala Lys Thr Ser Gly Gly Ser Leu
 65 70 75 80
 Ala Gly Glu Phe Val Thr Ala Thr Val Asn Phe Leu Asp Glu Ser Gly
 85 90 95
 Ala Val Val Ala Thr Glu Asp Gln Val Glu Thr Leu Ser Trp Glu Asp
 100 105 110
 Gln Glu Leu Val Leu Pro Val Ser His Tyr Lys Glu Asn Ser Ser Arg
 115 120 125
 Pro Glu Ile Thr Ser Ile Glu Ala Phe Leu Ser Val Thr Asp Tyr Gly
 130 135 140
 Ser Gly Gln Pro Asp Glu Thr Ala Leu Pro Val Leu Glu Thr Thr Asp
 145 150 155 160
 Ile Ser Asn Pro Tyr Ala Gly Ser Tyr Asn Ala Ser Phe Ala Leu Lys
 165 170 175

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Asn Asp Ser Ser Asp Asp Phe Lys Asn Leu Arg Val Gly Ile Val Cys
      180                               185                               190
Tyr Asn Glu Gln Thr Asp Ile Ile Gly Gly Gly Phe Lys Phe Pro Asn
      195                               200                               205
Leu Val Pro Ala Gly Gly Ser Ile Arg Met Asp Ala Ser Val Thr Val
      210                               215                               220
Ser Glu Met Pro Ala Ser Cys Lys Ala Tyr Leu Asn His
      225                               230                               235

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<210> 1567

<211> 3036

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(3013)

<223> RXA00054

<400> 1567

atgctgagat ccgctggggtg gcaccacacg aattggaatc ttggagtggtg gcacctgctg 60

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atatctctgc ggtgaaactt ctctgcgagc agcttgctta atg agc cca ttc gat      115
                Met Ser Pro Phe Asp
                1                               5

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tca aag ctt ggt cgc gat acc cat ttt gga ttc ctc gat aag acc act      163
Ser Lys Leu Gly Arg Asp Thr His Phe Gly Phe Leu Asp Lys Thr Thr
                10                               15                               20

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gct tcg caa caa ctg ctg aat oct tca ttg att tct aat gag gat ccg      211
Ala Ser Gln Gln Leu Leu Asn Pro Ser Leu Ile Ser Asn Glu Asp Pro
                25                               30                               35

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cac acc atg ttg cag gcg atc aag tta gag ctt cgt acc gca cag tct      259
His Thr Met Leu Gln Ala Ile Lys Leu Glu Leu Arg Thr Ala Gln Ser
                40                               45                               50

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ttt aca ttt tca gtc gct ttt att tcc agt cgc ggt atc gcg ttg ttg      307
Phe Thr Phe Ser Val Ala Phe Ile Ser Ser Arg Gly Ile Ala Leu Leu
                55                               60                               65

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aaa cag gca ttg ttg gac ttc aag ggt aaa gga cga att atc acg tcc      355
Lys Gln Ala Leu Leu Asp Phe Lys Gly Lys Gly Arg Ile Ile Thr Ser
                70                               75                               80                               85

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```

cgc tac ctg gat ttc aat gat cca acg atg ttt cgt gag ctt ctt act      403
Arg Tyr Leu Asp Phe Asn Asp Pro Thr Met Phe Arg Glu Leu Leu Thr
                90                               95                               100

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```

ttg gag aac gtg gaa gtc ctc ata cat caa ggc gat ggt ttc cac tcc      451
Leu Glu Asn Val Glu Val Leu Ile His Gln Gly Asp Gly Phe His Ser
                105                               110                               115

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aag ggc tac gtt ttc cat cac gac gtg gga atc acc gca gta gtg ggt      499
Lys Gly Tyr Val Phe His His Asp Val Gly Ile Thr Ala Val Val Gly
                120                               125                               130

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agt tcc aac ctc aca gat aat gct ctg ttg gta aac cgg gaa tgg aat 547
 Ser Ser Asn Leu Thr Asp Asn Ala Leu Leu Val Asn Arg Glu Trp Asn
 135 140 145

ctg aag ttc tct gcc agc aag aat ggc gac att gct ttt caa ctt gat 595
 Leu Lys Phe Ser Ala Ser Lys Asn Gly Asp Ile Ala Phe Gln Leu Asp
 150 155 160 165

gat gcg att aat cgc caa att gaa cga tcc acg cca ctg acg cct gaa 643
 Asp Ala Ile Asn Arg Gln Ile Glu Arg Ser Thr Pro Leu Thr Pro Glu
 170 175 180

tgg atc tca gag tat gag gca acc aga cgt gta cct gag cgt ttg gtg 691
 Trp Ile Ser Glu Tyr Glu Ala Thr Arg Arg Val Pro Glu Arg Leu Val
 185 190 195

tct cag aat att cct ctc gag gat caa agt aac gcc gga aca att gtt 739
 Ser Gln Asn Ile Pro Leu Glu Asp Gln Ser Asn Ala Gly Thr Ile Val
 200 205 210

cca aac gtc atg cag gaa gag gcc ctc gac gct cta ctt tct ttg acg 787
 Pro Asn Val Met Gln Glu Glu Ala Leu Asp Ala Leu Leu Ser Leu Thr
 215 220 225

gag aag gga gag aaa cgt ggt gtc att att tct gcg aca gga act ggc 835
 Glu Lys Gly Glu Lys Arg Gly Val Ile Ile Ser Ala Thr Gly Thr Gly
 230 235 240 245

aag act atc ctg gct gct cta gct aca aga atg ctc aag cct gaa cga 883
 Lys Thr Ile Leu Ala Ala Leu Ala Thr Arg Met Lys Pro Glu Arg
 250 255 260

gtt ttg ttt gtc gtg cac cgc gaa caa att ctg gat aag gcg cga tcc 931
 Val Leu Phe Val Val His Arg Glu Gln Ile Leu Asp Lys Ala Arg Ser
 265 270 275

gag ttc atc aaa gtt ctt gaa cgt ccc gct gtt gat ttc gga aaa atg 979
 Glu Phe Ile Lys Val Leu Glu Arg Pro Ala Val Asp Phe Gly Lys Met
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tct ggc tcg acc aag gag cta gat aag ccg ttt gtg ttt ggc acc atc 1027
 Ser Gly Ser Thr Lys Glu Leu Asp Lys Pro Phe Val Phe Gly Thr Ile
 295 300 305

caa acg ctg aca aag gaa gct aca ctt tcc cag atc tcc cct act gac 1075
 Gln Thr Leu Thr Lys Glu Ala Thr Leu Ser Gln Ile Ser Pro Thr Asp
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 Phe Asp Leu Val Ile Val Asp Glu Val His Arg Ala Gly Ala Glu Ser
 330 335 340

tat ttg gca ttg ctc aat cat ctg cag cca cag ttt tta ttg ggc ctg 1171
 Tyr Leu Ala Leu Leu Asn His Leu Gln Pro Gln Phe Leu Leu Gly Leu
 345 350 355

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 Thr Ala Thr Pro Glu Arg Thr Asp Gly Phe Asn Ile Tyr Glu Leu Phe
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Asp Phe Asn Val Pro Tyr Glu Ile Arg Leu Gln Ala Ala Leu Glu Ser	
375 380 385	
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Asn Met Leu Val Pro Phe His Tyr Tyr Gly Val Thr Asp Phe Thr Leu	
390 395 400 405	
gat tct gaa aca acg gtg act gat acc tcc aaa cta agt gcc ttg gtg	1363
Asp Ser Glu Thr Thr Val Thr Asp Thr Ser Lys Leu Ser Ala Leu Val	
410 415 420	
agc gaa gag aga gtc cat cac att ctg gag gcc ctc aaa act tat ggt	1411
Ser Glu Glu Arg Val His His Ile Leu Glu Ala Leu Lys Thr Tyr Gly	
425 430 435	
cat cca gaa aat gtt cgt gga ctg atc ttc tgt tcc aag act gaa gag	1459
His Pro Glu Asn Val Arg Gly Leu Ile Phe Cys Ser Lys Thr Glu Glu	
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Ala Glu Glu Leu Ser Lys Leu Leu Asp Gln Ser Leu Phe Asn Gly Ser	
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Leu Leu Lys Thr Lys Ala Leu Ser Ala Lys Asp Ser Ile Pro Tyr Arg	
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Glu Glu Val Val Ala Glu Leu Glu Ser Gly Asp Leu Asp Tyr Ile Leu	
490 495 500	
acg gtt gac atc ttc aat gaa ggc att gat att cct tcg gtg aat caa	1651
Thr Val Asp Ile Phe Asn Glu Gly Ile Asp Ile Pro Ser Val Asn Gln	
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Ile Val Met Ile Arg Ser Thr Gln Ser Ser Ile Val Phe Thr Gln Gln	
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Leu Gly Arg Gly Leu Arg Lys Ala Ala Gly Lys Asp His Leu Arg Val	
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Ile Asp Phe Ile Gly Asn Tyr Ala Asn Asn Tyr Leu Ile Pro Ile Ala	
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Leu Phe Gly Asp Asn Ser Arg Asn Lys Asn Ser Ile Arg Arg Arg Leu	
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Ile Glu Ser Asp Ile Asp Gly Thr Ile Ser Gly Val Ser Ser Val Asn	
585 590 595	
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Phe Asp Pro Ile Ala Gln Glu Arg Ile Phe Ala Ala Leu Lys Ala Ala	
600 605 610	
aag ttg gac tca aaa gca caa ttc aag cag gat att gtt cag ctt caa	1987

Lys	Leu	Asp	Ser	Lys	Ala	Gln	Phe	Lys	Gln	Asp	Ile	Val	Gln	Leu	Gln		
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gat	cga	ctc	aat	cat	gtg	cca	gca	ctg	tta	gac	ttc	gct	cgc	ttc	aat	2035	
Asp	Arg	Leu	Asn	His	Val	Pro	Ala	Leu	Leu	Asp	Phe	Ala	Arg	Phe	Asn		
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Thr	Val	Asp	Pro	Phe	Ile	Leu	Ala	Thr	His	Ser	Gly	Asn	Tyr	Trp	Ser		
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ctg	ctc	agt	tca	gtg	aag	ttt	gtc	gat	cac	gct	ccc	agc	gaa	tcg	gag	2131	
Leu	Leu	Ser	Ser	Val	Lys	Phe	Val	Asp	His	Ala	Pro	Ser	Asn	Ser	Glu		
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Lys	Tyr	Phe	Leu	Asp	Phe	Leu	Thr	Gly	Glu	Leu	Leu	Asn	Gly	Lys	Arg		
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cct	cat	gag	ctg	ttg	ctg	atc	cag	gaa	cta	atg	aaa	cag	cct	gaa	act	2227	
Pro	His	Glu	Leu	Leu	Leu	Ile	Gln	Glu	Leu	Met	Lys	Gln	Pro	Glu	Thr		
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Ser	Thr	Glu	Glu	Phe	Arg	Lys	Leu	Leu	Gln	Ala	Gln	Ser	Thr	Ser	Ser		
		710			715					720					725		
gat	gag	caa	aca	atc	aac	tcg	gtt	gaa	agg	att	ttg	agc	caa	gaa	ttc	2323	
Asp	Glu	Gln	Thr	Ile	Asn	Ser	Val	Glu	Arg	Ile	Leu	Ser	Gln	Glu	Phe		
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Tyr	Thr	Gly	Pro	Asn	Arg	Lys	Lys	Phe	Gly	Glu	His	Pro	Ile	Leu	Ser		
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gtt	caa	aac	cgc	acc	tac	tct	ttt	act	ccc	gag	ttc	cga	cgt	gcc	ctc	2419	
Val	Gln	Asn	Arg	Thr	Tyr	Ser	Phe	Thr	Pro	Glu	Phe	Arg	Arg	Ala	Leu		
		760					765					770					
gac	gaa	agc	cta	gaa	gtg	acg	gac	cga	gat	gag	gct	gct	cag	aat	ttt	2467	
Asp	Glu	Ser	Leu	Glu	Val	Thr	Asp	Arg	Asp	Glu	Ala	Ala	Gln	Asn	Phe		
		775				780					785						
aag	ttt	cac	gtc	caa	gac	atc	atc	gac	act	ggt	ttg	ttt	atc	gcc	aga	2515	
Lys	Phe	His	Val	Gln	Asp	Ile	Ile	Asp	Thr	Gly	Leu	Phe	Ile	Ala	Arg		
		790			795					800					805		
aac	aat	gga	ttt	tgg	caa	gga	aac	ctc	gtt	gtt	ggc	gag	aga	tac	tcc	2563	
Asn	Asn	Gly	Phe	Trp	Gln	Gly	Asn	Leu	Val	Val	Gly	Glu	Arg	Tyr	Ser		
				810					815					820			
cga	cga	gat	gtc	tgc	cga	att	ctc	aat	tgg	gaa	cga	aac	aac	gag	agc	2611	
Arg	Arg	Asp	Val	Cys	Arg	Ile	Leu	Asn	Trp	Glu	Arg	Asn	Asn	Glu	Ser		
				825				830						835			
acg	att	tat	gga	tac	aaa	gtg	gac	agt	tac	aca	tct	act	tgc	cca	atc	2659	
Thr	Ile	Tyr	Gly	Tyr	Lys	Val	Asp	Ser	Tyr	Thr	Ser	Thr	Cys	Pro	Ile		
			840				845					850					
ttt	gtg	acc	tat	cac	aag	gct	gat	gat	gta	tcc	gaa	agt	act	cgt	tac	2707	
Phe	Val	Thr	Tyr	His	Lys	Ala	Asp	Asp	Val	Ser	Glu	Ser	Thr	Arg	Tyr		

855	860	865	
cag gat gaa ctc gtc gat ccg aat acc ctt cat tgg tat tcc cgc ggc			2755
Gln Asp Glu Leu Val Asp Pro Asn Thr Leu His Trp Tyr Ser Arg Gly			
870	875	880	885
aac cga aag atc acg tct aat gag atc aag ccc atc gct gcg aat gct			2803
Asn Arg Lys Ile Thr Ser Asn Glu Ile Lys Pro Ile Ala Ala Asn Ala			
	890	895	900
gtg gat ctt cat gtt ttt gtg aag aag gac gat gcc gaa ggc ctt gat			2851
Val Asp Leu His Val Phe Val Lys Lys Asp Asp Ala Glu Gly Leu Asp			
	905	910	915
ttc ttc tac ctt ggt caa gcg cat tca gaa aac agc aaa cag tca tcg			2899
Phe Phe Tyr Leu Gly Gln Ala His Ser Glu Asn Ser Lys Gln Ser Ser			
	920	925	930
atg ccc gga aac aaa gga gtt gtg caa ccg gtg gtc aca atg gat cta			2947
Met Pro Gly Asn Lys Gly Val Val Gln Pro Val Val Thr Met Asp Leu			
	935	940	945
cag ttc gac aca ccc gtc gaa caa agc ctg ttt gag tac ctg agc aca			2995
Gln Phe Asp Thr Pro Val Glu Gln Ser Leu Phe Glu Tyr Leu Ser Thr			
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	20	25	30
Ser Asn Glu Asp Pro His Thr Met Leu Gln Ala Ile Lys Leu Glu Leu			
	35	40	45
Arg Thr Ala Gln Ser Phe Thr Phe Ser Val Ala Phe Ile Ser Ser Arg			
	50	55	60
Gly Ile Ala Leu Leu Lys Gln Ala Leu Leu Asp Phe Lys Gly Lys Gly			
	65	70	75
Arg Ile Ile Thr Ser Arg Tyr Leu Asp Phe Asn Asp Pro Thr Met Phe			
	85	90	95
Arg Glu Leu Leu Thr Leu Glu Asn Val Glu Val Leu Ile His Gln Gly			
	100	105	110
Asp Gly Phe His Ser Lys Gly Tyr Val Phe His His Asp Val Gly Ile			
	115	120	125

Thr Ala Val Val Gly Ser Ser Asn Leu Thr Asp Asn Ala Leu Leu Val
 130 135 140
 Asn Arg Glu Trp Asn Leu Lys Phe Ser Ala Ser Lys Asn Gly Asp Ile
 145 150 155 160
 Ala Phe Gln Leu Asp Asp Ala Ile Asn Arg Gln Ile Glu Arg Ser Thr
 165 170 175
 Pro Leu Thr Pro Glu Trp Ile Ser Glu Tyr Glu Ala Thr Arg Arg Val
 180 185 190
 Pro Glu Arg Leu Val Ser Gln Asn Ile Pro Leu Glu Asp Gln Ser Asn
 195 200 205
 Ala Gly Thr Ile Val Pro Asn Val Met Gln Glu Glu Ala Leu Asp Ala
 210 215 220
 Leu Leu Ser Leu Thr Glu Lys Gly Glu Lys Arg Gly Val Ile Ile Ser
 225 230 235 240
 Ala Thr Gly Thr Gly Lys Thr Ile Leu Ala Ala Leu Ala Thr Arg Met
 245 250 255
 Leu Lys Pro Glu Arg Val Leu Phe Val Val His Arg Glu Gln Ile Leu
 260 265 270
 Asp Lys Ala Arg Ser Glu Phe Ile Lys Val Leu Glu Arg Pro Ala Val
 275 280 285
 Asp Phe Gly Lys Met Ser Gly Ser Thr Lys Glu Leu Asp Lys Pro Phe
 290 295 300
 Val Phe Gly Thr Ile Gln Thr Leu Thr Lys Glu Ala Thr Leu Ser Gln
 305 310 315 320
 Ile Ser Pro Thr Asp Phe Asp Leu Val Ile Val Asp Glu Val His Arg
 325 330 335
 Ala Gly Ala Glu Ser Tyr Leu Ala Leu Leu Asn His Leu Gln Pro Gln
 340 345 350
 Phe Leu Leu Gly Leu Thr Ala Thr Pro Glu Arg Thr Asp Gly Phe Asn
 355 360 365
 Ile Tyr Glu Leu Phe Asp Phe Asn Val Pro Tyr Glu Ile Arg Leu Gln
 370 375 380
 Ala Ala Leu Glu Ser Asn Met Leu Val Pro Phe His Tyr Tyr Gly Val
 385 390 395 400
 Thr Asp Phe Thr Leu Asp Ser Glu Thr Thr Val Thr Asp Thr Ser Lys
 405 410 415
 Leu Ser Ala Leu Val Ser Glu Glu Arg Val His His Ile Leu Glu Ala
 420 425 430
 Leu Lys Thr Tyr Gly His Pro Glu Asn Val Arg Gly Leu Ile Phe Cys
 435 440 445
 Ser Lys Thr Glu Glu Ala Glu Glu Leu Ser Lys Leu Leu Asp Gln Ser

450					455					460					
Leu	Phe	Asn	Gly	Ser	Leu	Leu	Lys	Thr	Lys	Ala	Leu	Ser	Ala	Lys	Asp
465					470					475					480
Ser	Ile	Pro	Tyr	Arg	Glu	Glu	Val	Val	Ala	Glu	Leu	Glu	Ser	Gly	Asp
				485					490						495
Leu	Asp	Tyr	Ile	Leu	Thr	Val	Asp	Ile	Phe	Asn	Glu	Gly	Ile	Asp	Ile
			500					505					510		
Pro	Ser	Val	Asn	Gln	Ile	Val	Met	Ile	Arg	Ser	Thr	Gln	Ser	Ser	Ile
		515					520					525			
Val	Phe	Thr	Gln	Gln	Leu	Gly	Arg	Gly	Leu	Arg	Lys	Ala	Ala	Gly	Lys
		530				535					540				
Asp	His	Leu	Arg	Val	Ile	Asp	Phe	Ile	Gly	Asn	Tyr	Ala	Asn	Asn	Tyr
545						550					555				560
Leu	Ile	Pro	Ile	Ala	Leu	Phe	Gly	Asp	Asn	Ser	Arg	Asn	Lys	Asn	Ser
				565					570						575
Ile	Arg	Arg	Arg	Leu	Ile	Glu	Ser	Asp	Ile	Asp	Gly	Thr	Ile	Ser	Gly
				580				585					590		
Val	Ser	Ser	Val	Asn	Phe	Asp	Pro	Ile	Ala	Gln	Glu	Arg	Ile	Phe	Ala
				595					600				605		
Ala	Leu	Lys	Ala	Ala	Lys	Leu	Asp	Ser	Lys	Ala	Gln	Phe	Lys	Gln	Asp
				610			615					620			
Ile	Val	Gln	Leu	Gln	Asp	Arg	Leu	Asn	His	Val	Pro	Ala	Leu	Leu	Asp
625						630					635				640
Phe	Ala	Arg	Phe	Asn	Thr	Val	Asp	Pro	Phe	Ile	Leu	Ala	Thr	His	Ser
				645					650						655
Gly	Asn	Tyr	Trp	Ser	Leu	Leu	Ser	Ser	Val	Lys	Phe	Val	Asp	His	Ala
				660					665					670	
Pro	Ser	Glu	Ser	Glu	Lys	Tyr	Phe	Leu	Asp	Phe	Leu	Thr	Gly	Glu	Leu
				675				680					685		
Leu	Asn	Gly	Lys	Arg	Pro	His	Glu	Leu	Leu	Leu	Ile	Gln	Glu	Leu	Met
				690			695						700		
Lys	Gln	Pro	Glu	Thr	Ser	Thr	Glu	Glu	Phe	Arg	Lys	Leu	Leu	Gln	Ala
705						710					715				720
Gln	Ser	Thr	Ser	Ser	Asp	Glu	Gln	Thr	Ile	Asn	Ser	Val	Glu	Arg	Ile
				725					730						735
Leu	Ser	Gln	Glu	Phe	Tyr	Thr	Gly	Pro	Asn	Arg	Lys	Lys	Phe	Gly	Glu
				740				745						750	
His	Pro	Ile	Leu	Ser	Val	Gln	Asn	Arg	Thr	Tyr	Ser	Phe	Thr	Pro	Glu
				755				760					765		
Phe	Arg	Arg	Ala	Leu	Asp	Glu	Ser	Leu	Glu	Val	Thr	Asp	Arg	Asp	Glu
				770				775							780

Ala Ala Gln Asn Phe Lys Phe His Val Gln Asp Ile Ile Asp Thr Gly
785 790 795 800

Leu Phe Ile Ala Arg Asn Asn Gly Phe Trp Gln Gly Asn Leu Val Val
805 810 815

Gly Glu Arg Tyr Ser Arg Arg Asp Val Cys Arg Ile Leu Asn Trp Glu
820 825 830

Arg Asn Asn Glu Ser Thr Ile Tyr Gly Tyr Lys Val Asp Ser Tyr Thr
835 840 845

Ser Thr Cys Pro Ile Phe Val Thr Tyr His Lys Ala Asp Asp Val Ser
850 855 860

Glu Ser Thr Arg Tyr Gln Asp Glu Leu Val Asp Pro Asn Thr Leu His
865 870 875 880

Trp Tyr Ser Arg Gly Asn Arg Lys Ile Thr Ser Asn Glu Ile Lys Pro
885 890 895

Ile Ala Ala Asn Ala Val Asp Leu His Val Phe Val Lys Lys Asp Asp
900 905 910

Ala Glu Gly Leu Asp Phe Phe Tyr Leu Gly Gln Ala His Ser Glu Asn
915 920 925

Ser Lys Gln Ser Ser Met Pro Gly Asn Lys Gly Val Val Gln Pro Val
930 935 940

Val Thr Met Asp Leu Gln Phe Asp Thr Pro Val Glu Gln Ser Leu Phe
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<212> DNA

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gctcgtgtaa tctccgctta tctagctcaa aggaataactt atg aag ttc ttc ggg 115
Met Lys Phe Phe Gly
1 5

ttt tat cgt cct att gct tta att gct ggc att acc gtt tca gca tct 163
Phe Tyr Arg Pro Ile Ala Leu Ile Ala Gly Ile Thr Val Ser Ala Ser
10 15 20

att ctc aca tcc gta gct act gca gct gaa tct cca act agc ttt caa 211
Ile Leu Thr Ser Val Ala Thr Ala Ala Glu Ser Pro Thr Ser Phe Gln

25

30

35

gcg att aca cct gca ttc tct tca tca tcg gct cca gaa gca gac gca 259
 Ala Ile Thr Pro Ala Phe Ser Ser Ser Ala Pro Glu Ala Asp Ala
 40 45 50

gaa gca aac acc agt gaa gct acc gca gac ctg ctt tac gtg gca gaa 307
 Glu Ala Asn Thr Ser Glu Ala Thr Ala Asp Leu Leu Tyr Val Ala Glu
 55 60 65

aac caa cta ctt att aag ctt tct aac gcc gtc gtc gaa gat gtt aac 355
 Asn Gln Leu Leu Ile Lys Leu Ser Asn Ala Val Val Glu Asp Val Asn
 70 75 80 85

ggc gaa atc tta atg aaa gat aat aag ggc act ctt ctg gag aat ttg 403
 Gly Glu Ile Leu Met Lys Asp Asn Lys Gly Thr Leu Leu Asn Leu
 90 95 100

aca gct gaa ctt caa gcc caa cca ggc ttc tca atc gag aaa gtc gat 451
 Thr Ala Glu Leu Gln Ala Gln Pro Gly Phe Ser Ile Glu Lys Val Asp
 105 110 115

tcc cat act gct ttg ttg acc atg aat cca gat gag gtg cca gat tta 499
 Ser His Thr Thr Ala Leu Leu Thr Met Asn Pro Asp Glu Val Pro Asp Leu
 120 125 130

cag gac tgg cga tgc gga gtc ggc gct ttg tca ggc ggg gta gca ggt 547
 Gln Asp Trp Arg Cys Gly Val Gly Ala Leu Ser Gly Gly Val Ala Gly
 135 140 145

gtg gtg gca act ggt cta gct ctc gcc gct ttg gga gtt gcc aca ggt 595
 Val Val Ala Thr Gly Leu Ala Leu Ala Ala Leu Gly Val Ala Thr Gly
 150 155 160 165

ggc acg ggg ttt gct gtg ctt gca gca ggg gga ctt gct gga tat ggc 643
 Gly Thr Gly Phe Ala Val Leu Ala Ala Gly Gly Leu Ala Gly Tyr Gly
 170 175 180

act ggc gct gtc gcc aac tgc taaggagaaa taatgggaat tgt 687
 Thr Gly Ala Val Ala Asn Cys
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<210> 1570

<211> 188

<212> PRT

<213> Corynebacterium glutamicum

<400> 1570

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 20 25 30

Pro Thr Ser Phe Gln Ala Ile Thr Pro Ala Phe Ser Ser Ser Ser Ala
 35 40 45

Pro Glu Ala Asp Ala Glu Ala Asn Thr Ser Glu Ala Thr Ala Asp Leu
 50 55 60

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Leu Tyr Val Ala Glu Asn Gln Leu Leu Ile Lys Leu Ser Asn Ala Val
65              70              75              80

Val Glu Asp Val Asn Gly Glu Ile Leu Met Lys Asp Asn Lys Gly Thr
85              90              95

Leu Leu Glu Asn Leu Thr Ala Glu Leu Gln Ala Gln Pro Gly Phe Ser
100            105            110

Ile Glu Lys Val Asp Ser His Thr Ala Leu Leu Thr Met Asn Pro Asp
115            120            125

Glu Val Pro Asp Leu Gln Asp Trp Arg Cys Gly Val Gly Ala Leu Ser
130            135            140

Gly Gly Val Ala Gly Val Val Ala Thr Gly Leu Ala Leu Ala Ala Leu
145            150            155            160

Gly Val Ala Thr Gly Gly Thr Gly Phe Ala Val Leu Ala Ala Gly Gly
165            170            175

Leu Ala Gly Tyr Gly Thr Gly Ala Val Ala Asn Cys
180            185

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<211> 405

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(382)

<223> RXA00059

<400> 1571

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                                         Val Leu Thr Gly Ile
                                         1           5

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tta ctg gct atg gtc tct acc gcc cta cga atc cgc ttc gga tca ggg 163
Leu Leu Ala Met Val Ser Thr Ala Leu Arg Ile Arg Phe Gly Ser Gly
              10              15              20

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gta gct atc gct gca acc gtg ctg tgg aca gtt atc tca ata acc ttg 211
Val Ala Ile Ala Ala Thr Val Leu Trp Thr Val Ile Ser Ile Thr Leu
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ggc gga gat gtg cta gcc gag acc atg ctc tgg ctt gta gca gta cca 259
Gly Gly Asp Val Leu Ala Glu Thr Met Leu Trp Leu Val Ala Val Pro
              40              45              50

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tcc tgg cca gaa aca gcg gat act act acc cgc ttc ctt att gcg atg 307
Ser Trp Pro Glu Thr Ala Asp Thr Thr Thr Arg Phe Leu Ile Ala Met
              55              60              65

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cta ctg cag gca gtt ctt atc acc gcc agc act atc tgg gct atc cga 355
Leu Leu Gln Ala Val Leu Ile Thr Gly Ser Thr Ile Trp Ala Ile Arg
              70              75              80              85

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 Glu Ile Arg Asp Ser Glu Arg Arg Gly
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acg 405

<210> 1572

<211> 94

<212> PRT

<213> Corynebacterium glutamicum

<400> 1572

Val Leu Thr Gly Ile Leu Leu Ala Met Val Ser Thr Ala Leu Arg Ile
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Arg Phe Gly Ser Gly Val Ala Ile Ala Ala Thr Val Leu Trp Thr Val
 20 25 30

Ile Ser Ile Thr Leu Gly Gly Asp Val Leu Ala Glu Thr Met Leu Trp
 35 40 45

Leu Val Ala Val Pro Ser Trp Pro Glu Thr Ala Asp Thr Thr Thr Arg
 50 55 60

Phe Leu Ile Ala Met Leu Leu Gln Ala Val Leu Ile Thr Gly Ser Thr
 65 70 75 80

Ile Trp Ala Ile Arg Glu Ile Arg Asp Ser Glu Arg Arg Gly
 85 90

<210> 1573

<211> 396

<212> DNA

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<220>

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<222> (101)..(373)

<223> RXA00065

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gcattgcccc cggggacaga tcttgccgtg cgttaggaatt atg gcg aat ctt ccc 115
 Met Ala Asn Leu Pro
 1 5

caa gag ggt ttt tct gtg gtg cac gga att ttg gcg gat ccc cgc att 163
 Gln Glu Gly Phe Ser Val Val His Gly Ile Leu Ala Asp Pro Arg Ile
 10 15 20

tgg ggc ccg gag att ccg tat gtt cgt gaa gaa gca ggt caa gta aat 211
 Trp Gly Pro Glu Ile Pro Tyr Val Arg Glu Glu Ala Gly Gln Val Asn
 25 30 35

gtg gaa gca ccc gac gag gct ggc gat cta gcc cga ttg acg ttg cct 259
 Val Glu Ala Pro Asp Glu Ala Gly Asp Leu Ala Arg Leu Thr Leu Pro
 40 45 50

ctg cag ttg atc ctg ctc acg gag gaa gag ttt gcc atc gct ctc aac 307
 Leu Gln Leu Ile Leu Leu Thr Glu Glu Glu Phe Ala Ile Ala Leu Asn
 55 60 65

gag ggc agc gac gtc atg ttc gaa cga atg gcg gag caa gaa gtc gat 355
 Glu Gly Ser Asp Val Met Phe Glu Arg Met Ala Glu Gln Glu Val Asp
 70 75 80 85

ctt ctg gat ctg aaa cgt taagacggta ggctcaattc cgt 396
 Leu Leu Asp Leu Lys Arg
 90

<210> 1574

<211> 91

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1574

Met Ala Asn Leu Pro Gln Glu Gly Phe Ser Val Val His Gly Ile Leu
 1 5 10 15

Ala Asp Pro Arg Ile Trp Gly Pro Glu Ile Pro Tyr Val Arg Glu Glu
 20 25 30

Ala Gly Gln Val Asn Val Glu Ala Pro Asp Glu Ala Gly Asp Leu Ala
 35 40 45

Arg Leu Thr Leu Pro Leu Gln Leu Ile Leu Leu Thr Glu Glu Glu Phe
 50 55 60

Ala Ile Ala Leu Asn Glu Gly Ser Asp Val Met Phe Glu Arg Met Ala
 65 70 75 80

Glu Gln Glu Val Asp Leu Leu Asp Leu Lys Arg
 85 90

<210> 1575

<211> 705

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(682)

<223> RXA00068

<400> 1575
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atatagcacc ggcttaacag gccggtgcta ttctgttgcg atg act tcg aag gat 115
 Met Thr Ser Lys Asp
 1 5

ctg att gtg acc tcc tat acg tct tgg ggc aag cgt ttc aag aat gac 163
 Leu Ile Val Thr Ser Tyr Thr Ser Trp Gly Lys Arg Phe Lys Asn Asp
 10 15 20

ggg aag ctt ttt att aac cta ctt cgc agc acc act gat agt gct gat 211

Gly Lys Leu Phe Ile Asn Leu Leu Arg Ser Thr Thr Asp Ser Ala Asp
 25 30 35
 gaa aag gtt tta gcc act ttc ggt gaa gtt ccc agc aaa tca ttt gaa 259
 Glu Lys Val Leu Ala Thr Phe Gly Glu Val Pro Ser Lys Ser Phe Glu
 40 45 50
 acc acc gca acg gtt gat gag cag cag tgg gaa ctg tcc ttc agt att 307
 Thr Thr Ala Thr Val Asp Glu Gln Gln Trp Glu Leu Ser Phe Ser Ile
 55 60 65
 gat gga acg gca act gcc aag ctt cct gat ggt cgt gtg ttc agc gcg 355
 Asp Gly Thr Ala Thr Ala Lys Leu Pro Asp Gly Arg Val Phe Ser Ala
 70 75 80 85
 aat gca ggt gag aag acc ttt acc aag tcc aag cgg att gaa atc gac 403
 Asn Ala Gly Glu Lys Thr Phe Thr Lys Ser Lys Arg Ile Glu Ile Asp
 90 95 100
 atg gac ggc acc gcg atg gct gct gtt aat gaa gat aaa aac aat tgg 451
 Met Asp Gly Thr Ala Met Ala Ala Val Asn Glu Asp Lys Asn Asn Trp
 105 110 115
 att atc gac gat tct gaa gag aat aaa gtc gct cag ttt acc ggt atg 499
 Ile Ile Asp Asp Ser Glu Glu Asn Lys Val Ala Gln Phe Thr Gly Met
 120 125 130
 aac aac ggt gtg cgt cgc gcg att gtg gag ttt gag cct gac gta gaa 547
 Asn Asn Gly Val Arg Arg Ala Ile Val Glu Phe Glu Pro Asp Val Glu
 135 140 145
 gtc acc cag gag cag gaa att ttc ttg tgg gtt gct cgg aaa act 595
 Val Thr Gln Glu Gln Glu Ile Phe Leu Ser Trp Val Ala Arg Lys Thr
 150 155 160 165
 ctg gaa tcc cgc atg ttg ggc tcc agt tgg gga ctg act ctg ttt ttg 643
 Leu Glu Ser Arg Met Leu Gly Ser Ser Trp Gly Leu Thr Leu Phe Leu
 170 175 180
 atc att ttg acg cca atc att att ttc ctc act ttc agc taaaaggacc 692
 Ile Ile Leu Thr Pro Ile Ile Ile Phe Leu Thr Phe Ser
 185 190
 atgcaatggt aga 705

<210> 1576

<211> 194

<212> PRT

<213> Corynebacterium glutamicum

<400> 1576

Met Thr Ser Lys Asp Leu Ile Val Thr Ser Tyr Thr Ser Trp Gly Lys
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 Arg Phe Lys Asn Asp Gly Lys Leu Phe Ile Asn Leu Leu Arg Ser Thr
 20 25 30
 Thr Asp Ser Ala Asp Glu Lys Val Leu Ala Thr Phe Gly Glu Val Pro
 35 40 45

Ser Lys Ser Phe Glu Thr Thr Ala Thr Val Asp Glu Gln Gln Trp Glu
 50 55 60
 Leu Ser Phe Ser Ile Asp Gly Thr Ala Thr Ala Lys Leu Pro Asp Gly
 65 70 75 80
 Arg Val Phe Ser Ala Asn Ala Gly Glu Lys Thr Phe Thr Lys Ser Lys
 85 90 95
 Arg Ile Glu Ile Asp Met Asp Gly Thr Ala Met Ala Ala Val Asn Glu
 100 105 110
 Asp Lys Asn Asn Trp Ile Ile Asp Asp Ser Glu Glu Asn Lys Val Ala
 115 120 125
 Gln Phe Thr Gly Met Asn Asn Gly Val Arg Arg Ala Ile Val Glu Phe
 130 135 140
 Glu Pro Asp Val Glu Val Thr Gln Glu Gln Glu Ile Phe Leu Ser Trp
 145 150 155 160
 Val Ala Arg Lys Thr Leu Glu Ser Arg Met Leu Gly Ser Ser Trp Gly
 165 170 175
 Leu Thr Leu Phe Leu Ile Ile Leu Thr Pro Ile Ile Ile Phe Leu Thr
 180 185 190
 Phe Ser

<210> 1577
 <211> 345
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(322)
 <223> RXA00079

<400> 1577
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 ttgctttatc gaagccaaact cctccattt ggaatcccc atg ggc cta gtt cac 115
 Met Gly Leu Val His
 1 5
 acc gaa ttc acc cca ata aac acc tac gga atc ctc gac cac gta gtc 163
 Thr Glu Phe Thr Pro Ile Asn Thr Tyr Gly Ile Leu Asp His Val Val
 10 15 20
 acc ctc ccc gac gga act aaa gtg ctc aac cct ttc cga gtc atc ccc 211
 Thr Leu Pro Asp Gly Thr Lys Val Leu Asn Pro Phe Arg Val Ile Pro
 25 30 35
 cac gac acc ggc tcc gaa ctc att ttc acc gtc cgc ccc aac gaa aac 259
 His Asp Thr Gly Ser Glu Leu Ile Phe Thr Val Arg Pro Asn Glu Asn
 40 45 50
 ttc gaa gaa gat tgc caa gca gtc gca gca gac ctc gaa agg ctg gtc 307

Phe Glu Glu Asp Cys Gln Ala Val Ala Ala Asp Leu Glu Arg Leu Val
 55 60 65

gca ctg gcc gaa aaa tgacccacaca gaatggtctc taa 345
 Ala Leu Ala Glu Lys
 70

<210> 1578

<211> 74

<212> PRT

<213> Corynebacterium glutamicum

<400> 1578

Met Gly Leu Val His Thr Glu Phe Thr Pro Ile Asn Thr Tyr Gly Ile
 1 5 10 15

Leu Asp His Val Val Thr Leu Pro Asp Gly Thr Lys Val Leu Asn Pro
 20 25 30

Phe Arg Val Ile Pro His Asp Thr Gly Ser Glu Leu Ile Phe Thr Val
 35 40 45

Arg Pro Asn Glu Asn Phe Glu Glu Asp Cys Gln Ala Val Ala Ala Asp
 50 55 60

Leu Glu Arg Leu Val Ala Leu Ala Glu Lys
 65 70

<210> 1579

<211> 666

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> {80}..(643)

<223> RXA00082

<400> 1579

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tattcaagaa gatgggctagtg aac gtc act gaa caa tcc ggc gag tcc cat 112
 Val Asn Val Thr Glu Gln Ser Gly Glu Ser His
 1 5 10

atc gac atc ccg gaa tca cac cag ctg ccc gga cct cgt cca gtt ggc 160
 Ile Asp Ile 15 Pro Glu Ser His Gln Leu Pro Gly Pro Arg Pro Val Gly 25

gag ggc act ttc tgg gaa ggc cgc tcc ggg ctc atc atg ccc gca att 208
 Glu Gly Thr Phe Trp Glu Gly Arg Ser Gly Leu Ile Met Pro Ala Ile 30 35 40

ctt acg gca ttt agt ttg tat ttg ctc atc ggt gtt tta aac atg gat 256
 Leu Thr Ala Phe Ser Leu Tyr Leu Leu Ile Gly Val Leu Asn Met Asp 45 50 55

gtg ggc aat gca gca ttc cca gga cct cga ttc ttc cca aca atc ctc 304
 Val Gly Asn Ala Ala Phe Pro Gly Pro Arg Phe Phe Pro Thr Ile Leu

60	65	70	75	
ggc atc gcg ggt ttg ttg gtg gca gtg gca ttg acc att caa acc atc				352
Gly Ile Ala Gly Leu Leu Val Ala Val Ala Leu Thr Ile Gln Thr Ile	80	85	90	
aag tac ccc atg cat cca gaa aat gaa tct ggc cga agc tgg aaa ttc				400
Lys Tyr Pro Met His Pro Glu Asn Glu Ser Gly Arg Ser Trp Lys Phe	95	100	105	
cac tct gat tac gtc tca ctc gcg tgg gcg atc ggt ggc ttc ttc gcc				448
His Ser Asp Tyr Val Ser Leu Ala Trp Ala Ile Gly Gly Phe Phe Ala	110	115	120	
ttt gca gtc ttg ctt cca tat ctt ggc tgg gtc ctt gct ggc tcc ttg				496
Phe Ala Val Leu Leu Pro Tyr Leu Gly Trp Val Leu Ala Gly Ser Leu	125	130	135	
ttg ttc tgg aca atg acc agg gct ttc ggt tcc aaa cgc cca ggt ttc				544
Leu Phe Trp Thr Met Thr Arg Ala Phe Gly Ser Lys Arg Pro Gly Phe	140	145	150	155
gat gtt ctt gtt tcc ctc atg atg agc tcc gtg gtc tac ctc gca ttc				592
Asp Val Leu Val Ser Leu Met Met Ser Ser Val Val Tyr Leu Ala Phe	160	165	170	
gat gtg ggc ttg gga ctt aat ctt cct tcc gga ctt ttg ggt ggt ggc				640
Asp Val Gly Leu Gly Leu Asn Leu Pro Ser Gly Leu Leu Gly Gly Gly	175	180	185	
ttt taatggatat ttgtccctc ttg				666
Phe				
<210> 1580				
<211> 188				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 1580				
Val Asn Val Thr Glu Gln Ser Gly Glu Ser His Ile Asp Ile Pro Glu	1	5	10	15
Ser His Gln Leu Pro Gly Pro Arg Pro Val Gly Glu Gly Thr Phe Trp	20	25	30	
Glu Gly Arg Ser Gly Leu Ile Met Pro Ala Ile Leu Thr Ala Phe Ser	35	40	45	
Leu Tyr Leu Leu Ile Gly Val Leu Asn Met Asp Val Gly Asn Ala Ala	50	55	60	
Phe Pro Gly Pro Arg Phe Phe Pro Thr Ile Leu Gly Ile Ala Gly Leu	65	70	75	80
Leu Val Ala Val Ala Leu Thr Ile Gln Thr Ile Lys Tyr Pro Met His	85	90	95	
Pro Glu Asn Glu Ser Gly Arg Ser Trp Lys Phe His Ser Asp Tyr Val	100	105	110	

Ser Leu Ala Trp Ala Ile Gly Gly Phe Phe Ala Phe Ala Val Leu Leu
115 120 125

Pro Tyr Leu Gly Trp Val Leu Ala Gly Ser Leu Leu Phe Trp Thr Met
130 135 140

Thr Arg Ala Phe Gly Ser Lys Arg Pro Gly Phe Asp Val Leu Val Ser
145 150 155 160

Leu Met Met Ser Ser Val Val Tyr Leu Ala Phe Asp Val Gly Leu Gly
165 170 175

Leu Asn Leu Pro Ser Gly Leu Leu Gly Gly Gly Phe
180 185

<210> 1581

<211> 423

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(400)

<223> RXA00083

<400> 1581

gaagatacac ggggccacgg tgggggtggtg aacaagagca ggcacgaggc ctggtgata 60

cggattcgac caagaaaacg tacaccactc aggagcactc gtg ctt gcc ctt cca 115
Val Leu Ala Leu Pro
1 5

tcc tct atc atc gac ccc ctc tgg tgc cag ttc gcc gcg ctg atc cca 163
Ser Ser Ile Ile Asp Pro Leu Trp Cys Gln Phe Ala Ala Leu Ile Pro
10 15 20

ccc gtg acc gac acc cac cca ctt cgg tgc cac cgc cca cgc atc ccg 211
Pro Val Thr Asp Thr His Pro Leu Arg Cys His Arg Pro Arg Ile Pro
25 30 35

gac cgg atc atc ttc gac aag ctc atc cag gtc ctc gtc ctc gcc gcc 259
Asp Arg Ile Ile Phe Asp Lys Leu Ile Gln Val Leu Val Leu Gly Ala
40 45 50

tcc tat gcc aag atc gcc gac acg aca tgc tgg gcc acc acc ttg cgc 307
Ser Tyr Ala Lys Ile Ala Asp Thr Thr Cys Ser Ala Thr Thr Leu Arg
55 60 65

acc cgc cgg gac gag tgg atc acc gct gcc atc ttc gag cag ctg gaa 355
Thr Arg Arg Asp Glu Trp Ile Thr Ala Gly Ile Phe Glu Gln Leu Glu
70 75 80 85

cag atc tgt ttg gaa ttc tac gac cgt atc gtc gga ctc gat ctc 400
Gln Ile Cys Leu Glu Phe Tyr Asp Arg Ile Val Gly Leu Asp Leu
90 95 100

taagttcgga ttggtcgaa ttg 423

<210> 1582
 <211> 100
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1582
 Val Leu Ala Leu Pro Ser Ser Ile Ile Asp Pro Leu Trp Cys Gln Phe
 1 5 10 15
 Ala Ala Leu Ile Pro Pro Val Thr Asp Thr His Pro Leu Arg Cys His
 20 25 30
 Arg Pro Arg Ile Pro Asp Arg Ile Ile Phe Asp Lys Leu Ile Gln Val
 35 40 45
 Leu Val Leu Gly Ala Ser Tyr Ala Lys Ile Ala Asp Thr Thr Cys Ser
 50 55 60
 Ala Thr Thr Leu Arg Thr Arg Arg Asp Glu Trp Ile Thr Ala Gly Ile
 65 70 75 80
 Phe Glu Gln Leu Glu Gln Ile Cys Leu Glu Phe Tyr Asp Arg Ile Val
 85 90 95
 Gly Leu Asp Leu
 100

<210> 1583
 <211> 2346
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(2323)
 <223> RXA00093

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 gggcagaccg aacaatcatg cttagggatg gtgaaatcca gtg acc aca ctt cta 115
 Val Thr Thr Leu Leu
 1 5
 gca gca acc cgc ccc acc ctg cgc gat gcc ttt aaa cac cca tgg cga 163
 Ala Ala Thr Arg Pro Thr Leu Arg Asp Ala Phe Lys His Pro Trp Arg
 10 15 20
 tcg ctg gca gcc atc ttg ttg gtg gcc gta cgg atg ttc ctg gtg agt 211
 Ser Leu Ala Ala Ile Leu Leu Val Ala Val Pro Met Phe Leu Val Ser
 25 30 35
 ttc ttt ctt acc tat gat caa tca atc aac aat gca gct agc tat cct 259
 Phe Phe Leu Thr Tyr Asp Gln Ser Ile Asn Asn Ala Ala Ser Tyr Pro
 40 45 50
 ggt tcc cag gta caa gct cac tat gac gga gaa gga gcc tac caa ctc 307
 Gly Ser Gln Val Gln Ala His Tyr Asp Gly Glu Gly Ala Tyr Gln Leu
 55 60 65

ctc caa gaa aac ctt cca gaa gac ttc cac ctg gaa ctc ttt gcc aat	355
Leu Gln Glu Asn Leu Pro Glu Asp Phe His Leu Glu Leu Phe Ala Asn	
70 75 80 85	
ggt tat cca gaa gtc tcc ttc ggt gat gaa gaa gtc aat ttc ttt gtt	403
Gly Tyr Pro Glu Val Ser Phe Gly Asp Glu Glu Val Asn Phe Phe Val	
90 95 100	
gtg caa tca aca aac gta caa caa gcc tca ttt ccc gcc gat gca ctc	451
Val Gln Ser Thr Asn Val Gln Gln Ala Ser Phe Pro Ala Asp Ala Leu	
105 110 115	
gat gtt tta ggt gcc aca atc ggt gat acc gtg acc att cac ggc acc	499
Asp Val Leu Gly Ala Thr Ile Gly Asp Thr Val Thr Ile His Gly Thr	
120 125 130	
ccg gtg gaa gtt cag tcg att tct ccc aca aat atc tta ttg ccc gaa	547
Pro Val Glu Val Gln Ser Ile Ser Pro Thr Asn Ile Leu Leu Pro Glu	
135 140 145	
ggt act ctg ttt tct ctt gag aat ttc tcc gaa tca gaa act ttt tcc	595
Gly Thr Leu Phe Ser Leu Glu Asn Phe Ser Glu Ser Glu Thr Phe Ser	
150 155 160 165	
ggc acc tgg tac ttc ccc gga tcg aat ttc acc gaa gaa aac cga caa	643
Gly Thr Trp Tyr Phe Pro Gly Ser Asn Phe Thr Glu Glu Asn Arg Gln	
170 175 180	
gca cta gaa gca gtt ggc ttt gaa gtt aat gaa tat cgg cgc ggc ccc	691
Ala Leu Glu Ala Val Gly Phe Glu Val Asn Glu Tyr Arg Arg Gly Pro	
185 190 195	
ata tcc gtc gac cca aat ttg atc cca agc tac atc atg gga ttt tta	739
Ile Ser Val Asp Pro Asn Leu Ile Pro Ser Tyr Ile Met Gly Phe Leu	
200 205 210	
tcg acg aca att ctc gcc gtc gtt gca ctc atg ctg atc tca cca gta	787
Ser Thr Thr Ile Leu Ala Val Val Ala Leu Met Leu Ile Ser Pro Val	
215 220 225	
ttt aca att tcc gcc tca agg caa acc aga act ttc gca ctg ctc gcc	835
Phe Thr Ile Ser Ala Ser Arg Gln Thr Arg Thr Phe Ala Leu Leu Ala	
230 235 240 245	
tca cag ggt gcc aca cct aga cac att cgg tgg gca gtg ctt aca tat	883
Ser Gln Gly Ala Thr Pro Arg His Ile Arg Trp Ala Val Leu Thr Tyr	
250 255 260	
ggg ctc ttc gca ggt ctt gtt ggg gca tcc att ggt tta gtt ctg ggg	931
Gly Leu Phe Ala Gly Leu Val Gly Ala Ser Ile Gly Leu Val Leu Gly	
265 270 275	
caa ata ggc atc tac ggc tgg tgg aaa tac acc tat cct gaa ttc tcc	979
Gln Ile Gly Ile Tyr Gly Trp Trp Lys Tyr Thr Tyr Pro Glu Phe Ser	
280 285 290	
ctc acc acc ccc tgg cta gtt ctt gta ggt ttt tgg gcg ctg gca atc	1027
Leu Thr Thr Pro Trp Leu Val Leu Val Gly Phe Trp Ala Leu Ala Ile	
295 300 305	
atc gct tca acg att gct gca ttc tta ccg gca gtt ttt gtc agt aga	1075

Ile Ala Ser Thr Ile	Ala Ala Phe Leu Pro	Ala Val Phe Val Ser Arg	
310	315	320 325	
tca agc atc atc aac gga atc tac gga gga atc tcc gac aaa atc atc			1123
Ser Ser Ile Ile Asn Gly Ile Tyr Gly Gly Ile Ser Asp Lys Ile Ile			
	330 335	340	
cgg tgg agc cct cga atg ctc atc ggg cca atc gtc tta att gca gct			1171
Arg Trp Ser Pro Arg Met Leu Ile Gly Pro Ile Val Leu Ile Ala Ala			
	345 350	355	
gcg gta atc gcc ttg ttt atc ggt gac gga gag tgg gga gcc gtc gtc			1219
Ala Val Ile Ala Leu Phe Ile Gly Asp Gly Glu Trp Gly Gly Val Val			
	360 365	370	
aag caa tta tgc ttc ctg gca gcc gtc atc gcc ctg ccg gcc tca gtg			1267
Lys Gln Leu Cys Phe Leu Ala Ala Val Ile Ala Leu Pro Ala Ser Val			
	375 380	385	
cct gcg gtg ttg tgg gcg ctt ggg cgc ctg cct ggt ttg aca ttc aaa			1315
Pro Ala Val Leu Trp Ala Leu Gly Arg Leu Pro Gly Leu Thr Phe Lys			
	390 395	400 405	
cta gct acg cgc gat atg ctg cgc cga tca atg cac tcc att cct gcg			1363
Leu Ala Thr Arg Asp Met Leu Arg Arg Ser Met His Ser Ile Pro Ala			
	410 415	420	
att ggt gcg ctg gcg gca gtg att atg ctt ggt aca ttt atg caa aca			1411
Ile Gly Ala Leu Ala Ala Val Ile Met Leu Gly Thr Phe Met Gln Thr			
	425 430	435	
act gga ctt gca acc caa gcc agc gat aga gaa gct acc gcc tgc gtg			1459
Thr Gly Leu Ala Thr Gln Ala Ser Asp Arg Glu Ala Thr Ala Ser Val			
	440 445	450	
tat cct gag gcc gta ttc tta cgc ggt gac aca caa atc cct gga ctc			1507
Tyr Pro Glu Ala Val Phe Leu Arg Gly Asp Thr Gln Ile Pro Gly Leu			
	455 460	465	
atg ggg caa aaa atc gat gta tac ggt gat aac cat gcc ttt ggt atc			1555
Met Gly Gln Lys Ile Asp Val Tyr Gly Asp Asn His Gly Phe Gly Ile			
	470 475	480 485	
tat gaa cta gat gta gat ttt tac tgc gcc aac tat gtg ccc gca ctg			1603
Tyr Glu Leu Asp Val Asp Phe Tyr Ser Ala Asn Tyr Val Pro Ala Leu			
	490 495	500	
acc tca ttt ttt ggc gga cca gtt att gcc acg ccc aag att tta gac			1651
Thr Ser Phe Phe Gly Gly Pro Val Ile Ala Thr Pro Lys Ile Leu Asp			
	505 510	515	
atg ttc ggt gtc cac gaa caa gcc gac atc tac gcg cca tca acc tat			1699
Met Phe Gly Val His Glu Gln Ala Asp Ile Tyr Ala Pro Ser Thr Tyr			
	520 525	530	
aat tcc ggg ctg caa gaa tac gca ata tac ccc gcc gat gaa acc tac			1747
Asn Ser Gly Leu Gln Glu Tyr Ala Ile Tyr Pro Gly Asp Glu Thr Tyr			
	535 540	545	
atg cta gac acc gct gct gtt tta ccg ccg ctg tac tca cat gtt tta			1795
Met Leu Asp Thr Ala Ala Val Leu Pro Pro Leu Tyr Ser His Val Leu			

550	555	560	565	
tta agc cca gaa act ttt gaa gaa atc gga gga caa aca gaa ttc ttg	1843			
Leu Ser Pro Glu Thr Phe Glu Glu Ile Gly Gly Gln Thr Glu Phe Leu	570	575	580	
gga aca atc gtg ctt ccc caa gaa cta gat gac caa act gta caa gca	1891			
Gly Thr Ile Val Leu Pro Gln Glu Leu Asp Asp Gln Thr Val Gln Ala	585	590	595	
atc aat cgg tca aga gat gcg cat ttc agc cac gac ggc cat aat tct	1939			
Ile Asn Arg Ser Arg Asp Ala His Phe Ser His Asp Gly His Asn Ser	600	605	610	
tca ctt gct tcc agt gct goa cta act gcg gtg goa att gtg gtc gtt	1987			
Ser Leu Ala Ser Ser Ala Ala Leu Thr Ala Val Ala Ile Val Val Val	615	620	625	
tcc ctt gtg atc gtg ctg gct aat cgc aaa ctc caa cag cac gca ttg	2035			
Ser Leu Val Ile Val Leu Ala Asn Arg Lys Leu Gln Gln His Ala Leu	630	635	640	645
att gcc atc gga gca aca cct gga aca atc tac aaa gtc aat gcc tta	2083			
Ile Ala Ile Gly Ala Thr Pro Gly Thr Ile Tyr Lys Val Asn Ala Leu	650	655	660	
aat gca gcg ttg ctt gcc ctt gtc gga ggc atc atg ggc ctt gtc tcc	2131			
Asn Ala Ala Leu Leu Ala Leu Val Gly Gly Ile Met Gly Leu Val Ser	665	670	675	
gga tgg att gca gcg ctg ctg aca ggc acc act gat gaa att gtt gat	2179			
Gly Trp Ile Ala Ala Leu Leu Thr Gly Thr Thr Asp Glu Ile Val Asp	680	685	690	
gga gca att ttg aac tac ggc acg ctt gaa cac atg atg ctg ccg tgg	2227			
Gly Ala Ile Leu Asn Tyr Gly Thr Leu Glu His Met Met Leu Pro Trp	695	700	705	
cct ctg ttg gta agc ctc ctc gtt gtg gcg ccg ctg gtg tgc gcc gtg	2275			
Pro Leu Leu Val Ser Leu Leu Val Val Ala Pro Leu Val Cys Ala Val	710	715	720	725
att ggg gct ata gct tct cca tcg gga cgc cac caa gaa gca tca atc	2323			
Ile Gly Ala Ile Ala Ser Pro Ser Gly Arg His Gln Glu Ala Ser Ile	730	735	740	
taaccttgcc ggagaaaccg aaa	2346			
<210> 1584				
<211> 741				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 1584				
Val Thr Thr Leu Leu Ala Ala Thr Arg Pro Thr Leu Arg Asp Ala Phe	1	5	10	15
Lys His Pro Trp Arg Ser Leu Ala Ala Ile Leu Leu Val Ala Val Pro	20	25	30	

Met Phe Leu Val Ser Phe Phe Leu Thr Tyr Asp Gln Ser Ile Asn Asn
35 40 45

Ala Ala Ser Tyr Pro Gly Ser Gln Val Gln Ala His Tyr Asp Gly Glu
50 55 60

Gly Ala Tyr Gln Leu Leu Gln Glu Asn Leu Pro Glu Asp Phe His Leu
65 70 75 80

Glu Leu Phe Ala Asn Gly Tyr Pro Glu Val Ser Phe Gly Asp Glu Glu
85 90 95

Val Asn Phe Phe Val Val Gln Ser Thr Asn Val Gln Gln Ala Ser Phe
100 105 110

Pro Ala Asp Ala Leu Asp Val Leu Gly Ala Thr Ile Gly Asp Thr Val
115 120 125

Thr Ile His Gly Thr Pro Val Glu Val Gln Ser Ile Ser Pro Thr Asn
130 135 140

Ile Leu Leu Pro Glu Gly Thr Leu Phe Ser Leu Glu Asn Phe Ser Glu
145 150 155 160

Ser Glu Thr Phe Ser Gly Thr Trp Tyr Phe Pro Gly Ser Asn Phe Thr
165 170 175

Glu Glu Asn Arg Gln Ala Leu Glu Ala Val Gly Phe Glu Val Asn Glu
180 185 190

Tyr Arg Arg Gly Pro Ile Ser Val Asp Pro Asn Leu Ile Pro Ser Tyr
195 200 205

Ile Met Gly Phe Leu Ser Thr Thr Ile Leu Ala Val Val Ala Leu Met
210 215 220

Leu Ile Ser Pro Val Phe Thr Thr Ile Ser Ala Ser Arg Gln Thr Arg Thr
225 230 235 240

Phe Ala Leu Leu Ala Ser Gln Gly Ala Thr Pro Arg His Ile Arg Trp
245 250 255

Ala Val Leu Thr Tyr Gly Leu Phe Ala Gly Leu Val Gly Ala Ser Ile
260 265 270

Gly Leu Val Leu Gly Gln Ile Gly Ile Tyr Gly Trp Trp Lys Tyr Thr
275 280 285

Tyr Pro Glu Phe Ser Leu Thr Thr Pro Trp Leu Val Leu Val Gly Phe
290 295 300

Trp Ala Leu Ala Ile Ile Ala Ser Thr Ile Ala Ala Phe Leu Pro Ala
305 310 315 320

Val Phe Val Ser Arg Ser Ser Ile Ile Asn Gly Ile Tyr Gly Gly Ile
325 330 335

Ser Asp Lys Ile Ile Arg Trp Ser Pro Arg Met Leu Ile Gly Pro Ile
340 345 350

Val Leu Ile Ala Ala Ala Val Ile Ala Leu Phe Ile Gly Asp Gly Glu

355		360		365
Trp Gly Gly Val Val Lys Gln	Leu Cys Phe Leu Ala Ala Val Ile Ala			
370	375		380	
Leu Pro Ala Ser Val Pro Ala Val Leu Trp Ala Leu Gly Arg Leu Pro				
385	390		395	400
Gly Leu Thr Phe Lys Leu Ala Thr Arg Asp Met Leu Arg Arg Ser Met				
	405		410	415
His Ser Ile Pro Ala Ile Gly Ala Leu Ala Ala Val Ile Met Leu Gly				
	420		425	430
Thr Phe Met Gln Thr Thr Gly Leu Ala Thr Gln Ala Ser Asp Arg Glu				
	435		440	445
Ala Thr Ala Ser Val Tyr Pro Glu Ala Val Phe Leu Arg Gly Asp Thr				
	450		455	460
Gln Ile Pro Gly Leu Met Gly Gln Lys Ile Asp Val Tyr Gly Asp Asn				
	465		470	475
His Gly Phe Gly Ile Tyr Glu Leu Asp Val Asp Phe Tyr Ser Ala Asn				
	485		490	495
Tyr Val Pro Ala Leu Thr Ser Phe Phe Gly Gly Pro Val Ile Ala Thr				
	500		505	510
Pro Lys Ile Leu Asp Met Phe Gly Val His Glu Gln Ala Asp Ile Tyr				
	515		520	525
Ala Pro Ser Thr Tyr Asn Ser Gly Leu Gln Glu Tyr Ala Ile Tyr Pro				
	530		535	540
Gly Asp Glu Thr Tyr Met Leu Asp Thr Ala Ala Val Leu Pro Pro Leu				
	545		550	555
Tyr Ser His Val Leu Leu Ser Pro Glu Thr Phe Glu Glu Ile Gly Gly				
	565		570	575
Gln Thr Glu Phe Leu Gly Thr Ile Val Leu Pro Gln Glu Leu Asp Asp				
	580		585	590
Gln Thr Val Gln Ala Ile Asn Arg Ser Arg Asp Ala His Phe Ser His				
	595		600	605
Asp Gly His Asn Ser Ser Leu Ala Ser Ser Ala Ala Leu Thr Ala Val				
	610		615	620
Ala Ile Val Val Val Ser Leu Val Ile Val Leu Ala Asn Arg Lys Leu				
	625		630	635
Gln Gln His Ala Leu Ile Ala Ile Gly Ala Thr Pro Gly Thr Ile Tyr				
	645		650	655
Lys Val Asn Ala Leu Asn Ala Ala Leu Leu Val Gly Gly Ile				
	660		665	670
Met Gly Leu Val Ser Gly Trp Ile Ala Ala Leu Leu Thr Gly Thr Thr				
	675		680	685

Asp Glu Ile Val Asp Gly Ala Ile Leu Asn Tyr Gly Thr Leu Glu His
690 695 700

Met Met Leu Pro Trp Pro Leu Leu Val Ser Leu Leu Val Val Ala Pro
705 710 715 720

Leu Val Cys Ala Val Ile Gly Ala Ile Ala Ser Pro Ser Gly Arg His
725 730 735

Gln Glu Ala Ser Ile
740

<210> 1585

<211> 531

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(508)

<223> RXA00101

<400> 1585

taaaccgtgc aggagatgcc gaaccccaat cgtgaaagcc gagtggggg agcgataat 60

ctgggtgtgt ccgcgctgcc aaccgctaaa ctcgtgaagc atg aga cta ata ctc 115
Met Arg Leu Ile Leu
1 5

aac ctg att tgg tta ttc ttc ggt ggc att tgg ctc gcg ttg gga tac 163
Asn Leu Ile Trp Leu Phe Phe Gly Gly Ile Trp Leu Ala Leu Gly Tyr
10 15 20

gta ttc ttc gga atc atc gca tgt atc ttc atc gtg acg att ccc gcc 211
Val Phe Phe Gly Ile Ile Ala Cys Ile Phe Ile Val Thr Ile Pro Ala
25 30 35

ggt atc gca agc ttc cgc atg gct aac tac gcg ctg tgg ccg ttt ggt 259
Gly Ile Ala Ser Phe Arg Met Ala Asn Tyr Ala Leu Trp Pro Phe Gly
40 45 50

agg acg gtt gtt cgt aat cct aaa gcc gga ggg ttt tct gcc ctg agc 307
Arg Thr Val Val Arg Asn Pro Lys Ala Gly Gly Phe Ser Ala Leu Ser
55 60 65

aac gga ctg tgg ttt atc att gct gga ctg tgg ctg gcg atc ggg cac 355
Asn Gly Leu Trp Phe Ile Ile Ala Gly Leu Trp Leu Ala Ile Gly His
70 75 80 85

ctc acc acc gcg gct gcc cag gcg atc acc atc atc gga att cca ctg 403
Leu Thr Thr Ala Ala Ala Gln Ala Ile Thr Ile Ile Gly Ile Pro Leu
90 95 100

gcg atc gca aac atc cga atg atc ccc gtg acg tgt ttc ccg ttc ggc 451
Ala Ile Ala Asn Ile Arg Met Ile Pro Val Thr Cys Phe Pro Phe Gly
105 110 115

aaa gaa atc tat gac agc aac cgc att ccc ttc ggc tac gaa ccg atg 499
Lys Glu Ile Tyr Asp Ser Asn Arg Ile Pro Phe Gly Tyr Glu Pro Met

123456789101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100101102103104105106107108109110111112113114115116117118119120121122123124125126127128129130131132133134135136137138139140141142143144145146147148149150151152153154155156157158159160161162163164165166167168169170171172173174175176177178179180181182183184185186187188189190191192193194195196197198199200

120 125 130
 gtt aag ttt taattcggcg acggactaaa cca 531
 Val Lys Phe
 135

<210> 1586
 <211> 136
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1586
 Met Arg Leu Ile Leu Asn Leu Ile Trp Leu Phe Phe Gly Gly Ile Trp
 1 5 10 15

Leu Ala Leu Gly Tyr Val Phe Phe Gly Ile Ile Ala Cys Ile Phe Ile
 20 25 30

Val Thr Ile Pro Ala Gly Ile Ala Ser Phe Arg Met Ala Asn Tyr Ala
 35 40 45

Leu Trp Pro Phe Gly Arg Thr Val Val Arg Asn Pro Lys Ala Gly Gly
 50 55 60

Phe Ser Ala Leu Ser Asn Gly Leu Trp Phe Ile Ala Gly Leu Trp
 65 70 75 80

Leu Ala Ile Gly His Leu Thr Thr Ala Ala Ala Gln Ala Ile Thr Ile
 85 90 95

Ile Gly Ile Pro Leu Ala Ile Ala Asn Ile Arg Met Ile Pro Val Thr
 100 105 110

Cys Phe Pro Phe Gly Lys Glu Ile Tyr Asp Ser Asn Arg Ile Pro Phe
 115 120 125

Gly Tyr Glu Pro Met Val Lys Phe
 130 135

<210> 1587
 <211> 643
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(643)
 <223> RXA00108

<400> 1587
 gaattgggtt ttgagcatcg tggcgggtgct tgttgttgca agtgccatcg tcatgatgat 60
 tgcaagaagt cgtaaccaga aataagaggg tttattcacc atg aag aag ttt ttt 115
 Met Lys Lys Phe Phe
 1 5

gtc gca ggt gct gta ctg agc agt gcg ttg gtt atg gcg gcg tgt tcg 163
 Val Ala Gly Ala Val Leu Ser Ser Ala Leu Val Met Ala Ala Cys Ser
 10 15 20

cct gct aat caa agt gat tcc acc tcc acg agc gtg gag act act tcc 211
 Pro Ala Asn Gln Ser Asp Ser Thr Ser Thr Ser Val Glu Thr Thr Ser
 25 30 35
 tcc agc agc acg cag gta agc gat gct gtg atc acc acg gaa aac gct 259
 Ser Ser Ser Thr Gln Val Ser Asp Ala Val Ile Thr Thr Glu Asn Ala
 40 45 50
 gtt gtt cgt gcg tct gtg gag gac agc gac atg acg gca gtg ttc gct 307
 Val Val Arg Ala Ser Val Glu Asp Ser Asp Met Thr Ala Val Phe Ala
 55 60 65
 acg ttg gtg aac aat tct gat gat gag atc aac gtt tct ggc ttt act 355
 Thr Leu Val Asn Asn Ser Asp Asp Glu Ile Asn Val Ser Gly Phe Thr
 70 75 80 85
 gct gat gtt gat gct gcc agc ttt gag gtc cat gag gtt gtt gat ggc 403
 Ala Asp Val Asp Ala Ala Ser Phe Glu Val His Glu Val Val Asp Gly
 90 95 100
 gtc atg cag gaa aag cca ggt ggt ttt gtg atc cct gca ggg gag agc 451
 Val Met Gln Glu Lys Pro Gly Gly Phe Val Ile Pro Ala Gly Glu Ser
 105 110 115
 atc gag ctg gca cca ggt ggc gat cat ttg atg atc atg ggg ctt gcg 499
 Ile Glu Leu Ala Pro Gly Gly Asp His Leu Met Ile Met Gly Leu Ala
 120 125 130
 aac cca atc gag gct ggc gat gaa gtg acg gtc act ctt gaa ttg gct 547
 Asn Pro Ile Glu Ala Gly Asp Glu Val Thr Val Thr Leu Glu Leu Ala
 135 140 145
 gat ggt tct gaa gtt aag ctt gat ccg atc ccg gcg cgc acc att gct 595
 Asp Gly Ser Glu Val Lys Leu Asp Pro Ile Pro Ala Arg Thr Ile Ala
 150 155 160 165
 gct ggt gat gag gat tat ggc gat ctg gga act gaa ggc cac gag ggc 643
 Ala Gly Asp Glu Asp Tyr Gly Asp Leu Gly Thr Glu Gly His Glu Gly
 170 175 180

<210> 1588

<211> 181

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1588

Met Lys Lys Phe Phe Val Ala Gly Ala Val Leu Ser Ser Ala Leu Val
 1 5 10 15
 Met Ala Ala Cys Ser Pro Ala Asn Gln Ser Asp Ser Thr Ser Thr Ser
 20 25 30
 Val Glu Thr Thr Ser Ser Ser Thr Thr Gln Val Ser Asp Ala Val Ile
 35 40 45
 Thr Thr Glu Asn Ala Val Val Arg Ala Ser Val Glu Asp Ser Asp Met
 50 55 60
 Thr Ala Val Phe Ala Thr Leu Val Asn Asn Ser Asp Asp Glu Ile Asn

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65              70              75              80
Val Ser Gly Phe Thr Ala Asp Val Asp Ala Ala Ser Phe Glu Val His
      85              90
Glu Val Val Asp Gly Val Met Gln Glu Lys Pro Gly Gly Phe Val Ile
      100              105              110
Pro Ala Gly Glu Ser Ile Glu Leu Ala Pro Gly Gly Asp His Leu Met
      115              120              125
Ile Met Gly Leu Ala Asn Pro Ile Glu Ala Gly Asp Glu Val Thr Val
      130              135              140
Thr Leu Glu Leu Ala Asp Gly Ser Glu Val Lys Leu Asp Pro Ile Pro
      145              150              155              160
Ala Arg Thr Ile Ala Ala Gly Asp Glu Asp Tyr Gly Asp Leu Gly Thr
      165              170              175
Glu Gly His Glu Gly
      180

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<210> 1589
<211> 672
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(649)
<223> RXA00110

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<400> 1589
atatcgaatg tccagtcacg ctaaaacttca cccaagatga gatttcgtgg caccgattggg 60

aataacgaac gctaatttta aacactggag gagcttcac gtg agc aac aaa gac 115
Val Ser Asn Lys Asp
1 5

ggc ctt ttt act gac ggt aac agc acg ttt gca cct aag gtg gat tca 163
Gly Leu Phe Thr Asp Gly Asn Ser Thr Phe Ala Pro Lys Val Asp Ser
10 15 20

att ccc ctc agc gat gtg gat acc agc gtt agc ggt gaa gcc tcc atc 211
Ile Pro Leu Ser Asp Val Asp Thr Ser Val Ser Gly Glu Ala Ser Ile
25 30 35

ggc acg ctg atc tcc aac gca acc tcc caa atg tcc agc ctt ttc cgc 259
Gly Thr Leu Ile Ser Asn Ala Thr Ser Gln Met Ser Ser Leu Phe Arg
40 45 50

gca gaa gtt gag ctg gcg aag act gaa ctc gca ggc gaa gcc aag aaa 307
Ala Glu Val Glu Leu Ala Lys Thr Glu Leu Ala Gly Glu Ala Lys Lys
55 60 65

gct gcc atc ggc ggc ggc gca ttc agc gtt gct ggc gta atc gca ctg 355
Ala Ala Ile Gly Gly Gly Ala Phe Ser Val Ala Gly Val Ile Ala Leu
70 75 80 85

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tac agc tcc ttc ttc ttt ttc ttc ttc gtc gca gca ctg ctg agc gag 403
 Tyr Ser Ser Phe Phe Phe Phe Phe Phe Val Ala Ala Leu Leu Ser Glu
 90 95 100

tgg att aag cct tgg gca gca ttc ctc atc gtg ttc ctc ttc atg ctg 451
 Trp Ile Lys Pro Trp Ala Ala Phe Leu Ile Val Phe Leu Phe Met Leu
 105 110 115

gtc atc gcc gca gct ctc gca ctg ttc gcc tgg cgc aag gtg aag aag 499
 Val Ile Ala Ala Ala Leu Ala Leu Phe Gly Trp Arg Lys Val Lys Lys
 120 125 130

atg gcc gct ccg aag aac acc atc caa tcg gtc aac caa ctg aag aac 547
 Met Gly Ala Pro Lys Asn Thr Ile Gln Ser Val Asn Gln Leu Lys Asn
 135 140 145

ctg gtc cca ggt cag gca tcc gag aag ctg gag aag gcc aac aag cgt 595
 Leu Val Pro Gly Gln Ala Ser Glu Lys Leu Glu Lys Ala Asn Lys Arg
 150 155 160 165

gcc ctc tac acc tcc gcg tcc ttc cac agc ccc gcc gcc atc act gcc 643
 Gly Leu Tyr Thr Ser Ala Ser Phe His Ser Pro Gly Ala Ile Thr Gly
 170 175 180

gac cac taaaaaagga gacttcgatg gcc 672
 Asp His

<210> 1590
 <211> 183
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1590
 Val Ser Asn Lys Asp Gly Leu Phe Thr Asp Gly Asn Ser Thr Phe Ala
 1 5 10 15
 Pro Lys Val Asp Ser Ile Pro Leu Ser Asp Val Asp Thr Ser Val Ser
 20 25 30
 Gly Glu Ala Ser Ile Gly Thr Leu Ile Ser Asn Ala Thr Ser Gln Met
 35 40 45
 Ser Ser Leu Phe Arg Ala Glu Val Glu Leu Ala Lys Thr Glu Leu Ala
 50 55 60
 Gly Glu Ala Lys Lys Ala Ala Ile Gly Gly Gly Ala Phe Ser Val Ala
 65 70 75 80
 Gly Val Ile Ala Leu Tyr Ser Ser Phe Phe Phe Phe Phe Val Ala
 85 90 95
 Ala Leu Leu Ser Glu Trp Ile Lys Pro Trp Ala Ala Phe Leu Ile Val
 100 105 110
 Phe Leu Phe Met Leu Val Ile Ala Ala Ala Leu Ala Leu Phe Gly Trp
 115 120 125
 Arg Lys Val Lys Lys Met Gly Ala Pro Lys Asn Thr Ile Gln Ser Val
 130 135 140

Asn Gln Leu Lys Asn Leu Val Pro Gly Gln Ala Ser Glu Lys Leu Glu
145 150 155 160

Lys Ala Asn Lys Arg Gly Leu Tyr Thr Ser Ala Ser Phe His Ser Pro
165 170 175

Gly Ala Ile Thr Gly Asp His
180

<210> 1591

<211> 714

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(691)

<223> RXA00117

<400> 1591

gttgatccca cagtataccc ccacccctat cttgaatacc cccaggggta tatggcacac 60

ttggaatcgc ccataccttt gagattgaaa aggacaaggt atg act tcc gct caa 115
Met Thr Ser Ala Gln
1 5

cgc att act tcc gta gat gca cag act cta aaa tcg tgg atc gat aag 163
Pro Ile Thr Ser Val Asp Ala Gln Thr Leu Lys Ser Trp Ile Asp Lys
10 15 20

cat gaa gga ctc acc gtc att gac gtc cgc act gca cat gag ttt tca 211
His Glu Gly Leu Thr Val Ile Asp Val Arg Thr Ala His Glu Phe Ser
25 30 35

aat ttg cac att aaa ggc tct tac aac gtg cct cta act aca ctt gct 259
Asn Leu His Ile Lys Gly Ser Tyr Asn Val Pro Leu Thr Thr Leu Ala
40 45 50

gag cat tcc gaa gag att tcc tct cgt gtt gga gaa cat gtt gtt ttg 307
Glu His Ser Glu Glu Ile Ser Ser Arg Val Gly Glu His Val Val Leu
55 60 65

gtg tgt caa tcc ggc att cga gca ggt cag gca caa caa aag ctg gca 355
Val Cys Gln Ser Gly Ile Arg Ala Gly Gln Ala Gln Gln Lys Leu Ala
70 75 80 85

cct ttg gga att tcc acc gtg gct gtt ttg gag ggt ggc atc aat agt 403
Pro Leu Gly Ile Ser Thr Val Ala Val Leu Glu Gly Gly Ile Asn Ser
90 95 100

ttt gct aag gct gac ggt gat gtg gtc cgc gga acc cag gtg tgg gat 451
Phe Ala Lys Ala Asp Gly Asp Val Val Arg Gly Thr Gln Val Trp Asp
105 110 115

atc gaa cgt cag gtg cgt ttt gcc gct gga tca ttg gtg ctc gca ggg 499
Ile Glu Arg Gln Val Arg Phe Ala Ala Gly Ser Leu Val Leu Ala Gly
120 125 130

ctt gcg gga ggt aaa ttc ctt tca cca aaa gtt cgc acc ctg tcg gga 547

Leu Ala Gly Gly Lys Phe Leu Ser Pro Lys Val Arg Thr Leu Ser Gly
 135 140 145
 att att ggt gcg ggt ctg aca ttt tct ggc gtt tcc aac acc tgt gcc 595
 Ile Ile Gly Ala Gly Leu Thr Phe Ser Gly Val Ser Asn Thr Cys Ala
 150 155 160 165
 atg ggc aaa gct ctg tcc gcc ttg ccg tgg aat aaa act aag cca gtt 643
 Met Gly Lys Ala Leu Ser Ala Leu Pro Trp Asn Lys Thr Lys Pro Val
 170 175 180
 cct acc gaa acc gag aca ttg agc aag ctt cca agc cct aag gag aac 691
 Pro Thr Glu Thr Glu Thr Leu Ser Lys Leu Pro Ser Pro Lys Glu Asn
 185 190 195
 taaatgtcta tcaccattac tga 714

<210> 1592

<211> 197

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1592

Met Thr Ser Ala Gln Pro Ile Thr Ser Val Asp Ala Gln Thr Leu Lys
 1 5 10 15
 Ser Trp Ile Asp Lys His Glu Gly Leu Thr Val Ile Asp Val Arg Thr
 20 25 30
 Ala His Glu Phe Ser Asn Leu His Ile Lys Gly Ser Tyr Asn Val Pro
 35 40 45
 Leu Thr Thr Leu Ala Glu His Ser Glu Glu Ile Ser Ser Arg Val Gly
 50 55 60
 Glu His Val Val Leu Val Cys Gln Ser Gly Ile Arg Ala Gly Gln Ala
 65 70 75 80
 Gln Gln Lys Leu Ala Pro Leu Gly Ile Ser Thr Val Ala Val Leu Glu
 85 90 95
 Gly Gly Ile Asn Ser Phe Ala Lys Ala Asp Gly Asp Val Val Arg Gly
 100 105 110
 Thr Gln Val Trp Asp Ile Glu Arg Gln Val Arg Phe Ala Ala Gly Ser
 115 120 125
 Leu Val Leu Ala Gly Leu Ala Gly Gly Lys Phe Leu Ser Pro Lys Val
 130 135 140
 Arg Thr Leu Ser Gly Ile Ile Gly Ala Gly Leu Thr Phe Ser Gly Val
 145 150 155 160
 Ser Asn Thr Cys Ala Met Gly Lys Ala Leu Ser Ala Leu Pro Trp Asn
 165 170 175
 Lys Thr Lys Pro Val Pro Thr Glu Thr Glu Thr Leu Ser Lys Leu Pro
 180 185 190
 Ser Pro Lys Glu Asn

195

<210> 1593
 <211> 378
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(355)
 <223> RXA00118

<400> 1593
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 actgtgggat caacgttcca gggcaacaaa aggagaaaaa atg caa ctc aat cct 115
 Met Gln Leu Asn Pro
 1 5
 gat gag atc acc cca gtg ctc aac cga ctc aag cgc gcc caa ggt caa 163
 Asp Glu Ile Thr Pro Val Leu Asn Arg Leu Lys Arg Ala Gln Gly Gln
 10 15 20
 ctc acc gga gta atc cga atg ctt gat gaa ggc gaa gac tgt aaa gcc 211
 Leu Thr Gly Val Ile Arg Met Leu Asp Glu Gly Glu Asp Cys Lys Ala
 25 30 35
 gta gtc acc caa ctt gcc gca gtc aca aaa gcg ctg gac agg gca gcc 259
 Val Val Thr Gln Leu Ala Ala Val Thr Lys Ala Leu Asp Arg Ala Gly
 40 45 50
 ttc gcc atc att gcc aca ggt ttg gaa cag tgc ctc acc aac cct gat 307
 Phe Ala Ile Ile Ala Thr Gly Leu Glu Gln Cys Leu Thr Asn Pro Asp
 55 60 65
 ggc gac atg gac aaa aag gaa cta gaa aaa ctg ttc ctg tcg ctg gct 355
 Gly Asp Met Asp Lys Lys Glu Leu Glu Lys Leu Phe Leu Ser Leu Ala
 70 75 80 85
 taactatggc ctagttcagg gcg 378

<210> 1594
 <211> 85
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 1594
 Met Gln Leu Asn Pro Asp Glu Ile Thr Pro Val Leu Asn Arg Leu Lys
 1 5 10 15
 Arg Ala Gln Gly Gln Leu Thr Gly Val Ile Arg Met Leu Asp Glu Gly
 20 25 30
 Glu Asp Cys Lys Ala Val Val Thr Gln Leu Ala Ala Val Thr Lys Ala
 35 40 45
 Leu Asp Arg Ala Gly Phe Ala Ile Ile Ala Thr Gly Leu Glu Gln Cys
 50 55 60

Leu Thr Asn Pro Asp Gly Asp Met Asp Lys Lys Glu Leu Glu Lys Leu
65 70 75 80

Phe Leu Ser Leu Ala
85

<210> 1595

<211> 882

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(859)

<223> RXA00119

<400> 1595

actaatgaga actgtttttc aattggtgca ggatttccac aaggaagcta ggggagaggg 60

gcttccaatc aagtggggtc catgcgtgg agaatttggc atg ctg gag ttt cct 115
Met Leu Glu Phe Pro
1 5

gca gat gtc att ccc gag aac atc aaa cac att gcg cag aca aag ttc 163
Ala Asp Val Ile Pro Glu Asn Ile Lys His Ile Ala Gln Thr Lys Phe
10 15 20

cag act gaa gca act tcg gtg gag gat att cgt cgt gcg att aac ctg 211
Gln Thr Glu Ala Thr Ser Val Glu Asp Ile Arg Arg Ala Ile Asn Leu
25 30 35

ctg agt gat cag gcg gag cgt gcg ggt gcg tcc ttt aat cct ggt ttc 259
Leu Ser Asp Gln Ala Glu Arg Ala Gly Ala Ser Phe Asn Pro Gly Phe
40 45 50

att ctt gcg cag gtg ggc tcc acc atc gtg gag gtt tat ggc ggt gct 307
Ile Leu Ala Gln Val Gly Ser Thr Ile Val Glu Val Tyr Gly Gly Ala
55 60 65

ccg gtt gct tgg ctg gat gcg gtt gag ctg ttg att agt cct gat gtg 355
Pro Val Ala Trp Leu Asp Ala Val Glu Leu Leu Ile Ser Pro Asp Val
70 75 80 85

gag tgg gtt ggg gtt cat ggc tca agg aag ctc gat att aat gtc agc 403
Glu Trp Val Gly Val His Gly Ser Arg Lys Leu Asp Ile Asn Val Ser
90 95 100

gga gaa ttg tcc ggg gtg att tct gct ggt gac aag ttg ggt gaa ctg 451
Gly Glu Leu Ser Gly Val Ile Ser Ala Gly Asp Lys Leu Gly Glu Leu
105 110 115

ctt ggc gat gat tgg aca atc aac att gtt cac ggc gag tac aaa atc 499
Leu Gly Asp Asp Trp Thr Ile Asn Ile Val His Gly Glu Tyr Lys Ile
120 125 130

cag atc gaa gat gct cga cca agt act gca ttc ctt gcg gac gcg act 547
Gln Ile Glu Asp Ala Arg Pro Ser Thr Ala Phe Leu Ala Asp Ala Thr
135 140 145

gaa ctg att aat cag gca aac tct gag att gtt ccg ttc cat gtt cgg 595

Glu Leu Ile Asn Gln Ala Asn Ser Glu Ile Val Pro Phe His Val Arg 150 155 160 165
 atg ctc agc aac tcg aaa att gtg atg tct ggc ttt agt gat tat tca 643
 Met Leu Ser Asn Ser Lys Ile Val Met Ser Gly Phe Ser Asp Tyr Ser 170 175 180
 cta gcg ggt gat gcg att aca tct gcg gga aaa ctg gct gaa ttg gcg 691
 Leu Ala Gly Asp Ala Ile Thr Ser Ala Gly Lys Leu Ala Glu Leu Ala 185 190 195
 agg cct ttt gcc cac tgg aaa gaa aac gtc att cct acg ata gaa ata 739
 Arg Pro Phe Ala His Trp Lys Glu Asn Val Ile Pro Thr Ile Glu Ile 200 205 210
 gcc atg gac tat gaa cca tca ccg gtg gca gat ctt tgg cag gga gat 787
 Ala Met Asp Tyr Glu Pro Ser Pro Val Ala Asp Leu Trp Gln Gly Asp 215 220 225
 tct tcg gag aca cct gag cct ttc gac gat ttt gag cgc tta ttg cgg 835
 Ser Ser Glu Thr Pro Glu Pro Phe Asp Asp Phe Glu Arg Leu Leu Arg 230 235 240 245
 gaa gaa atg ctt att cct gag att tagctgggtca tagacctgct gtt 882
 Glu Glu Met Leu Ile Pro Glu Ile 250
 <210> 1596
 <211> 253
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 1596
 Met Leu Glu Phe Pro Ala Asp Val Ile Pro Glu Asn Ile Lys His Ile 1 5 10 15
 Ala Gln Thr Lys Phe Gln Thr Glu Ala Thr Ser Val Glu Asp Ile Arg 20 25 30
 Arg Ala Ile Asn Leu Leu Ser Asp Gln Ala Glu Arg Ala Gly Ala Ser 35 40 45
 Phe Asn Pro Gly Phe Ile Leu Ala Gln Val Gly Ser Thr Ile Val Glu 50 55 60
 Val Tyr Gly Gly Ala Pro Val Ala Trp Leu Asp Ala Val Glu Leu Leu 65 70 75 80
 Ile Ser Pro Asp Val Glu Trp Val Gly Val His Gly Ser Arg Lys Leu 85 90 95
 Asp Ile Asn Val Ser Gly Glu Leu Ser Gly Val Ile Ser Ala Gly Asp 100 105 110
 Lys Leu Gly Glu Leu Leu Gly Asp Asp Trp Thr Ile Asn Ile Val His 115 120 125
 Gly Glu Tyr Lys Ile Gln Ile Glu Asp Ala Arg Pro Ser Thr Ala Phe 130 135 140

Leu Ala Asp Ala Thr Glu Leu Ile Asn Gln Ala Asn Ser Glu Ile Val 145 150 155 160
 Pro Phe His Val Arg Met Leu Ser Asn Ser Lys Ile Val Met Ser Gly 165 170 175
 Phe Ser Asp Tyr Ser Leu Ala Gly Asp Ala Ile Thr Ser Ala Gly Lys 180 185 190
 Leu Ala Glu Leu Ala Arg Pro Phe Ala His Trp Lys Glu Asn Val Ile 195 200 205
 Pro Thr Ile Glu Ile Ala Met Asp Tyr Glu Pro Ser Pro Val Ala Asp 210 215 220
 Leu Trp Gln Gly Asp Ser Ser Glu Thr Pro Glu Pro Phe Asp Asp Phe 225 230 235 240
 Glu Arg Leu Leu Arg Glu Glu Met Leu Ile Pro Glu Ile 245 250

<210> 1597
 <211> 834
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(811)
 <223> RXA00121

<400> 1597
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 cgctgtcgac cccatcttct aaacaagaaa ggcccoctcca atg ttg agc gat ctg 115
 Met Leu Ser Asp Leu 5
 1
 agc tcc att ttt gac ttc caa gac ctc tcc ggc acc ttc tct gtc gtc 163
 Ser Ser Ile Phe Asp Phe Gln Asp Leu Ser Gly Thr Phe Ser Val Val 20
 10 15
 gac gtt ctc atc act ttg gtc ttg tcc ttc gtc ctg acc tcc atc gtg 211
 Asp Val Leu Ile Thr Leu Val Leu Ser Phe Val Leu Thr Ser Ile Val 35
 25 30
 ggt gtg gtg tac caa aag acc cac cgc cac atc tcc tac agc cag tca 259
 Gly Val Val Tyr Gln Lys Thr His Arg His Ile Ser Tyr Ser Gln Ser 50
 40 45
 ttc gta caa acg ttg gtg ctg gtg gga atg gtc att gca atc atc atg 307
 Phe Val Gln Thr Leu Val Leu Val Gly Met Val Ile Ala Ile Ile Met 65
 55 60
 ctg gtg gtc ggc tcc aac att gca cgt gca ttc gcc ctg gtt ggc gcg 355
 Leu Val Val Gly Ser Asn Ile Ala Arg Ala Phe Ala Leu Val Gly Ala 85
 70 75 80
 ctt tcg gtg att cga ttc cgc aac gca gtg aaa gaa acc cga gat gtg 403
 Leu Ser Val Ile Arg Phe Arg Asn Ala Val Lys Glu Thr Arg Asp Val

	90	95	100	
ggc ttc ctt ttc ctt gcc atg gca atc ggc atg act tgc ggt acc cgc				451
Gly Phe Leu Phe Leu Ala Met Ala Ile Gly Met Thr Cys Gly Thr Arg	105	110	115	
ttc tac gtt ctg gcg atc gct gca acc atc gtt gtc tgt ggc gtt ctg				499
Phe Tyr Val Leu Ala Ile Ala Thr Ile Val Val Cys Gly Val Leu	120	125	130	
ttc atc atg tac cgc ttc gac tgg ttc aag gct gat atc cag cgc cag				547
Phe Ile Met Tyr Arg Phe Asp Trp Phe Lys Ala Asp Ile Gln Arg Gln	135	140	145	
gtc atc aag gtg cag gtc cca gcc gat gga caa gct gat tcc ggc agg				595
Val Ile Lys Val Gln Val Pro Ala Asp Gly Gln Ala Asp Ser Gly Arg	150	155	160	165
tcc tac gca gaa gaa gtt gaa ctg atc ctc gca cag tac tgc act tcc				643
Ser Tyr Ala Glu Glu Val Glu Leu Ile Leu Ala Gln Tyr Cys Thr Ser	170	175	180	
ttt gag atg atg tcc gct gaa tct gtc cgc ggc gga gcc ctg acc gag				691
Phe Glu Met Met Ser Ala Glu Ser Val Arg Gly Gly Ala Leu Thr Glu	185	190	195	
ttc tcc tac acc gct caa atg cgc aag aac gtg aag cca cat gag ctg				739
Phe Ser Tyr Thr Ala Gln Met Arg Lys Asn Val Lys Pro His Glu Leu	200	205	210	
gtc gcc aag atg cgc gat gtg aac tac ggc caa aaa gcg act gtc ctg				787
Val Ala Lys Met Arg Asp Val Asn Tyr Gly Gln Lys Ala Thr Val Leu	215	220	225	
acc ggt cac gat caa acg gat gta tagaaaaatgc ctacgtttaa atc				834
Thr Gly His Asp Gln Thr Asp Val	230	235		
<210> 1598				
<211> 237				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 1598				
Met Leu Ser Asp Leu Ser Ser Ile Phe Asp Phe Gln Asp Leu Ser Gly	1	5	10	15
Thr Phe Ser Val Val Asp Val Leu Ile Thr Leu Val Leu Ser Phe Val	20	25	30	
Leu Thr Ser Ile Val Gly Val Val Tyr Gln Lys Thr His Arg His Ile	35	40	45	
Ser Tyr Ser Gln Ser Phe Val Gln Thr Leu Val Leu Val Gly Met Val	50	55	60	
Ile Ala Ile Ile Met Leu Val Val Gly Ser Asn Ile Ala Arg Ala Phe	65	70	75	80
Ala Leu Val Gly Ala Leu Ser Val Ile Arg Phe Arg Asn Ala Val Lys				

[illegible]

1000

400> 1599															
gatgcgcgat gtgaactacg gccaaaaagc gactgtcctg accggtcacg atcaaacgga															60
tgtatagaaa atgcctagct ttaaatctgc tcgatggagg															
Met Asn Arg Arg Leu															115
1 5															
ttc cta gga act tcc gca gct atc atc gct gtc ggt gtg ctc ggt															163
Phe Leu Gly Thr Ser Ala Ala Ile Ile Ala Val Gly Gly Val Leu Gly															
10 15 20															
gga gtg cag gtt gta cct tat att tcc tct ggt gaa atc caa acg tca															211
Gly Val Gln Val Val Pro Tyr Ile Ser Ser Gly Glu Ile Gln Thr Ser															
25 30 35															
gca tca tcc act gcc acg atc asp gtc ggt gca ggc aat gtc gat att															259
Ala Ser Ser Thr Ala Thr Ile Asp Val Gly Ala Gly Asn Val Asp Ile															
40 45 50															
ttt gat acc tcc gtt tcc cat gaa atc agc ctg cag gtt tcc gaa gaa															307
Phe Asp Thr Ser Val Ser His Gly Ile Ser Leu Gln Val Ser Gln Glu															

55	60	65	
agc ctc gat gag atg ctc gcg gac tat caa gaa gac ggt tcc aaa acc			355
Ser Leu Asp Glu Met Leu Ala Asp Tyr Gln Glu Asp Gly Ser Lys Thr			
70	75	80	85
tgg gtg aaa gca acc atc acg att gat ggc gtg acc att gaa aac gtc			403
Trp Val Lys Ala Thr Ile Thr Ile Asp Gly Val Thr Ile Glu Asn Val			
	90	95	100
ggc atc cgc ctc aag ggc aac tcc acg ctg tcc ggg ttg ggt cga aca			451
Gly Ile Arg Leu Lys Gly Asn Ser Thr Leu Ser Gly Leu Gly Arg Thr			
	105	110	115
tct gaa gaa ggc gga cct cag gca cca gaa ggc gtc gaa gag ttt aca			499
Ser Glu Glu Gly Gly Pro Gln Ala Pro Glu Gly Val Glu Glu Phe Thr			
	120	125	130
gat ctc agt gaa gag gaa atc gcc cag ttt gag gaa cag ttc gcg gcg			547
Asp Leu Ser Glu Glu Ile Ala Gln Phe Glu Glu Gln Phe Ala Ala			
	135	140	145
cag caa gag act act gac gct tca gag acc ggt gaa act gcg gaa aat			595
Gln Gln Glu Thr Thr Asp Ala Ser Glu Thr Gly Glu Thr Ala Glu Asn			
	150	155	160
gaa gag act cgc ggc ccc ggc ggt ggc atg ggt ggt ggc ggc atg ggt			643
Glu Glu Thr Arg Gly Pro Gly Gly Gly Met Gly Gly Gly Met Gly			
	170	175	180
ggc atg act tcg gtc gat gcc gac gat gtc agc acc tgg cca ctt ctg			691
Gly Met Thr Ser Val Asp Ala Asp Asp Val Ser Thr Trp Pro Leu Leu			
	185	190	195
atc agc ttc gac aaa tac gaa gac ggc cgc gtc tac caa ggc atg acc			739
Ile Ser Phe Asp Lys Tyr Glu Asp Gly Arg Val Tyr Gln Gly Met Thr			
	200	205	210
caa ctg gca cta cgc ccc ggc acc acc gtg gtc aac gaa gca atg gcg			787
Gln Leu Ala Leu Arg Pro Gly Thr Thr Val Val Asn Glu Ala Met Ala			
	215	220	225
ctg gcc ctg acc gca gaa acc ggc cag gtc tcg cag caa tcc agc ttc			835
Leu Ala Leu Thr Ala Glu Thr Gly Gln Val Ser Gln Gln Ser Ser Phe			
	230	235	240
aca acg ttt tcg ctt aac gac gag ccc tcc acc act cga ctc ctt ttg			883
Thr Thr Phe Ser Leu Asn Asp Glu Pro Ser Thr Thr Arg Leu Leu Leu			
	250	255	260
aag cac ccc gat gaa aat tat gcc gac gcg ctc ggc aac gga gtc ctc			931
Lys His Pro Asp Glu Asn Tyr Ala Asp Ala Leu Gly Asn Gly Val Leu			
	265	270	275
ttc aaa gca gat tcc aac agt tcc ttc acc tac caa ggc gaa gac caa			979
Phe Lys Ala Asp Ser Asn Ser Ser Phe Thr Tyr Gln Gly Glu Asp Gln			
	280	285	290
act gaa tac gac gga cag ttc aag cag atc aac ggt gac ggc aac gga			1027
Thr Glu Tyr Asp Gly Gln Phe Lys Gln Ile Asn Gly Asp Gly Asn Gly			
	295	300	305

gac atc caa ccg atc atc aac ctg ctg aaa tgg ctc gac acc gca agc Asp Ile Gln Pro Ile Ile Asn Leu Leu Lys Trp Leu Asp Thr Ala Ser 310 315 320 325	1075
gat gaa gag ttt gct gaa cac ctc tct gac tac gtc gat gtg gaa agc Asp Glu Glu Phe Ala Glu His Leu Ser Asp Tyr Val Asp Val Glu Ser 330 335 340	1123
ttt gct cgc tac gtt gcc act caa aac ctg ttg gta aat tcc gac gac Phe Ala Arg Tyr Val Ala Thr Gln Asn Leu Leu Val Asn Ser Asp Asp 345 350 355	1171
atg gct ggt ccc ggt agt aat tac tac ctg tgg tac gac tac gac acc Met Ala Gly Pro Gly Ser Asn Tyr Tyr Leu Trp Tyr Asp Tyr Asp Thr 360 365 370	1219
ggc ctg atc agc gtg atc tct tgg gat ttg aac ctc gca atg tcc ggc Gly Leu Ile Ser Val Ile Ser Trp Asp Leu Asn Ala Met Ser Gly 375 380 385	1267
tca act gat gct ggc cca gat gat gaa atc tcc atg ggc gga ggt ggc Ser Thr Asp Ala Gly Pro Asp Asp Glu Ile Ser Met Gly Gly Gly Gly 390 395 400 405	1315
ggt ggc gga atg cgt cct ggt gga acg acc gac act gaa att gaa ggt Gly Gly Gly Met Arg Pro Gly Gly Thr Thr Asp Thr Glu Ile Glu Gly 410 415 420	1363
act gcg acc gag gat atg cct gac atg ggc aat atg cag caa cgt gaa Thr Ala Thr Glu Asp Met Pro Asp Met Gly Asn Met Gln Gln Arg Glu 425 430 435	1411
cgc cct gaa gga atg cca gac atg ggt gag atg cct gat atg ggt gac Arg Pro Glu Gly Met Pro Asp Met Gly Glu Met Pro Asp Met Gly Asp 440 445 450	1459
cgg gaa ggc ggt gga tcg atg gga gga aac cag ctc aag gaa cgt ttc Arg Glu Gly Gly Gly Ser Met Gly Gly Asn Gln Leu Lys Glu Arg Phe 455 460 465	1507
ctc gct tcc gat gca ttc acg gaa atc tat gag cag gtg tac tgg gag Leu Ala Ser Asp Ala Phe Thr Glu Ile Tyr Glu Gln Val Tyr Trp Glu 470 475 480 485	1555
ctg tat gaa gaa atg tat ggt tcc gga act gcc atc gag ttg ttg gat Leu Tyr Glu Glu Met Tyr Gly Ser Gly Thr Ala Ile Glu Leu Leu Asp 490 495 500	1603
gag att gca gcg tca att cca gaa act gat gcg gtg act gca gat gag Glu Ile Ala Ala Ser Ile Pro Glu Thr Asp Ala Val Thr Ala Asp Glu 505 510 515	1651
atc gct acg gaa gtg gcg tca atg cgg gaa tgg atc act gcc cgc aca Ile Ala Thr Glu Val Ala Ser Met Arg Glu Trp Ile Thr Ala Arg Thr 520 525 530	1699
gaa gcg ttg gct gct ttg caa gag tgatcaaaact agaaaaccaa caa Glu Ala Leu Ala Ala Leu Gln Glu 535 540	1746

<210> 1600
 <211> 541
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 1600
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 Gly Gly Val Leu Gly Gly Val Gln Val Val Pro Tyr Ile Ser Ser Gly
 20 25 30
 Glu Ile Gln Thr Ser Ala Ser Ser Thr Ala Thr Ile Asp Val Gly Ala
 35 40 45
 Gly Asn Val Asp Ile Phe Asp Thr Ser Val Ser His Glu Ile Ser Leu
 50 55 60
 Gln Val Ser Gln Glu Ser Leu Asp Glu Met Leu Ala Asp Tyr Gln Glu
 65 70 75 80
 Asp Gly Ser Lys Thr Trp Val Lys Ala Thr Ile Thr Ile Asp Gly Val
 85 90 95
 Thr Ile Glu Asn Val Gly Ile Arg Leu Lys Gly Asn Ser Thr Leu Ser
 100 105 110
 Gly Leu Gly Arg Thr Ser Glu Glu Gly Gly Pro Gln Ala Pro Glu Gly
 115 120 125
 Val Glu Glu Phe Thr Asp Leu Ser Glu Glu Glu Ile Ala Gln Phe Glu
 130 135 140
 Glu Gln Phe Ala Ala Gln Gln Glu Thr Thr Asp Ala Ser Glu Thr Gly
 145 150 155 160
 Glu Thr Ala Glu Asn Glu Glu Thr Arg Gly Pro Gly Gly Gly Met Gly
 165 170 175
 Gly Gly Gly Met Gly Gly Met Thr Ser Val Asp Ala Asp Asp Val Ser
 180 185 190
 Thr Trp Pro Leu Leu Ile Ser Phe Asp Lys Tyr Glu Asp Gly Arg Val
 195 200 205
 Tyr Gln Gly Met Thr Gln Leu Ala Leu Arg Pro Gly Thr Thr Val Val
 210 215 220
 Asn Glu Ala Met Ala Leu Ala Leu Thr Ala Glu Thr Gly Gln Val Ser
 225 230 235 240
 Gln Gln Ser Ser Phe Thr Thr Phe Ser Leu Asn Asp Glu Pro Ser Thr
 245 250 255
 Thr Arg Leu Leu Leu Lys His Pro Asp Glu Asn Tyr Ala Asp Ala Leu
 260 265 270
 Gly Asn Gly Val Leu Phe Lys Ala Asp Ser Asn Ser Ser Phe Thr Tyr
 275 280 285

Gln Gly Glu Asp Gln Thr Glu Tyr Asp Gly Gln Phe Lys Gln Ile Asn
 290 295 300
 Gly Asp Gly Asn Gly Asp Ile Gln Pro Ile Ile Asn Leu Leu Lys Trp
 305 310 315 320
 Leu Asp Thr Ala Ser Asp Glu Glu Phe Ala Glu His Leu Ser Asp Tyr
 325 330 335
 Val Asp Val Glu Ser Phe Ala Arg Tyr Val Ala Thr Gln Asn Leu Leu
 340 345 350
 Val Asn Ser Asp Asp Met Ala Gly Pro Gly Ser Asn Tyr Tyr Leu Trp
 355 360 365
 Tyr Asp Tyr Asp Thr Gly Leu Ile Ser Val Ile Ser Trp Asp Leu Asn
 370 375 380
 Leu Ala Met Ser Gly Ser Thr Asp Ala Gly Pro Asp Asp Glu Ile Ser
 385 390 395 400
 Met Gly Gly Gly Gly Gly Gly Gly Met Arg Pro Gly Gly Thr Thr Asp
 405 410 415
 Thr Glu Ile Glu Gly Thr Ala Thr Glu Asp Met Pro Asp Met Gly Asn
 420 425 430
 Met Gln Gln Arg Glu Arg Pro Glu Gly Met Pro Asp Met Gly Glu Met
 435 440 445
 Pro Asp Met Gly Asp Arg Glu Gly Gly Gly Ser Met Gly Gly Asn Gln
 450 455 460
 Leu Lys Glu Arg Phe Leu Ala Ser Asp Ala Phe Thr Glu Ile Tyr Glu
 465 470 475 480
 Gln Val Tyr Trp Glu Leu Tyr Glu Glu Met Tyr Gly Ser Gly Thr Ala
 485 490 495
 Ile Glu Leu Leu Asp Glu Ile Ala Ala Ser Ile Pro Glu Thr Asp Ala
 500 505 510
 Val Thr Ala Asp Glu Ile Ala Thr Glu Val Ala Ser Met Arg Glu Trp
 515 520 525
 Ile Thr Ala Arg Thr Glu Ala Leu Ala Ala Leu Gln Glu
 530 535 540

<210> 1601

<211> 579

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> {101}..(556)

<223> RXA00127

<400> 1601

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aacattggcg cggttgatt tagatttacc ggtgtggacg ttg tgc ccg tat gac 115
 Leu Ser Pro Tyr Asp
 1 5

ggc ccg cat cgc aac gtg ctc att gcg ctg aag gag cac ggc cgt gca 163
 Gly Pro His Arg Asn Val Leu Ile Ala Leu Lys Glu His Gly Arg Ala
 10 15 20

gac ctt gtg gcg ttt gtg ggc gcg gtg gtg ggg gcg tgc ata agc tat 211
 Asp Leu Val Ala Phe Val Gly Ala Val Val Gly Ala Ser Ile Ser Tyr
 25 30 35

ctg gcg gct cag ggg gaa att gag cac gac atc acg ctg gtt ccg gcg 259
 Leu Ala Ala Gln Gly Glu Ile Glu His Asp Ile Thr Leu Val Pro Ala
 40 45 50

ccc acc cgc gcc acc tgc cga cgc cgg cgg ggc ggc gat ccg gtt gag 307
 Pro Thr Arg Ala Thr Ser Arg Arg Arg Gly Asp Pro Val Glu
 55 60 65

cgg gtg tgc aat gca tca cgc tta tgc acg ttt ccc tgc ctt caa atc 355
 Arg Val Cys Asn Ala Ser Arg Leu Ser Thr Phe Pro Cys Leu Gln Ile
 70 75 80 85

tca tcc cgc aca cca gac tcc gtc ggt caa act gcg caa cag cga aga 403
 Ser Ser Arg Thr Pro Asp Ser Val Gly Gln Thr Ala Gln Arg Arg
 90 95 100

ctc aat atg cga gtg gag tta gtc cga caa cct cgg ggt tct gtc ttg 451
 Leu Asn Met Arg Val Glu Leu Val Arg Gln Pro Arg Gly Ser Val Leu
 105 110 115

atc atc gac gat gtg gta aca acg ggg gca act att tcc gca tct gca 499
 Ile Ile Asp Asp Val Val Thr Thr Gly Ala Thr Ile Ser Ala Ser Ala
 120 125 130

aac gtt ctt cgc gca gcg ggt gtg cag gtc aga gga gct tta act tat 547
 Asn Val Leu Arg Ala Ala Gly Val Gln Val Arg Gly Ala Leu Thr Tyr
 135 140 145

tgc caa gcg tgatcttggg tataaaaggg gcc 579
 Cys Gln Ala
 150

<210> 1602

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 1602

Leu Ser Pro Tyr Asp Gly Pro His Arg Asn Val Leu Ile Ala Leu Lys
 1 5 10 15

Glu His Gly Arg Ala Asp Leu Val Ala Phe Val Gly Ala Val Val Gly
 20 25 30

Ala Ser Ile Ser Tyr Leu Ala Ala Gln Gly Glu Ile Glu His Asp Ile
 35 40 45

Thr Leu Val Pro Ala Pro Thr Arg Ala Thr Ser Arg Arg Arg Gly
 50 55 60

Gly Asp Pro Val Glu Arg Val Cys Asn Ala Ser Arg Leu Ser Thr Phe
 65 70 75 80

Pro Cys Leu Gln Ile Ser Ser Arg Thr Pro Asp Ser Val Gly Gln Thr
 85 90 95

Ala Gln Gln Arg Arg Leu Asn Met Arg Val Glu Leu Val Arg Gln Pro
 100 105 110

Arg Gly Ser Val Leu Ile Ile Asp Asp Val Val Thr Thr Gly Ala Thr
 115 120 125

Ile Ser Ala Ser Ala Asn Val Leu Arg Ala Ala Gly Val Gln Val Arg
 130 135 140

Gly Ala Leu Thr Tyr Cys Gln Ala
 145 150

<210> 1603
 <211> 693
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(670)
 <223> RXA00134

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 tccccacccc tgtgcgtaac gacagctaga atctcaagtt atg gcc gtt cat tta 115
 Met Ala Val His Leu
 1 5

acc aag atc tat acg cga acc ggg gac gat gga acc acg ggg ctc tca 163
 Thr Lys Ile Tyr Thr Arg Thr Gly Asp Asp Gly Thr Thr Gly Leu Ser
 10 15 20

aat ttt gag cga gtt ccc aag gac gat ccc cgc ctt att gca tac gcc 211
 Asn Phe Glu Arg Val Pro Lys Asp Asp Pro Arg Leu Ile Ala Tyr Ala
 25 30 35

gac tcc gat gaa gca aac tgt gcg att ggc caa gtg ctt gca ctc agc 259
 Asp Ser Asp Glu Ala Asn Cys Ala Ile Gly Gln Val Leu Ala Leu Ser
 40 45 50

agc cct acg gaa gat atg gca acc tta ttg cgg act att caa aat gaa 307
 Ser Pro Thr Glu Asp Met Ala Thr Leu Leu Arg Thr Ile Gln Asn Glu
 55 60 65

ctt ttt gat gtg ggc gca gac tta gca acc ccg att gag gag aat ccg 355
 Leu Phe Asp Val Gly Ala Asp Leu Ala Thr Pro Ile Glu Glu Asn Pro
 70 75 80 85

aag tat ccc cca ctt cga gtt ctt ccg gaa tat atc gaa cga ctt gag 403
 Lys Tyr Pro Pro Leu Arg Val Leu Pro Glu Tyr Ile Glu Arg Leu Glu

	90	95	100	
aag gag tgc gat aaa tgg aac gag gat		gtg ccg gcg ttg gat tcc ttc	451	
Lys Glu Cys Asp Lys Trp Asn Glu Asp		Val Pro Ala Leu Asn Ser Phe		
	105	110	115	
att ttg ccg ggt ggc acg cca gca gcg gca ctc ttg cac acc gca agg			499	
Ile Leu Pro Gly Gly Thr Pro Ala Ala Leu Leu His Thr Ala Arg				
	120	125	130	
gta att acg agg cgc gcg gag aga gca gct tgg ata gcg gtg cgg gaa			547	
Val Ile Thr Arg Arg Ala Glu Arg Ala Ala Trp Ile Ala Val Arg Glu				
	135	140	145	
ttt ccg agc acc acc tct acc ttg cca gcc caa tac ctg aat cgt ctt			595	
Phe Pro Ser Thr Thr Ser Thr Leu Pro Ala Gln Tyr Leu Asn Arg Leu				
	150	155	165	
agc gat ctg ctg ttt att ctt tcc cgt gtt gcc aac aat ggc aat gat			643	
Ser Asp Leu Leu Phe Ile Leu Ser Arg Val Ala Asn Asn Gly Asn Asp				
	170	175	180	
gtg aag tgg gtt ccg ggc gga aaa aga tga		tgaaaaccac cctgcgaccg	690	
Val Lys Trp Val Pro Gly Gly Lys Arg				
	185	190		
tga			693	
<210> 1604				
<211> 190				
<212> FRT				
<213> Corynebacterium glutamicum				
<400> 1604				
Met Ala Val His Leu Thr Lys Ile Tyr Thr Arg Thr Gly Asp Asp Gly				
	1	5	10	
Thr Thr Gly Leu Ser Asn Phe Glu Arg Val Pro Lys Asp Asp Pro Arg				
	20	25	30	
Leu Ile Ala Tyr Ala Asp Ser Asp Glu Ala Asn Cys Ala Ile Gly Gln				
	35	40	45	
Val Leu Ala Leu Ser Ser Pro Thr Glu Asp Met Ala Thr Leu Leu Arg				
	50	55	60	
Thr Ile Gln Asn Glu Leu Phe Asp Val Gly Ala Asp Leu Ala Thr Pro				
	65	70	75	
Ile Glu Glu Asn Pro Lys Tyr Pro Pro Leu Arg Val Leu Pro Glu Tyr				
	85	90	95	
Ile Glu Arg Leu Glu Lys Glu Cys Asp Lys Trp Asn Glu Asp Val Pro				
	100	105	110	
Ala Leu Asp Ser Phe Ile Leu Pro Gly Gly Thr Pro Ala Ala Ala Leu				
	115	120	125	
Leu His Thr Ala Arg Val Ile Thr Arg Arg Ala Glu Arg Ala Ala Trp				
	130	135	140	

Ile Ala Val Arg Glu Phe Pro Ser Thr Thr Ser Thr Leu Pro Ala Gln
145 150 155 160

Tyr Leu Asn Arg Leu Ser Asp Leu Leu Phe Ile Leu Ser Arg Val Ala
165 170 175

Asn Asn Gly Asn Asp Val Lys Trp Val Pro Gly Gly Lys Arg
180 185 190

<210> 1605

<211> 309

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(286)

<223> RXA00140

<400> 1605

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caagatgccg tagccaatgc aggcaaggaa atcggtctaac atg tcg gac gag tcc 115
Met Ser Asp Glu Ser
1 5

atc gaa gag cag gaa aaa gaa ctc gcg gcg ctg aag gct caa atc gat 163
Ile Glu Glu Gln Glu Lys Glu Leu Ala Ala Leu Lys Ala Gln Ile Asp
10 15 20

gaa ctg gaa aag aaa gac aag cag aac aag cta atc atc gag att ttg 211
Glu Leu Glu Lys Lys Asp Lys Gln Asn Lys Leu Ile Ile Glu Ile Leu
25 30 35

tcc aag gcc gtc gaa aag aat gtg gca gag gca gaa gcg aaa aga gcc 259
Ser Lys Ala Val Glu Lys Asn Val Ala Glu Ala Glu Ala Lys Arg Ala
40 45 50

cgc aaa tat ccg ccc aat ccc ctg tgg tgaattctaa ggcgctogaac 306
Arg Lys Tyr Pro Pro Asn Pro Leu Trp
55 60

ttt 309

<210> 1606

<211> 62

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1606

Met Ser Asp Glu Ser Ile Glu Glu Gln Glu Lys Glu Leu Ala Leu
1 5 10 15

Lys Ala Gln Ile Asp Glu Leu Glu Lys Lys Asp Lys Gln Asn Lys Leu
20 25 30

Ile Ile Glu Ile Leu Ser Lys Ala Val Glu Lys Asn Val Ala Glu Ala
35 40 45

Glu Ala Lys Arg Ala Arg Lys Tyr Pro Pro Asn Pro Leu Trp
 50 55 60

<210> 1607

<211> 585

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)...(562)

<223> RXA00141

<400> 1607

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cagcaattcc cagatctagt cacctggaag gacgaacacc atg acc act gat tcc 115
 Met Thr Thr Asp Ser
 1 5

aat tct gcg aca atc cca acc cca aag ccg att cca gtg acc atc gac 163
 Asn Ser Ala Thr Ile Pro Thr Pro Lys Pro Ile Pro Val Thr Ile Asp
 10 15 20

cga atc tcc ctc atc atg aaa gaa ttc ggc att gac cta tcc atc gcc 211
 Arg Ile Ser Leu Ile Met Lys Glu Phe Gly Ile Asp Leu Ser Ile Ala
 25 30 35

gat gaa caa ggc acc gga tcc caa gta gcc agc gcc aac ctc aac ggc 259
 Asp Glu Gln Gly Thr Gly Ser Gln Val Ala Ser Ala Asn Leu Asn Gly
 40 45 50

cat cac gtc atg ttc gct gtc atc ggt tca gtc ctg atc gtt cgt gcc 307
 His His Val Met Phe Ala Val Ile Gly Ser Val Leu Ile Val Arg Ala
 55 60 65

gat cgc gcc acc gaa atg cca gtc tcc gac ggc aac ccc gca tgg cat 355
 Asp Arg Ala Thr Glu Met Pro Val Ser Asp Gly Asn Pro Ala Trp His
 70 75 80 85

ctc gcc tgc aac caa gtc aac tgt ttc aac ttc gct gcc aag gct gtc 403
 Leu Ala Cys Asn Gln Val Asn Cys Phe Asn Phe Ala Ala Lys Ala Val
 90 95 100

gta gtt gat cgc acc gac aac atc gtg atc cgc gcc gag aag gat gtc 451
 Val Val Asp Arg Thr Asp Asn Ile Val Ile Arg Ala Glu Lys Asp Val
 105 110 115

ccc atc gcc gct ggg ctc aac gat att cag ctt tcc gca atg ctg aaa 499
 Pro Ile Ala Ala Gly Leu Asn Asp Ile Gln Leu Ser Ala Met Leu Lys
 120 125 130

aac gcc atc gat cac gtc ctc gcg att caa gat gcc gta gcc aat gca 547
 Asn Ala Ile Asp His Val Leu Ala Ile Gln Asp Ala Val Ala Asn Ala
 135 140 145

ggc aag gaa atc ggc taacatgtcg gacgagtcca tcg 585
 Gly Lys Glu Ile Gly
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<210> 1608

<211> 154

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1608

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Met Thr Thr Asp Ser Asn Ser Ala Thr Ile Pro Thr Pro Lys Pro Ile
 1          5          10          15

Pro Val Thr Ile Asp Arg Ile Ser Leu Ile Met Lys Glu Phe Gly Ile
          20          25          30

Asp Leu Ser Ile Ala Asp Glu Gln Gly Thr Gly Ser Gln Val Ala Ser
          35          40          45

Ala Asn Leu Asn Gly His His Val Met Phe Ala Val Ile Gly Ser Val
          50          55          60

Leu Ile Val Arg Ala Asp Arg Ala Thr Glu Met Pro Val Ser Asp Gly
          65          70          75          80

Asn Pro Ala Trp His Leu Ala Cys Asn Gln Val Asn Cys Phe Asn Phe
          85          90          95

Ala Ala Lys Ala Val Val Val Asp Arg Thr Asp Asn Ile Val Ile Arg
          100          105          110

Ala Glu Lys Asp Val Pro Ile Ala Ala Gly Leu Asn Asp Ile Gln Leu
          115          120          125

Ser Ala Met Leu Lys Asn Ala Ile Asp His Val Leu Ala Ile Gln Asp
          130          135          140

Ala Val Ala Asn Ala Gly Lys Glu Ile Gly
          145          150

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<210> 1609

<211> 600

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(577)

<223> RXA00142

<400> 1609

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atcctcaatt tccgccgtaa gcgcaacgac taaaaccacc atctgtagtgt tgggtggaaaa 60

gttactttta aaaggatttt ggaaggactg aaactcccca gtg cct caa tca ccc 115
          Val Pro Gln Ser Pro
          1          5

aca gca cac gac ccc aac gac atc cag gaa ttt aac ctc gat gcc gtt 163
Thr Ala His Asp Pro Asn Asp Ile Gln Glu Phe Asn Leu Asp Ala Val
          10          15          20

gca ggg att ctc cag gac gaa aaa ctg gac tac cgc atc gat gaa cac 211

```

Ala Gly Ile Leu Gln Asp Glu Lys Leu Asp Tyr Arg Ile Asp Glu His	
25 30 35	
gac ggc gaa aaa gta atc cgc acc gga ttc atc aac gcc gcc atc agc	259
Asp Gly Glu Lys Val Ile Arg Thr Gly Phe Ile Asn Ala Ala Ile Ser	
40 45 50	
ttc atc ctc tta gac ggc agc tta acc atg gaa gcc atg tgg cga gga	307
Phe Ile Leu Leu Asp Gly Ser Leu Thr Met Glu Ala Met Trp Arg Gly	
55 60 65	
gcc ccc tcc acc gat gct gcc gca caa gtt ctc gcg gcc acc aac gaa	355
Ala Pro Ser Thr Asp Ala Ala Ala Gln Val Leu Ala Ala Thr Asn Glu	
70 75 80 85	
tgg aac ctc acc cag ttc gca ccc acc att cga ttc ttc gaa ctc aac	403
Trp Asn Leu Thr Gln Phe Ala Pro Thr Ile Arg Phe Phe Glu Leu Asn	
90 95 100	
gaa ggc acc ctc gcc atc aat gca ctg cga cac gtc gtt gtt tcc gca	451
Glu Gly Thr Leu Ala Ile Asn Ala Leu Arg His Val Val Ser Ala	
105 110 115	
ggc atg agc cac aac caa gtc ggc tcc tac gtt atg agc tcc atc gaa	499
Gly Met Ser His Asn Gln Val Gly Ser Tyr Val Met Ser Ser Ile Glu	
120 125 130	
tcc gct gtt cag tgc ttc gaa tgg ctt gag cag caa ttc cca gat cta	547
Ser Ala Val Gln Cys Phe Glu Trp Leu Glu Gln Gln Phe Pro Asp Leu	
135 140 145	
gtc acc tgg aag gac gaa cac cat gac cac tgattccaat tctgcgacaa	597
Val Thr Trp Lys Asp Glu His His Asp His	
150 155	
tcc	600
<210> 1610	
<211> 159	
<212> PRT	
<213> <i>Corynebacterium glutamicum</i>	
<400> 1610	
Val Pro Gln Ser Pro Thr Ala His Asp Pro Asn Asp Ile Gln Glu Phe	
1 5 10 15	
Asn Leu Asp Ala Val Ala Gly Ile Leu Gln Asp Glu Lys Leu Asp Tyr	
20 25 30	
Arg Ile Asp Glu His Asp Gly Glu Lys Val Ile Arg Thr Gly Phe Ile	
35 40 45	
Asn Ala Ala Ile Ser Phe Ile Leu Leu Asp Gly Ser Leu Thr Met Glu	
50 55 60	
Ala Met Trp Arg Gly Ala Pro Ser Thr Asp Ala Ala Ala Gln Val Leu	
65 70 75 80	
Ala Ala Thr Asn Glu Trp Asn Leu Thr Gln Phe Ala Pro Thr Ile Arg	
85 90 95	

Phe Phe Glu Leu Asn Glu Gly Thr Leu Ala Ile Asn Ala Leu Arg His
100 105 110

Val Val Val Ser Ala Gly Met Ser His Asn Gln Val Gly Ser Tyr Val
115 120 125

Met Ser Ser Ile Glu Ser Ala Val Gln Cys Phe Glu Trp Leu Glu Gln
130 135 140

Gln Phe Pro Asp Leu Val Thr Trp Lys Asp Glu His His Asp His
145 150 155

<210> 1611

<211> 897

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(874)

<223> RXA00150

<400> 1611

agctgagcag ggcacggcac tagcttctac tacgataacg agaactttgt ttcaatacat 60

tcaaaatggc ggaatatattt gatcacgggg gtgcaactgt atg gtg ttt tct atg 115
Met Val Phe Ser Met
1 5

cat gac aaa ggt gag acc cag gag aat cct gcg gac atg tca gga cgc 163
His Asp Lys Gly Glu Thr Gln Glu Asn Pro Ala Asp Met Ser Gly Arg
10 15 20

cta aac aca cca att tcc acg gtc ttt cac ttc ttt agc tca ctt ttc 211
Leu Asn Thr Pro Ile Ser Thr Val Phe His Phe Phe Ser Ser Leu Phe
25 30 35

cat gac gct ctg cgc agt gtt gcc cag tgg agt gcg tgg aag aaa atc 259
His Asp Ala Leu Arg Ser Val Ala Gln Trp Ser Ala Trp Lys Lys Ile
40 45 50

gct gta tcg gtt gtc atc gtc gca att att tcc gta act ttt ctt gtc 307
Ala Val Ser Val Val Ile Val Ala Ile Ile Ser Val Thr Phe Leu Val
55 60 65

gat gtc ccc ccg att tcg gtt tat cgt gac tgg gca aac aac gcc ggc 355
Asp Val Pro Pro Ile Ser Val Tyr Arg Asp Trp Ala Asn Asn Ala Gly
70 75 80 85

gac gct ttt gtc tta gtt ttt tgc gcc ttt tat atc ctc att act cag 403
Asp Ala Phe Val Leu Val Phe Cys Ala Phe Tyr Ile Leu Ile Thr Gln
90 95 100

ttc cct atc ccc cgc aca gtt ctc aca ctg gcc tcc ggc gtg ctg ttc 451
Phe Pro Ile Pro Arg Thr Val Leu Thr Leu Ala Ser Gly Val Leu Phe
105 110 115

ggg ccg gtt ctt gga tca gtc gtg gcg ctg ggt tcc acc aca gtg tca 499
Gly Pro Val Leu Gly Ser Val Val Ala Leu Gly Ser Thr Thr Val Ser

1611 897 DNA RXA00150

120	125	130	
gcg gta atc tgg ctc ctc att gtt cgg ggt ctg ctt ggc gat tgg atg			547
Ala Val Ile Ser Leu Leu Ile Val Arg Gly Leu Leu Gly Asp Trp Met			
135	140	145	
gcg cca cgt tta acg cac ccc gca gtc tca cgc atc aat acc cga ctt			595
Ala Pro Arg Leu Thr His Pro Ala Val Ser Arg Ile Asn Thr Arg Leu			
150	155	160	165
gag caa cgt gga tgg ctg gcg att acc tct tta aga atg atc gcc gct			643
Glu Gln Arg Gly Trp Leu Ala Ile Thr Ser Leu Arg Met Ile Ala Ala			
170	175	180	
atc ccc ttt tcc atc ctc aac tat gtt gca gcc ttg act agc gtt cct			691
Ile Pro Phe Ser Ile Leu Asn Tyr Val Ala Ala Leu Thr Ser Val Pro			
185	190	195	
gtt ttt tct ttt gcc atc gct acc ttg atc gga tct gca cca gga acc			739
Val Phe Ser Phe Ala Ile Ala Thr Leu Ile Gly Ser Ala Pro Gly Thr			
200	205	210	
atc gtc acc gtc gtt ttg gga gat gca gtc aca ggt tct gga aac tgg			787
Ile Val Thr Val Val Leu Gly Asp Ala Val Thr Gly Ser Gly Asn Trp			
215	220	225	
act gcc gtt gca ttc acg gta ttt tta gcg att ttg ggt gtt tta ggt			835
Thr Ala Val Ala Phe Thr Val Phe Leu Ala Ile Leu Gly Val Leu Gly			
230	235	240	245
atc ttt tta gat caa aag atg cca gtc aag cct gga aag tagacaatat			884
Ile Phe Leu Asp Gln Lys Met Pro Val Lys Pro Gly Lys			
250	255		
aaggtagggt tgg			897
<210> 1612			
<211> 258			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 1612			
Met Val Phe Ser Met His Asp Lys Gly Glu Thr Gln Glu Asn Pro Ala			
1	5	10	15
Asp Met Ser Gly Arg Leu Asn Thr Pro Ile Ser Thr Val Phe His Phe			
20	25	30	
Phe Ser Ser Leu Phe His Asp Ala Leu Arg Ser Val Ala Gln Trp Ser			
35	40	45	
Ala Trp Lys Lys Ile Ala Val Ser Val Val Ile Val Ala Ile Ile Ser			
50	55	60	
Val Thr Phe Leu Val Asp Val Pro Pro Ile Ser Val Tyr Arg Asp Trp			
65	70	75	80
Ala Asn Asn Ala Gly Asp Ala Phe Val Leu Val Phe Cys Ala Phe Tyr			
85	90	95	

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Ile Leu Ile Thr Gln Phe Pro Ile Pro Arg Thr Val Leu Thr Leu Ala
    100                      105                      110

Ser Gly Val Leu Phe Gly Pro Val Leu Gly Ser Val Val Ala Leu Gly
    115                      120                      125

Ser Thr Thr Val Ser Ala Val Ile Ser Leu Leu Ile Val Arg Gly Leu
    130                      135                      140

Leu Gly Asp Trp Met Ala Pro Arg Leu Thr His Pro Ala Val Ser Arg
    145                      150                      155                      160

Ile Asn Thr Arg Leu Glu Gln Arg Gly Trp Leu Ala Ile Thr Ser Leu
    165                      170                      175

Arg Met Ile Ala Ala Ile Pro Phe Ser Ile Leu Asn Tyr Val Ala Ala
    180                      185                      190

Leu Thr Ser Val Pro Val Phe Ser Phe Ala Ile Ala Thr Leu Ile Gly
    195                      200                      205

Ser Ala Pro Gly Thr Ile Val Thr Val Val Leu Gly Asp Ala Val Thr
    210                      215                      220

Gly Ser Gly Asn Trp Thr Ala Val Ala Phe Thr Val Phe Leu Ala Ile
    225                      230                      235                      240

Leu Gly Val Leu Gly Ile Phe Leu Asp Gln Lys Met Pro Val Lys Pro
    245                      250                      255

Gly Lys

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<210> 1613

<211> 720

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(697)

<223> RXA00151

<400> 1613

aagtagacaa tataaggtag ggttgagaa gattctttac ttcttcactc attcgccctg 60

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acagcgaatc cactacaata aacaaagggg gcagccaccc atg tgg gca ctg cat    115
                Met Trp Ala Leu His
                1                      5

```

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gcc aga tac cgc ggc cga gac aca cga cga gcc gaa ttg gtt aaa aga    163
Ala Arg Tyr Arg Gly Arg Asp Thr Arg Arg Ala Glu Leu Val Lys Arg
                10                      15                      20

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ttt gca gaa gct ttg tcc acc ctc gaa ggt gct ggc cag ttt gaa gtc    211
Phe Ala Glu Ala Leu Ser Thr Leu Glu Gly Ala Gly Gln Phe Glu Val
                25                      30                      35

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att ggt gtc gaa gac atc cga gca cac atc acc tca ccg tta acc aca    259
Ile Gly Val Glu Asp Ile Arg Ala His Ile Thr Ser Pro Leu Thr Thr

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40	45	50	
tgt gat gtt gtc atg gcg cta ctc gca gct ggc gat tgg gca atc gga			307
Cys Asp Val Val Met Ala Leu Leu Ala Ala Gly Val Asp Trp Ala Ile Gly			
55	60	65	
att ggt gtt atc ccc acc gtt gac gga aca gtc gat gaa tcg gat gag			355
Ile Gly Val Ile Pro Thr Val Asp Gly Thr Val Asp Glu Ser Asp Glu			
70	75	80	85
gcc atc atc gaa cag gta aag aaa att tcc tct gat gct ctg cgc ccc			403
Ala Ile Ile Glu Gln Val Lys Lys Ile Ser Ser Asp Ala Leu Arg Pro			
90	95	100	
acc gcc aag gcg gga acg gtc aaa gtt agg atc gcc gga acc aaa cgg			451
Thr Ala Lys Ala Gly Thr Val Lys Val Arg Ile Ala Gly Thr Lys Arg			
105	110	115	
gac aat act caa gcc ttc aac atc tcc gct gca ttc acg ttg att ggg			499
Asp Asn Thr Gln Ala Phe Asn Ile Ser Ala Ala Phe Thr Leu Ile Gly			
120	125	130	
caa gtt ctg tca aag cgc acc atc gaa gga cgc gaa gcc acc gca ctc			547
Gln Val Leu Ser Lys Arg Thr Ile Glu Gly Arg Glu Ala Thr Ala Leu			
135	140	145	
gtc cgt tct gga ctg aat caa aat gag gca gcc caa gag ctc ggt att			595
Val Arg Ser Ser Gly Leu Asn Gln Asn Glu Ala Ala Gln Glu Leu Gly Ile			
150	155	160	165
tcc aag cag gca atg tcg cag cga ttg cag gcg gca ggt tgg cag gcg			643
Ser Lys Gln Ala Met Ser Gln Arg Leu Gln Ala Ala Gly Trp Gln Ala			
170	175	180	
gaa tct gct ggt tgg caa ttg gcc gta aac ctc atc gag cag gct ggc			691
Glu Ser Ala Gly Trp Gln Leu Ala Val Asn Leu Ile Glu Gln Ala Gly			
185	190	195	
aag cgc tagcaggcga ttttaagacc tga			720
Lys Arg			

<210> 1614

<211> 199

<212> FRT

<213> Corynebacterium glutamicum

<400> 1614

Met	Trp	Ala	Leu	His	Ala	Arg	Tyr	Arg	Gly	Arg	Asp	Thr	Arg	Arg	Ala
1				5					10					15	

Glu	Leu	Val	Lys	Arg	Phe	Ala	Glu	Ala	Leu	Ser	Thr	Leu	Glu	Gly	Ala
			20					25					30		

Gly	Gln	Phe	Glu	Val	Ile	Gly	Val	Glu	Asp	Ile	Arg	Ala	His	Ile	Thr
			35				40				45				

Ser	Pro	Leu	Thr	Thr	Cys	Asp	Val	Val	Met	Ala	Leu	Leu	Ala	Ala	Gly
		50				55					60				


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Asp Trp Ala Ile Gly Ile Gly Val Ile Pro Thr Val Asp Gly Thr Val
 65                      70                      75                      80

Asp Glu Ser Asp Glu Ala Ile Ile Glu Gln Val Lys Lys Ile Ser Ser
                      85                      90                      95

Asp Ala Leu Arg Pro Thr Ala Lys Ala Gly Thr Val Lys Val Arg Ile
                100                105                110

Ala Gly Thr Lys Arg Asp Asn Thr Gln Ala Phe Asn Ile Ser Ala Ala
                115                120                125

Phe Thr Leu Ile Gly Gln Val Leu Ser Lys Arg Thr Ile Glu Gly Arg
                130                135                140

Glu Ala Thr Ala Leu Val Arg Ser Gly Leu Asn Gln Asn Glu Ala Ala
                145                150                155                160

Gln Glu Leu Gly Ile Ser Lys Gln Ala Met Ser Gln Arg Leu Gln Ala
                165                170                175

Ala Gly Trp Gln Ala Glu Ser Ala Gly Trp Gln Leu Ala Val Asn Leu
                180                185                190

Ile Glu Gln Ala Gly Lys Arg
                195

```

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<210> 1615
<211> 549
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(526)
<223> RXA00153

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<400> 1615
cctcgatttg agtaaagagc acgtcctcgc ctgatttttc ggggtgtgttt ttgcgtggcg 60

agccctgcct ggcccttcca aattatgtag ggtggcctgc gtg gga gca ata att 115
                               Val Gly Ala Ile Ile
                               1                               5

tgg ttt atc gga gca ttg gtt ctt gct ggc ttg gaa ttg gca gta ggt 163
Trp Phe Ile Gly Ala Leu Val Leu Ala Gly Leu Glu Leu Ala Val Gly
                10                15                20

gag ttc acc tta ttg atg ctc ggc ggt gca gct ttg gca acc gcc gcc 211
Glu Phe Thr Leu Leu Met Leu Gly Gly Ala Ala Leu Ala Thr Ala Gly
                25                30                35

gtg gca ctc atc ggt gtc cca gta tgg gct gaa ttt gtc acc ttc gcg 259
Val Ala Leu Ile Gly Val Pro Val Trp Ala Glu Phe Val Thr Phe Ala
                40                45                50

gtg gcc tca gct gct cta ctg atg ttc att agg ccg gcc att aga aag 307
Val Ala Ser Ala Ala Leu Leu Met Phe Ile Arg Pro Ala Ile Arg Lys
                55                60                65

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cgt ctg ctg aaa cca aag gtt ctg gac tct tca cca cga gca ctt gtt 355
Arg Leu Leu Lys Pro Lys Val Leu Asp Ser Ser Pro Arg Ala Leu Val
70 75 80
ggc cac cgt gct gaa gtg ctc gaa gat gtc gga gcg acc agc ggg cag 403
Gly His Arg Ala Glu Val Leu Glu Asp Val Gly Ala Thr Ser Gly Gln
90 95 100
gtc cgc ctg gat ggt tca att tgg tcc gcc cgc agc atg gat ccc aca 451
Val Arg Leu Asp Gly Ser Ile Trp Ser Ala Arg Ser Met Asp Pro Thr
105 110 115
cac acc ttc gcg gaa ggt gaa att gtc agt gtc att gat atc caa ggc 499
His Thr Phe Ala Glu Gly Glu Ile Val Ser Val Ile Asp Ile Gln Gly
120 125 130
acg acc gcg att gta tgg aaa gaa gcc taaattttta acaatcaaat 546
Thr Thr Ala Ile Val Trp Lys Glu Ala
135 140
agt 549

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<210> 1616
<211> 142
<212> PRT
<213> Corynebacterium glutamicum

<400> 1616
Val Gly Ala Ile Ile Trp Phe Ile Gly Ala Leu Val Leu Ala Gly Leu
1 5 10 15
Glu Leu Ala Val Gly Glu Phe Thr Leu Leu Met Leu Gly Gly Ala Ala
20 25 30
Leu Ala Thr Ala Gly Val Ala Leu Ile Gly Val Pro Val Trp Ala Glu
35 40 45
Phe Val Thr Phe Ala Val Ala Ser Ala Ala Leu Met Phe Ile Arg
50 55 60
Pro Ala Ile Arg Lys Arg Leu Leu Lys Pro Lys Val Leu Asp Ser Ser
65 70 75 80
Pro Arg Ala Leu Val Gly His Arg Ala Glu Val Leu Glu Asp Val Gly
85 90 95
Ala Thr Ser Gly Gln Val Arg Leu Asp Gly Ser Ile Trp Ser Ala Arg
100 105 110
Ser Met Asp Pro Thr His Thr Phe Ala Glu Gly Glu Ile Val Ser Val
115 120 125
Ile Asp Ile Gln Gly Thr Thr Ala Ile Val Trp Lys Glu Ala
130 135 140

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<210> 1617
<211> 906
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(883)
<223> RXA00155

<400> 1617
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ccacctagt caaagcactg cactacactt ccctaacact      atg gaa att cga gca 115
                                         Met Glu Ile Arg Ala
                                         1                               5

aac gtt tat tca ccg ctt caa aat act gcc gtc tgg cta ggt gcg tgg 163
Asn Val Tyr Ser Pro Leu Gln Asn Thr Ala Val Trp Leu Gly Ala Trp
                               10                               15                               20

ctc tat gaa tta gtg ccc acc gaa gat gtc atc gat gcg ttc gtc gat 211
Leu Tyr Glu Leu Val Pro Thr Glu Asp Val Ile Asp Ala Phe Val Asp
                               25                               30                               35

ctc ggc ggc ccg cac acc ttc ggc gac ggc ggg ctg ctc gat atg ctg 259
Leu Gly Gly Pro His Thr Phe Gly Asp Gly Gly Leu Leu Asp Met Leu
                               40                               45                               50

cga act tta aaa gaa tta aca agc acg ctt atc gac gcc ccc ttc cac 307
Arg Thr Leu Lys Glu Leu Thr Ser Thr Leu Ile Asp Ala Pro Phe His
                               55                               60                               65

ggg cgc att tta act ctc gca ctc agc ggc cca ggc caa gtg ccg gcg 355
Gly Pro Ile Leu Thr Leu Ala Leu Ser Gly Pro Gly Gln Val Pro Ala
                               70                               75                               80                               85

ttg ccg gca ggt tca cgc gct gcg gtc ttg gcc tcc gcc tcg aag gag 403
Leu Pro Ala Gly Ser Arg Ala Ala Val Leu Ala Ser Ala Ser Lys Glu
                               90                               95                               100

ggg gcg ttg gtg ctg ggc ggc gtc gat aag cag cat tct tgg gcg ctt 451
Gly Ala Leu Val Leu Gly Gly Val Asp Lys Gln His Ser Trp Ala Leu
                               105                               110                               115

att cct acg cgc ggt aag gat gcc act gag tgg aat ttg gtg gag gtg 499
Ile Pro Thr Arg Gly Lys Asp Ala Thr Glu Trp Asn Leu Val Glu Val
                               120                               125                               130

gag ggc ttt ttg ccg gcg att gcg act gtc tcg ccc ggt gag gcg gat 547
Glu Gly Phe Leu Pro Ala Ile Ala Thr Val Ser Pro Gly Glu Ala Asp
                               135                               140                               145

cag ctg ctc cgt cag gcg aca gat cag gcg gca aat atc att gag tta 595
Gln Leu Leu Arg Gln Ala Thr Asp Gln Ala Asn Ile Ile Glu Leu
                               150                               155                               160                               165

agt ggc tac gct tca ctt gcg ccg aaa tct ttg aag aat ccg cga cta 643
Ser Gly Tyr Ala Ser Leu Ala Pro Lys Ser Leu Lys Asn Pro Arg Leu
                               170                               175                               180

acc gtg ggc atg ctg tca gat ttt tac gac acc ccg ggg ctt ccc tat 691
Thr Val Gly Met Leu Ser Asp Phe Tyr Asp Thr Pro Gly Leu Pro Tyr
                               185                               190                               195

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gca gtc cca gag agg tcg gcg aag ctt ttt gcg cgc gca gat cgc gtg 739
Ala Val Pro Glu Arg Ser Ala Lys Leu Phe Ala Arg Ala Asp Arg Val
      200                205                210

gct gcc atc gca gag acc gtg cag gaa acc atc ggc gat cac agc ctg 787
Ala Ala Ile Ala Glu Thr Val Gln Glu Thr Ile Gly Asp His Ser Leu
      215                220                225

gat cca cag ttg att ttc ctg tgg agc cat att cgg acc gcg cgc atg 835
Asp Pro Gln Leu Ile Phe Leu Trp Ser His Ile Arg Thr Ala Arg Met
      230                235                240                245

gct ggg gtg agt tat gcc ctc gca gag ttt gcg agg gac tat cac tcc 883
Ala Gly Val Ser Tyr Ala Leu Ala Glu Phe Ala Arg Asp Tyr His Ser
      250                255                260

tagttggcag ctggcgccgc tga 906

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<210> 1618

<211> 261

<212> PRT

<213> Corynebacterium glutamicum

<400> 1618

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Met Glu Ile Arg Ala Asn Val Tyr Ser Pro Leu Gln Asn Thr Ala Val
  1              5              10              15

Trp Leu Gly Ala Trp Leu Tyr Glu Leu Val Pro Thr Glu Asp Val Ile
      20              25              30

Asp Ala Phe Val Asp Leu Gly Gly Pro His Thr Phe Gly Asp Gly Gly
      35              40              45

Leu Leu Asp Met Leu Arg Thr Leu Lys Glu Leu Thr Ser Thr Leu Ile
      50              55              60

Asp Ala Pro Phe His Gly Pro Ile Leu Thr Leu Ala Leu Ser Gly Pro
      65              70              75              80

Gly Gln Val Pro Ala Leu Pro Ala Gly Ser Arg Ala Ala Val Leu Ala
      85              90              95

Ser Ala Ser Lys Glu Gly Ala Leu Val Leu Gly Gly Val Asp Lys Gln
      100             105             110

His Ser Trp Ala Leu Ile Pro Thr Arg Gly Lys Asp Ala Thr Glu Trp
      115             120             125

Asn Leu Val Glu Val Glu Gly Phe Leu Pro Ala Ile Ala Thr Val Ser
      130             135             140

Pro Gly Glu Ala Asp Gln Leu Leu Arg Gln Ala Thr Asp Gln Ala Ala
      145             150             155             160

Asn Ile Ile Glu Leu Ser Gly Tyr Ala Ser Leu Ala Pro Lys Ser Leu
      165             170             175

Lys Asn Pro Arg Leu Thr Val Gly Met Leu Ser Asp Phe Tyr Asp Thr
      180             185             190

```

Pro Gly Leu Pro Tyr Ala Val Pro Glu Arg Ser Ala Lys Leu Phe Ala
 195 200 205

Arg Ala Asp Arg Val Ala Ala Ile Ala Glu Thr Val Gln Glu Thr Ile
 210 215 220

Gly Asp His Ser Leu Asp Pro Gln Leu Ile Phe Leu Trp Ser His Ile
 225 230 235 240

Arg Thr Ala Arg Met Ala Gly Val Ser Tyr Ala Leu Ala Glu Phe Ala
 245 250 255

Arg Asp Tyr His Ser
 260

<210> 1619

<211> 1305

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1282)

<223> RXA00159

<400> 1619

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gtgtgcgatg gtgcaatgat ccccgctaac ctgggattcc atg gag aat gtt agt 115
 Met Glu Asn Val Ser
 1 5

tcc gtc acg tcg gat ggt tcg gta gcg gat gtg cat gcc gaa cgg tgg 163
 Ser Val Thr Ser Asp Gly Ser Val Ala Asp Val His Ala Glu Arg Trp
 10 15 20

caa gaa ttg ctc gca cgt ttg gat gcc gat gcg ccg gat att gcg gag 211
 Gln Glu Leu Leu Ala Arg Leu Asp Ala Asp Ala Pro Asp Ile Ala Glu
 25 30 35

ggc acc gcc gca aag ttg ctc gct acg atc ccg ggc tat gag ctc gtt 259
 Gly Thr Ala Ala Lys Leu Leu Ala Thr Ile Pro Gly Tyr Glu Leu Val
 40 45 50

gac gcg ggg ccg atc agg gag tcg tcg ata cgc aat acg gcc ttg att 307
 Asp Ala Gly Pro Ile Arg Glu Ser Ser Ile Arg Asn Thr Ala Leu Ile
 55 60 65

att cgc gtg att aac gcg ggc acc gag cca aag gcc gag gac ttg cct 355
 Ile Arg Val Ile Asn Ala Gly Thr Glu Pro Lys Ala Glu Asp Leu Pro
 70 75 80 85

gag gct tta agg ctt gcc gac gaa cgt ata gcg caa aat gtg ccg ctg 403
 Glu Ala Leu Arg Leu Ala Asp Glu Arg Ile Ala Gln Asn Val Pro Leu
 90 95 100

gga agt gtg ctg cac ggt ttt ccg atg tct ctg ggg gaa att ctg gag 451
 Gly Ser Val Leu His Gly Phe Arg Met Ser Leu Gly Glu Ile Leu Glu
 105 110 115

cat ttg gtg cag ttg ggc ccg gaa tac aat att gat ccc ggc aga atg	499
His Leu Val Gln Leu Gly Pro Glu Tyr Asn Ile Asp Pro Gly Arg Met	
120 125 130	
ctg cgc tgg tcc aca ctg atg tgg cgc gtc aat gat gcc ttt tct acg	547
Leu Arg Trp Ser Thr Leu Met Trp Ala Val Asn Asp Ala Phe Ser Thr	
135 140 145	
cgt gcc aca agg gtg tac cgc gat cac gag gtc gcc acg gcg atc gcc	595
Arg Ala Thr Arg Val Tyr Arg Asp His Glu Val Ala Thr Ala Ile Ala	
150 155 160 165	
gat tcg gtg cga agg tca gaa tgg atc ggc aaa gcg gtc tcg gaa ggc	643
Asp Ser Val Arg Arg Ser Glu Trp Ile Gly Lys Ala Val Ser Glu Gly	
170 175 180	
tct gaa ctg tca gag ctt tta tgg ggt gct gcg atg tat gac gtt ccc	691
Ser Glu Leu Ser Glu Leu Leu Trp Gly Ala Ala Met Tyr Asp Val Pro	
185 190 195	
gcc gac act cct cta aga gca ttg gca gcc acc tca cct gat cat gcg	739
Ala Asp Thr Pro Leu Arg Ala Leu Ala Ala Thr Ser Pro Asp His Ala	
200 205 210	
aaa gct gaa aca cag atc cag aag tgg act cag cgc gcc gga gtg cgg	787
Lys Ala Glu Thr Gln Ile Gln Lys Trp Thr Gln Arg Ala Gly Val Arg	
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Val Leu Ala Ser Val Gln Pro Ser Val Ile Val Gly Ile Val Ile Gly	
230 235 240 245	
gag ccg aag cga aac gtg gac ggc cct ggt ttt gct gtg ggt ttg ggt	883
Glu Pro Lys Arg Asn Val Asp Gly Pro Gly Phe Ala Val Gly Leu Gly	
250 255 260	
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Arg Ala Glu Val Leu Ser Lys Leu Ala Asp Ser Tyr Lys Asp Ala Ser	
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ctt gta ttg aag gct gcc gat aat ctg aaa ctt aat gag gtg cag cgg	979
Leu Val Leu Lys Ala Ala Asp Asn Leu Lys Leu Asn Glu Val Gln Arg	
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gca caa gat ttg tca tgg aag ttg gct atc cat gca agc cca cgg gtg	1027
Ala Gln Asp Leu Ser Trp Lys Leu Ala Ile His Ala Ser Pro Arg Val	
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Thr Glu Ile Leu Ala Gln Lys Tyr Val Lys Pro Leu Arg Glu Ser Gly	
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Glu Phe Ala His Glu Ile Val Glu Ser Leu Arg Ala Tyr Val Asp Asn	
330 335 340	
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Gln Met Asn Ile Pro Ala Ala Ala Arg Ser Ile Pro Val His Val Asn	
345 350 355	
acg ctt cgc tat cgg ttg cgc cgg ttt gag gag tta acg ggc tgc tat	1219

Thr Leu Arg Tyr Arg Leu Arg Arg Phe Glu Glu Leu Thr Gly Cys Tyr
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 ttg gag gat aca tcc acg gtc att gaa gtg tgc tgg gtg ctg gaa gtc 1267
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<210> 1620

<211> 394

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1620

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 Pro Asp Ile Ala Glu Gly Thr Ala Ala Lys Leu Leu Ala Thr Ile Pro
 35 40 45
 Gly Tyr Glu Leu Val Asp Ala Gly Pro Ile Arg Glu Ser Ser Ile Arg
 50 55 60
 Asn Thr Ala Leu Ile Ile Arg Val Ile Asn Ala Gly Thr Glu Pro Lys
 65 70 75 80
 Ala Glu Asp Leu Pro Glu Ala Leu Arg Leu Ala Asp Glu Arg Ile Ala
 85 90 95
 Gln Asn Val Pro Leu Gly Ser Val Leu His Gly Phe Arg Met Ser Leu
 100 105 110
 Gly Glu Ile Leu Glu His Leu Val Gln Leu Gly Pro Glu Tyr Asn Ile
 115 120 125
 Asp Pro Gly Arg Met Leu Arg Trp Ser Thr Leu Met Trp Ala Val Asn
 130 135 140
 Asp Ala Phe Ser Thr Arg Ala Thr Arg Val Tyr Arg Asp His Glu Val
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 Ala Thr Ala Ile Ala Asp Ser Val Arg Arg Ser Glu Trp Ile Gly Lys
 165 170 175
 Ala Val Ser Glu Gly Ser Glu Leu Ser Glu Leu Leu Trp Gly Ala Ala
 180 185 190
 Met Tyr Asp Val Pro Ala Asp Thr Pro Leu Arg Ala Leu Ala Ala Thr
 195 200 205
 Ser Pro Asp His Ala Lys Ala Glu Thr Gln Ile Gln Lys Trp Thr Gln
 210 215 220
 Arg Ala Gly Val Arg Val Leu Ala Ser Val Gln Pro Ser Val Ile Val

[illegible]


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aag tat ttg cag tat gag aat gag tcc att gag tta gaa aac atg gaa 355
Lys Tyr Leu Gln Tyr Glu Asn Glu Ser Ile Glu Leu Glu Asn Met Glu
70 75 80 85

gcc aaa atg atg gcg gag caa ggc aaa aca cca gtt gcg caa tca gag 403
Ala Lys Met Met Ala Glu Gln Gly Lys Thr Pro Val Ala Gln Ser Glu
90 95 100

cag gaa gat agc ttc gtt cag ctc tct cac cgt ccg agc ctg gtg gaa 451
Gln Glu Asp Ser Phe Val Gln Leu Ser His Arg Pro Ser Leu Val Glu
105 110 115

gat gac agc gtc aag gaa atc gac gaa tcc ttc ctg ccg tct cgc ccg 499
Asp Asp Ser Ser Val Lys Glu Ile Asp Glu Ser Phe Leu Pro Ser Arg Pro
120 125 130

acg atg gat gtg gaa gag ttc aac agg ttg aat gat ccg cat gca cgg 547
Thr Met Asp Val Glu Glu Phe Asn Arg Leu Asn Asp Pro His Ala Arg
135 140 145

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Arg Arg Arg Lys Ala
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<210> 1622
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<212> PRT
<213> Corynebacterium glutamicum

<400> 1622
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35 40 45

Gln Asn Leu Gly Tyr Ala Phe Gln Trp Pro Leu Ile Gly Ala Phe Phe
50 55 60

Val Tyr Ala Tyr Arg Lys Tyr Leu Gln Tyr Glu Asn Glu Ser Ile Glu
65 70 75 80

Leu Glu Asn Met Glu Ala Lys Met Met Ala Glu Gln Gly Lys Thr Pro
85 90 95

Val Ala Gln Ser Glu Gln Glu Asp Ser Phe Val Gln Leu Ser His Arg
100 105 110

Pro Ser Leu Val Glu Asp Asp Ser Val Lys Glu Ile Asp Glu Ser Phe
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130

135

140

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<210> 1623

<211> 2196

<212> DNA

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<220>

<221> CDS

<222> (101)..(2173)

<223> RXA00169

<400> 1623

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Met Ser Leu Gly Asn
1 5

cca gca gca atg ctc gct gcg tac aac acc agc acg cag gtg gca ccg 163
Pro Ala Ala Met Leu Ala Ala Tyr Asn Thr Ser Thr Gln Val Ala Pro
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Gln Pro Gln Leu Gly Pro Arg Ala Gly Glu Val Gln Leu Ser Ser Glu
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Gln Gln Ala Met Ile Asp Tyr Val Leu Ala Gly Lys Asp Val Ile Val
40 45 50

gat gcc acc gta ggc tcg ggc aaa act acc gct att caa cga ctg tgt 307
Asp Ala Thr Val Gly Ser Gly Lys Thr Thr Ala Ile Gln Arg Leu Cys
55 60 65

tcg atc atg ggt gca gac cat gac gtg ctg tat ttg acg tat tcg aag 355
Ser Ile Met Gly Ala Asp His Asp Val Leu Tyr Leu Thr Tyr Ser Lys
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Leu Leu Lys Val Asp Ala Gln Gln Arg Val Arg Gly Ala Lys Val Gln
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aac tat cac ggc att gtc tat ccg cat cta ctc aag gcc ggc atc aag 451
Asn Tyr His Gly Ile Val Tyr Pro His Leu Leu Lys Ala Gly Ile Lys
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Cys Gly Ile Ser Glu Ser Ile Arg Glu Phe Asn Lys Asn Phe Lys His
120 125 130

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Ile Ser Arg Thr Phe Pro Ser Tyr Asp Leu Leu Val Ile Asp Glu Tyr
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Val Arg Ser Asp Thr Thr Leu Asp Pro Gln Glu Phe Ala Ala Gln Leu				190		195	
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Cys Glu Asp Pro Val Phe Ala Pro Phe Thr Gln Ser Phe Arg Ile Gly							
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320				325		330	
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cca gtg gtc atg cgc aat gtg ttt ttg gtg gca gca tca cgc ggt aaa	1171						
Pro Val Val Met Arg Asn Val Phe Leu Val Ala Ala Ser Arg Gly Lys							
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Asn Lys Val Val Phe Val Arg Ser Asp Ser Leu Gln Ala Ala Tyr Glu							
365				370		375	
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Ala Gly Ala Asp Trp Ala Ala Gly Leu Ala Val Gly Val Val Asp Asn							
380				385		390	
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Asn Thr Glu Val Ala Pro Glu Val Asp Ala His Thr Pro Ala Glu Glu							
395				400		405	

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Ser Lys Gly Asp Val Gly Glu Val Gln Ser Gln Ile Glu Arg Met Met	
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Gly Phe Ile Pro Val Ser Val Phe Lys Glu Leu Phe Asp Ala Pro	
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Ser Glu Tyr Ala Arg Pro Ile Ser Val Thr Glu Ala Phe Asp Phe Lys	
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Tyr Ala Glu Asn Val Glu Ala Cys Phe Asp Leu Asp Val Lys Arg	
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Leu Asp Asn Gly Lys Gly Ala Ala Ile Glu Val Asn Arg Ser Asp Gly	
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Leu Ile Asp Leu Ser Pro Thr Val Gly Asn Phe Gln Glu Ala Val Phe	
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Phe Lys Asp Tyr Asn Val His Thr Ala Leu Ser Ala Tyr Pro Ser Gln	
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Phe Ala Lys Asn Leu Lys Arg Leu Val Lys Lys Asn Asn Ser Val Trp	
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cgt aac tgc ctt att gtc aca gca gcg tcc aca gag cag atg ccg tat	1747
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Val Asp Gln Val Arg Ser Ser Ile Pro Val Ala Ala Glu Lys Ala Leu	
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Val Ser Arg Leu Ser Thr Arg Leu Asn Ala Asp Ser Arg Asn Gln Ile	
570 575 580	
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Pro Leu Ile Leu Asp Gly Glu Ala Val Gln Ser Lys Val Val Arg Thr	
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Pro Met Ser Phe Ala Gly Val Ala Asp Ala Val His Lys Gly Val Leu	
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Tyr Glu Leu Lys Phe Val Ser Glu Leu Thr His Pro Met Phe Leu Gln	
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ctc gca atg tat ttg gtc atg tct ggg atg aag gac ggt att ttg tgg	2035
Leu Ala Met Tyr Leu Val Met Ser Gly Met Lys Asp Gly Ile Leu Trp	
630 635 640 645	

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 650 655 660

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<211> 691

<212> PRT

<213> Corynebacterium glutamicum

<400> 1624

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 35 40 45
 Lys Asp Val Ile Val Asp Ala Thr Val Gly Ser Gly Lys Thr Thr Ala
 50 55 60
 Ile Gln Arg Leu Cys Ser Ile Met Gly Ala Asp His Asp Val Leu Tyr
 65 70 75 80
 Leu Thr Tyr Ser Lys Leu Leu Lys Val Asp Ala Gln Gln Arg Val Arg
 85 90 95
 Gly Ala Lys Val Gln Asn Tyr His Gly Ile Val Tyr Pro His Leu Leu
 100 105 110
 Lys Ala Gly Ile Lys Cys Gly Ile Ser Glu Ser Ile Arg Glu Phe Asn
 115 120 125
 Lys Asn Phe Lys His Ile Ser Arg Thr Phe Pro Ser Tyr Asp Leu Leu
 130 135 140
 Val Ile Asp Glu Tyr Gln Asp Ile Asn Glu Asp Tyr Ala Glu Leu Leu
 145 150 155 160
 Arg Asn Ile Lys Ser Val Asn Pro Leu Met Gln Ile Val Met Val Gly
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 Asp Leu Glu Gln Lys Val Arg Ser Asp Thr Thr Leu Asp Pro Gln Glu
 180 185 190
 Phe Ala Ala Gln Leu Cys Glu Asp Pro Val Phe Ala Pro Phe Thr Gln
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 Ser Phe Arg Ile Gly Glu Ala Met Ala Ala Gly Leu Ala Asp Ala Trp

210					215					220					
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Leu	Leu	Cys	Leu	Gly	Ser	Arg	Asn	Gly	Gln	Met	Ser	Asp	Ala	Leu	Asn
			260					265					270		
Val	Val	Glu	Arg	Lys	Ser	Pro	Ala	Lys	Phe	Asn	Lys	Lys	Thr	Val	Phe
		275					280					285			
Ala	Ser	Ile	Arg	Asp	Gly	Asp	Ser	Gln	Ile	Ala	His	Pro	Asn	Asp	Ala
		290				295					300				
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						310					315				320
Cys	Val	Val	Phe	Asp	Tyr	Asp	Glu	Glu	Phe	Trp	Asp	Met	Arg	Leu	Gly
				325					330					335	
Tyr	Pro	Asn	Val	Asp	Pro	Val	Val	Met	Arg	Asn	Val	Phe	Leu	Val	Ala
			340					345					350		
Ala	Ser	Arg	Gly	Lys	Asn	Lys	Val	Val	Phe	Val	Arg	Ser	Asp	Ser	Leu
			355				360					365			
Gln	Ala	Ala	Tyr	Glu	Ala	Gly	Ala	Asp	Trp	Ala	Ala	Gly	Leu	Ala	Val
		370				375					380				
Gly	Val	Val	Asp	Asn	Asn	Thr	Glu	Val	Ala	Pro	Glu	Val	Asp	Ala	His
				385		390					395				400
Thr	Pro	Ala	Glu	Glu	Ser	Lys	Gly	Asp	Val	Gly	Glu	Val	Gln	Ser	Gln
				405				410						415	
Ile	Glu	Arg	Met	Met	Gly	Phe	Ile	Pro	Val	Ser	Val	Phe	Lys	Glu	Leu
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Pro	Glu	Leu	Ala	Pro	Ser	Glu	Tyr	Ala	Arg	Pro	Ile	Ser	Val	Thr	Glu
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Ala	Phe	Asp	Phe	Lys	Tyr	Ala	Glu	Asn	Val	Glu	Ala	Cys	Phe	Asp	Leu
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		465				470					475			480	
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Gln	Glu	Ala	Val	Phe	Phe	Lys	Asp	Tyr	Asn	Val	His	Thr	Ala	Leu	Ser
			500				505						510		
Ala	Tyr	Pro	Ser	Gln	Phe	Ala	Lys	Asn	Leu	Lys	Arg	Leu	Val	Lys	Lys
			515				520					525			
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Glu Gln Met Arg Tyr Val Asp Gln Val Arg Ser Ser Ile Pro Val Ala
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Ala Glu Lys Ala Leu Val Ser Arg Leu Ser Thr Arg Leu Asn Ala Asp
565 570 575

Ser Arg Asn Gln Ile Pro Leu Ile Leu Asp Gly Glu Ala Val Gln Ser
580 585 590

Lys Val Val Arg Thr Pro Met Ser Phe Ala Gly Val Ala Asp Ala Val
595 600 605

His Lys Gly Val Leu Tyr Glu Leu Lys Phe Val Ser Glu Leu Thr His
610 615 620

Pro Met Phe Leu Gln Leu Ala Met Tyr Leu Val Met Ser Gly Met Lys
625 630 635 640

Asp Gly Ile Leu Trp Asn Thr Arg Thr Asp Glu Ala Trp Gln Val Arg
645 650 655

Val Pro Asp Pro Lys Arg Phe Leu Asn Ala Val Val Leu Cys Val Ser
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<210> 1625

<211> 1977

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1954)

<223> RXA00170

<400> 1625

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Met Leu Leu Ala Ile
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ggg gtt gca tct ccg gta gct caa gca caa gtg gaa gat caa ttt gag 163
Gly Val Ala Ser Pro Val Ala Gln Ala Gln Val Glu Asp Gln Phe Glu
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Leu Val Lys Glu Ile Ser Asp Glu Gln Phe Ala Asp Asp Gly Val Asp
25 30 35

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Tyr Val Pro Asn Arg Asn Ala Pro Thr Val Lys Glu Gln Leu Glu Asp
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cca acc tct ggt ccg atg gat aca aac tat ccc ctt act cag cga cag Pro Thr Ser Gly Pro Met Asp Thr Asn Tyr Pro Leu Thr Gln Arg Gln 215 220 225	787
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Leu Gly Arg Glu Thr Gly Arg Leu Gly Phe Pro Glu Ala Asp Glu Thr	
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cct gag gtt tct ggt cta ttc cat gtg gtg aat ttt gcg gag cgc ggg	1123
Pro Glu Val Ser Gly Leu Phe His Val Val Asn Phe Ala Glu Arg Gly	
330 335 340	
gtg att gcg tgg aat gga atc cta gcc gcc aga gag ctg tat ggt gat	1171
Val Ile Ala Trp Asn Gly Ile Leu Gly Ala Arg Glu Leu Thr Tyr Gly Asp	
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gtt tac tcc ctg tgg ctg caa tac caa aat acc gat act cct tta ggg	1219
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tgg cgg ata cca tca ttg aca tca tta aat gag tca ctc gaa caa gaa	1267
Trp Pro Ile Pro Ser Leu Thr Ser Leu Asn Glu Ser Leu Glu Gln Glu	
375 380 385	
ttc acc aga ggt gtt gtt tta ggc tca ggt gat gca ctg aca tgg att	1315
Phe Thr Arg Gly Val Val Leu Gly Ser Gly Asp Ala Leu Thr Trp Ile	
390 395 400 405	
cct gac gat gaa gaa aga agt ttg gag gat ttc ctc cca att gga agt	1363
Pro Asp Asp Glu Glu Arg Ser Leu Glu Asp Phe Leu Pro Ile Gly Ser	
410 415 420	
agc ggc tca tcc tca tgc agc caa gag atg acc ctg ttt tcc cag cgt	1411
Ser Gly Ser Ser Ser Ser Ser Gln Glu Met Thr Leu Phe Ser Gln Arg	
425 430 435	
gca caa tac gtg gat tgc aag aat ctt ccc gat tta gat gag cag aga	1459
Ala Gln Tyr Val Asp Cys Lys Asn Leu Pro Asp Leu Asp Glu Gln Arg	
440 445 450	
aaa act gaa aac aac att gaa aag aat ggt ggc ccg atc aaa aaa gag	1507
Lys Thr Glu Asn Asn Ile Glu Lys Asn Gly Gly Pro Ile Lys Lys Glu	
455 460 465	
tat agt tgc cga ggt ttc ccc acc gag ttc aga ttt gtc gtg aga aaa	1555
Tyr Ser Ser Arg Gly Phe Pro Thr Glu Phe Arg Phe Val Val Arg Lys	
470 475 480 485	
ggg cat tat gac cgt tac agg aat gaa ggc tgg gga tat tta aaa aac	1603
Gly His Tyr Asp Arg Tyr Arg Asn Glu Gly Trp Gly Tyr Leu Lys Asn	
490 495 500	
tat tgc aaa cac aac ttc gcc aac cac gct atg gct gag gcc gta gta	1651
Tyr Cys Lys His Asn Phe Ala Asn His Ala Met Ala Glu Ala Val Val	
505 510 515	
gat aaa gcg gtg att gat tat ggc tca tgc cca gga acc agc tat tac	1699
Asp Lys Ala Val Ile Asp Tyr Gly Ser Ser Pro Gly Thr Ser Tyr Tyr	
520 525 530	
aag ttc gag aaa acg gtg tac ttt cta gat tgc aga act tat aca ttc	1747
Lys Phe Glu Lys Thr Val Tyr Phe Leu Asp Cys Arg Thr Tyr Thr Phe	

535	540	545	
aat aag aac tca gga tgt	aaa gaa atg cac gct ccg	caa tgg gtg act	1795
Asn Lys Asn Ser Gly Cys	Lys Glu Met His Ala Pro	Gln Trp Val Thr	
550	555	560	565
att att tac aat cct cat	act ttc act gga gca	aat tgg aac aga ccc	1843
Ile Ile Tyr Asn Pro His	Thr Phe Thr Gly Ala	Asn Ser Asn Arg Pro	
570	575	580	
aag ggg gta att tca gca	tgg tgt aat tca acc	cca cct ggt gga atc	1891
Lys Gly Val Ile Ser Ala	Trp Cys Asn Ser Thr	Pro Pro Gly Gly Ile	
585	590	595	
gaa cac gag cct gaa att	tcc caa tgt cct gat	cat gtg aat ctt tat	1939
Glu His Glu Pro Glu Ile	Ser Gln Cys Pro Asp	His Val Asn Leu Tyr	
600	605	610	
aat aag ctt cgc ata	tgacagaacc ccatcaactg	tcg	1977
Asn Lys Leu Arg Ile			
615			

<210> 1626
 <211> 618
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1626
 Met Leu Leu Ala Ile Gly Val Ala Ser Pro Val Ala Gln Ala Gln Val
 1 5 10 15
 Glu Asp Gln Phe Glu Leu Val Lys Glu Ile Ser Asp Glu Gln Phe Ala
 20 25 30
 Asp Asp Gly Val Asp Tyr Val Pro Asn Arg Asn Ala Pro Thr Val Lys
 35 40 45
 Glu Gln Leu Glu Asp Phe Glu Ser Ala His Pro Glu Val Val Ile Glu
 50 55 60
 Tyr His Glu His Val Asn Asp Ser Lys Asp Asn Val Glu Glu Leu Pro
 65 70 75 80
 Leu Pro Lys Arg Asp Ile Val Ala Gly Glu Met Arg Ser Asp Val Ile
 85 90 95
 Glu Leu Pro Glu Gly Val Ser Lys Asp Glu Ala Asp Gln Val Glu Val
 100 105 110
 Ala Glu Ala Arg Leu Asn Glu Gly Ala Arg Leu Met Ala Ala Thr Gly
 115 120 125
 Cys Glu Ala Met Trp Pro Thr Gly Phe Ser Val Cys Gly Arg Ile Leu
 130 135 140
 Asp Ala Tyr Arg Gln Val Gly Gly Gln Leu Ser Trp Leu Gly Pro Pro
 145 150 155 160
 Lys Ser Asn Glu Leu Thr Asn Pro Asp Gly Val Gly Lys Arg Ser Glu
 165 170 175

Phe Val Gly Gly Ala Ile Tyr Trp His Pro Asp Thr Gly Ala Tyr Ala
 180 185 190
 Val Thr Leu Asp Gly Leu Arg Gln Trp Gly Thr Leu Asn Trp Glu Ser
 195 200 205
 Gly Pro Leu Gly Tyr Pro Thr Ser Gly Pro Met Asp Thr Asn Tyr Pro
 210 215 220
 Leu Thr Gln Arg Gln Thr Phe Gln Gly Gly Asp Asn Tyr Tyr Asn Pro
 225 230 235 240
 Leu Thr Gly Gly Ala Val Trp Gly Asp Ile Lys Gln Arg Tyr Glu Glu
 245 250 255
 Leu Gly Gly Ser Asn His Ala Ile Gly Ile Pro Ile Thr Asn Glu Leu
 260 265 270
 Pro Ser Gly Thr Glu Tyr Phe Tyr Asn Asn Phe Phe Asn Gly Thr Ile
 275 280 285
 Ser Trp Arg Asn Asp Arg Gln Thr Arg Phe Met Tyr Leu Ala Thr Gln
 290 295 300
 Arg Val Trp Asp Ala Leu Gly Arg Glu Thr Gly Arg Leu Gly Phe Pro
 305 310 315 320
 Glu Ala Asp Glu Thr Pro Glu Val Ser Gly Leu Phe His Val Val Asn
 325 330 335
 Phe Ala Glu Arg Gly Val Ile Ala Trp Asn Gly Ile Leu Gly Ala Arg
 340 345 350
 Glu Leu Tyr Gly Asp Val Tyr Ser Leu Trp Leu Gln Tyr Gln Asn Thr
 355 360 365
 Asp Thr Pro Leu Gly Trp Pro Ile Pro Ser Leu Thr Ser Leu Asn Glu
 370 375 380
 Ser Leu Glu Gln Glu Phe Thr Arg Gly Val Val Leu Gly Ser Gly Asp
 385 390 395 400
 Ala Leu Thr Trp Ile Pro Asp Asp Glu Glu Arg Ser Leu Glu Asp Phe
 405 410 415
 Leu Pro Ile Gly Ser Ser Gly Ser Ser Ser Ser Ser Gln Glu Met Thr
 420 425 430
 Leu Phe Ser Gln Arg Ala Gln Tyr Val Asp Cys Lys Asn Leu Pro Asp
 435 440 445
 Leu Asp Glu Gln Arg Lys Thr Glu Asn Asn Ile Glu Lys Asn Gly Gly
 450 455 460
 Pro Ile Lys Lys Glu Tyr Ser Ser Arg Gly Phe Pro Thr Glu Phe Arg
 465 470 475 480
 Phe Val Val Arg Lys Gly His Tyr Asp Arg Tyr Arg Asn Glu Gly Trp
 485 490 495

gct cgc acc gac gca gca agc gcc att cat gaa gca gaa gct gaa ttt 403
 Ala Arg Thr Asp Ala Ala Ser Ala Ile His Glu Ala Glu Ala Glu Phe
 90 95 100

tac aac caa ctt gct gcg gtc ctt gct cag tgatttaatg tggccgacac 453
 Tyr Asn Gln Leu Ala Ala Val Leu Ala Gln
 105 110

acc 456

<210> 1628

<211> 111

<212> PRT

<213> Corynebacterium glutamicum

<400> 1628

Met Ser Thr Thr Ile Lys Ala Ala Ala Pro Tyr Ser Leu His Ala His
 1 5 10 15

Asp Leu Glu Gln Leu Ala Val Asp Leu Thr Leu Val Thr Thr Phe Asp
 20 25 30

Ser Asn Ala Ala Val Asp Val Thr Pro Thr His Thr Glu Ala Pro Gly
 35 40 45

Phe Thr Leu His Glu Gly Thr Asp Thr Ala Pro Met Ala Pro Thr Leu
 50 55 60

Val Val Pro Ile Ser Ser Asp Ile Ser Thr Ala Val Ser Glu Ile Ser
 65 70 75 80

Thr Leu Val Gln Gln Ala Arg Thr Asp Ala Ala Ser Ala Ile His Glu
 85 90 95

Ala Glu Ala Glu Phe Tyr Asn Gln Leu Ala Ala Val Leu Ala Gln
 100 105 110

<210> 1629

<211> 408

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(385)

<223> RXA00174

<400> 1629

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taagccactg ggaatcataa aaaagaaagt agcactagct atg cct aat cac cca 115
 Met Pro Asn His Pro
 1 5

cct att tcc acc ttc gat gac cgt cgc tct gct atg cgc gaa ggc att 163
 Pro Ile Ser Thr Phe Asp Asp Arg Arg Ser Ala Met Arg Glu Gly Ile
 10 15 20

act gat tac ctt gcc aat aca aat gca aat ggg tta ggc ggt tac agc 211
 Thr Asp Tyr Leu Ala Asn Thr Asn Ala Asn Gly Leu Gly Gly Tyr Ser
 25 30 35

atc agc gac acc cac ctc gac aat ctt gct gag aaa ttc acc cgc aca 259
 Ile Ser Asp Thr His Leu Asp Asn Leu Ala Glu Lys Phe Thr Arg Thr
 40 45 50

cat ggt gaa gca cag tac gat gcc ggc ttt gat ccc aat gat ctt gaa 307
 His Gly Glu Ala Gln Tyr Asp Ala Gly Phe Asp Pro Asn Asp Leu Glu
 55 60 65

cca gag act ttt gtt cgt gac att gag atg agc tgg gat gag cgt gct 355
 Pro Glu Thr Phe Val Arg Asp Ile Glu Met Ser Trp Asp Glu Arg Ala
 70 75 80 85

att gat cgt gcc ctg atc cac aca caa ctg tgaagaaaga agccgcaatg 405
 Ile Asp Arg Ala Leu Ile His Thr Gln Leu
 90 95

tcc 408

<210> 1630
 <211> 95
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1630
 Met Pro Asn His Pro Pro Ile Ser Thr Phe Asp Asp Arg Arg Ser Ala
 1 5 10 15

Met Arg Glu Gly Ile Thr Asp Tyr Leu Ala Asn Thr Asn Ala Asn Gly
 20 25 30

Leu Gly Gly Tyr Ser Ile Ser Asp Thr His Leu Asp Asn Leu Ala Glu
 35 40 45

Lys Phe Thr Arg Thr His Gly Glu Ala Gln Tyr Asp Ala Gly Phe Asp
 50 55 60

Pro Asn Asp Leu Glu Pro Glu Thr Phe Val Arg Asp Ile Glu Met Ser
 65 70 75 80

Trp Asp Glu Arg Ala Ile Asp Arg Ala Leu Ile His Thr Gln Leu
 85 90 95

<210> 1631
 <211> 753
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(730)
 <223> RXA00175

<400> 1631
 agctcgacag ccgtaaagaa gttgtaggtc tttttcgctt gggatactga tgctctccca 60

agcgaacatg	ggcgggagcc	catgtcgggg	tgttgtcgca	atg	gct	gtg	tgt	caa	115
				Met	Ala	Val	Cys	Gln	
				1				5	
cta cct cag cct gag aaa aca aca ctt ata aag aaa gac ctt tta ctc	163								
Leu Pro Gln Pro Glu Lys Thr Thr Leu Ile Lys Lys Asp Leu Leu Leu									
	10			15			20		
atg act tct aca act aac tcc acc gcc atg ttc aac gac cac ctt atc	211								
Met Thr Ser Thr Asn Ser Thr Ala Met Phe Asn Asp His Leu Ile									
	25			30			35		
cct atg gca gag ctt gat gaa caa gct ctg cgc gac agc gtt ggt tct	259								
Pro Met Ala Glu Leu Asp Glu Gln Ala Leu Arg Arg Asp Ser Val Gly Ser									
	40			45			50		
tgg gca cag tac aag cac ccg ctt gac cag cgc aaa gaa cca gag ctc	307								
Trp Ala Gln Tyr Lys His Pro Leu Asp Gln Arg Lys Glu Pro Glu Leu									
	55			60			65		
gtc ctt att cgt cgc gtc aac agc tca gag cgt gtg tgg gtc tta agt	355								
Val Leu Ile Arg Arg Val Asn Ser Ser Glu Arg Val Trp Val Leu Ser									
	70			75			80		85
ttc act gac ctg cgt cgt gat gca ggt ctt gtg cct cgt agc aca ccg	403								
Phe Thr Asp Leu Arg Ala Asp Ala Gly Leu Val Pro Arg Ser Thr Pro									
	90			95			100		
aat gct gac ccc tcc aat atc cgc aat acc att ttc tct gtc gct gtc	451								
Asn Ala Asp Pro Ser Asn Ile Arg Asn Thr Ile Phe Ser Val Ala Val									
	105			110			115		
cgc gat ctt gtc ctt gat cgc tca ctt ccc cgg ctg ctt aac ctc aac	499								
Arg Asp Leu Val Leu Asp Arg Ser Leu Pro Arg Leu Leu Asn Leu Asn									
	120			125			130		
ggg caa cca cca gca ggt gaa tgg gaa gaa ggc ttt gtc tac gtc gat	547								
Gly Gln Pro Pro Ala Gly Glu Trp Glu Glu Gly Phe Val Tyr Val Asp									
	135			140			145		
tat gac cag agc gac acc gta gat ggc tac ctc att gag cac agc gaa	595								
Tyr Asp Gln Ser Asp Thr Val Asp Gly Tyr Leu Ile Glu His Ser Glu									
	150			155			160		165
cct gtc tcc att gaa agt caa acc acc ggt gaa atg cac tat ttc gat	643								
Pro Val Ser Ile Glu Ser Gln Thr Thr Gly Glu Met His Tyr Phe Asp									
	170			175			180		
aag gtg cca ggc ggt gtg gct gtt acc aac aat ccc gat ggc act gaa	691								
Lys Val Pro Gly Gly Val Ala Val Thr Asn Asn Pro Asp Gly Thr Glu									
	185			190			195		
caa ggt gat gca cgc cgc tgg gta agc cac tgg gaa tca taaaaaagaa	740								
Gln Gly Asp Ala Arg Arg Trp Val Ser His Trp Glu Ser									
	200			205			210		
agtagcacta gct	750								

<210> 1632

 $\langle 211 \rangle$ 210

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1632

Met Ala Val Cys Gln Leu Pro Gln Pro Glu Lys Thr Thr Leu Ile Lys
 1 5 10 15

Lys Asp Leu Leu Met Thr Ser Thr Thr Asn Ser Thr Ala Met Phe
 20 25 30

Asn Asp His Leu Ile Pro Met Ala Glu Leu Asp Glu Gln Ala Leu Arg
 35 40 45

Asp Ser Val Gly Ser Trp Ala Gln Tyr Lys His Pro Leu Asp Gln Arg
 50 55 60

Lys Glu Pro Glu Leu Val Leu Ile Arg Arg Val Asn Ser Ser Glu Arg
 65 70 75 80

Val Trp Val Leu Ser Phe Thr Asp Leu Arg Ala Asp Ala Gly Leu Val
 85 90 95

Pro Arg Ser Thr Pro Asn Ala Asp Pro Ser Asn Ile Arg Asn Thr Ile
 100 105 110

Phe Ser Val Ala Val Arg Asp Leu Val Leu Asp Arg Ser Leu Pro Arg
 115 120 125

Leu Leu Asn Leu Asn Gly Gln Pro Pro Ala Gly Glu Trp Glu Glu Gly
 130 135 140

Phe Val Tyr Val Asp Tyr Asp Gln Ser Asp Thr Val Asp Gly Tyr Leu
 145 150 155 160

Ile Glu His Ser Glu Pro Val Ser Ile Glu Ser Gln Thr Thr Gly Glu
 165 170 175

Met His Tyr Phe Asp Lys Val Pro Gly Gly Val Ala Val Thr Asn Asn
 180 185 190

Pro Asp Gly Thr Glu Gln Gly Asp Ala Arg Arg Trp Val Ser His Trp
 195 200 205

Glu Ser
 210

<210> 1633

<211> 582

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(559)

<223> RXA00179

<400> 1633

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caaccataat tgaagaggtcc accagcccggt gaccaccatc atg atc gct att cac 115

Met Ile Ala Ile His
1 5

gct att gca gca atc ctg ttc cta gga cca gca aca gta gct aac tct 163
Ala Ile Ala Ala Ile Leu Phe Leu Gly Pro Ala Thr Val Ala Asn Ser
10 15 20

cag ttc cac gtc cgc gcg tac gat gca cac aac ggc aac acc caa gcc 211
Gln Phe His Val Arg Ala Tyr Asp Ala His Asn Gly Asn Thr Gln Ala
25 30 35

gct ggc tcc gca aaa acc ctt ttc aag att tcc cag tcc tac ggc atg 259
Ala Gly Ser Ala Lys Thr Leu Phe Lys Ile Ser Gln Ser Tyr Gly Met
40 45 50

ctg tcc ctg ctc gtg cct ttg ctg ggt atc gcc atc atg ctt ctc gat 307
Leu Ser Leu Leu Val Pro Leu Leu Gly Ile Ala Ile Met Leu Leu Asp
55 60 65

tgg tct ttc tac aag tct gaa ggc cag ttc cac gca gca atc gct ctc 355
Trp Ser Phe Tyr Lys Ser Glu Gly Gln Phe His Ala Ala Ile Ala Leu
70 75 80 85

agt gtt atc acc tgg gcg ctg ctt ctc ttc gtt atc ttc cca cgc cag 403
Ser Val Ile Thr Trp Ala Leu Leu Leu Phe Val Ile Phe Pro Arg Gln
90 95 100

aag aag atg atg ggt gct ctt gac ctt ctg gag gac gat gag cag gct 451
Lys Lys Met Met Gly Ala Leu Asp Leu Leu Glu Asp Asp Gln Ala
105 110 115

gca aag act tac gag atc gaa aac tgg gac aag gcg aag agc cag ctg 499
Ala Lys Thr Tyr Glu Ile Glu Asn Trp Asp Lys Ala Lys Ser Gln Leu
120 125 130

tcc atg ttc ggc ggc atc tgg gct ctg ctg tgg gtc atc atc gct gtg 547
Ser Met Phe Gly Gly Ile Trp Ala Leu Leu Trp Val Ile Ile Ala Val
135 140 145

ctg atg ttc atc taacacatct caaattgccaaa 582
Leu Met Phe Ile
150

<210> 1634

<211> 153

<212> PRT

<213> Corynebacterium glutamicum

<400> 1634

Met Ile Ala Ile His Ala Ile Ala Ala Ile Leu Phe Leu Gly Pro Ala
1 5 10 15

Thr Val Ala Asn Ser Gln Phe His Val Arg Ala Tyr Asp Ala His Asn
20 25 30

Gly Asn Thr Gln Ala Ala Gly Ser Ala Lys Thr Leu Phe Lys Ile Ser
35 40 45

Gln Ser Tyr Gly Met Leu Ser Leu Leu Val Pro Leu Leu Gly Ile Ala
50 55 60

Ile Met Leu Leu Asp Trp Ser Phe Tyr Lys Ser Glu Gly Gln Phe His
65 70 75 80

Ala Ala Ile Ala Leu Ser Val Ile Thr Trp Ala Leu Leu Leu Phe Val
85 90 95

Ile Phe Pro Arg Gln Lys Lys Met Met Gly Ala Leu Asp Leu Leu Glu
100 105 110

Asp Asp Glu Gln Ala Ala Lys Thr Tyr Glu Ile Glu Asn Trp Asp Lys
115 120 125

Ala Lys Ser Gln Leu Ser Met Phe Gly Gly Ile Trp Ala Leu Leu Trp
130 135 140

Val Ile Ile Ala Val Leu Met Phe Ile
145 150

<210> 1635

<211> 663

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(640)

<223> RXA00180

<400> 1635

aaacgaggat gttgatttcg ctgacgcagc tcagaagcgtt tcgaaagaaa gttaagcctt 60

agagggaaacc aaacgccaaag gcgatgagtc taaccgcagat atg aag aac ttt att 115
Met Lys Asn Phe Ile
1 5

cgg gta ctc atc gcc ttt agt gtt ttc ctc tgt ata tat acc gtt gct 163
Arg Val Leu Ile Ala Phe Ser Val Phe Leu Cys Ile Tyr Thr Val Ala
10 15 20

ccc cac att ggc cga ggt cct gga gac ctc gca cca gtt aca gca atc 211
Pro His Ile Gly Arg Gly Pro Gly Asp Leu Ala Pro Val Thr Ala Ile
25 30 35

ccc caa cga gcc aca gtc cta ggc tat gac aga gcc tcc atg ttt ggc 259
Pro Gln Arg Ala Thr Val Leu Gly Tyr Asp Arg Ala Ser Met Phe Gly
40 45 50

gga tgg ttg ggt ggc gtg cgg gaa ggc atc gtg gat gaa gcc ggc gac 307
Gly Trp Leu Gly Gly Val Arg Glu Gly Ile Val Asp Glu Ala Gly Asp
55 60 65

act gat cca tac tcc ggg aat cga tta gac ctc tct agt gcc gag gtg 355
Thr Asp Pro Tyr Ser Gly Asn Arg Leu Asp Leu Ser Ser Ala Glu Val
70 75 80 85

gat cat att ctc ccg ctc agc gcc gcc tgg gat cta ggc gca cac cgg 403
Asp His Ile Leu Pro Leu Ser Ala Ala Trp Asp Leu Gly Ala His Arg
90 95 100

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tgg agc gct ggc gag aga atc agc ttt gcc aac gac ccc ctc aac ctc 451
 Trp Ser Ala Gly Glu Arg Ile Ser Phe Ala Asn Asp Pro Leu Asn Leu
 105 110 115
 gtg ctc gtc tca aaa gct gag aac caa gaa aaa tcc gat caa ctt ccc 499
 Val Leu Val Ser Lys Ala Glu Asn Gln Glu Lys Ser Asp Gln Leu Pro
 120 125 130
 agc gag tgg ctc ccc tct gat cga agt gca cga tgt tgg tac gtg gaa 547
 Ser Glu Trp Leu Pro Ser Asp Arg Ser Ala Arg Cys Trp Tyr Val Glu
 135 140 145
 cgc ctt ttc gcc gtg gcc aac gca tac gaa ctt ccg tta cca gaa aac 595
 Arg Leu Phe Ala Val Ala Asn Ala Tyr Glu Leu Pro Leu Pro Glu Asn
 150 155 160 165
 gac att cgg gtt gga cga aaa cag tgc ggg ttc gcc aaa cct tgg 640
 Asp Ile Arg Val Gly Arg Lys Gln Cys Gly Phe Ala Lys Pro Trp
 170 175 180
 tgatctcgtt agtgtatgta tca 663

<210> 1636

<211> 180

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1636

Met Lys Asn Phe Ile Arg Val Leu Ile Ala Phe Ser Val Phe Leu Cys
 1 5 10 15
 Ile Tyr Thr Val Ala Pro His Ile Gly Arg Gly Pro Gly Asp Leu Ala
 20 25 30
 Pro Val Thr Ala Ile Pro Gln Arg Ala Thr Val Leu Gly Tyr Asp Arg
 35 40 45
 Ala Ser Met Phe Gly Gly Trp Leu Gly Gly Val Arg Glu Gly Ile Val
 50 55 60
 Asp Glu Ala Gly Asp Thr Asp Pro Tyr Ser Gly Asn Arg Leu Asp Leu
 65 70 75 80
 Ser Ser Ala Glu Val Asp His Ile Leu Pro Leu Ser Ala Ala Trp Asp
 85 90 95
 Leu Gly Ala His Arg Trp Ser Ala Gly Glu Arg Ile Ser Phe Ala Asn
 100 105 110
 Asp Pro Leu Asn Leu Val Leu Val Ser Lys Ala Glu Asn Gln Glu Lys
 115 120 125
 Ser Asp Gln Leu Pro Ser Glu Trp Leu Pro Ser Asp Arg Ser Ala Arg
 130 135 140
 Cys Trp Tyr Val Glu Arg Leu Phe Ala Val Ala Asn Ala Tyr Glu Leu
 145 150 155 160
 Pro Leu Pro Glu Asn Asp Ile Arg Val Gly Arg Lys Gln Cys Gly Phe
 165 170 175

Ala Lys Pro Trp
180

<210> 1637

<211> 975

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(952)

<223> RXA00183

<400> 1637

ctggccagcg ccatcggtggg cgagggcgaa ggctggatca ccgaactcaa cccagaagaa 60

ttggctatgc tgatgagtta ccgcgaaaag gaggggtgcag atg act gaa tca cgc 115
Met Thr Glu Ser Arg
1 5

cgc gtg aaa atg gat aac gtt att tac gcc aat ttt ggc agc aaa cag 163
Arg Val Lys Met Asp Asn Val Ile Tyr Ala Asn Phe Gly Ser Lys Gln
10 15 20

cgc gta tct act cct gat gac cgc acc cag gtg att aat aaa tca cga 211
Arg Val Ser Thr Pro Asp Asp Arg Thr Gln Val Ile Asn Lys Ser Arg
25 30 35

cac aaa caa ttc agc cca gcg ggt act cgt acc gtg atg ttg acg gag 259
His Lys Gln Phe Ser Pro Ala Gly Thr Arg Thr Val Met Leu Thr Glu
40 45 50

aaa aac gcc gac agc gga cga cgg tcc cgc ggt gag cag tac tac cga 307
Lys Asn Ala Asp Ser Gly Arg Arg Ser Arg Gly Glu Gln Tyr Tyr Arg
55 60 65

aac ggc aat gtc acc ggc atg act gtg ctg gaa ggc cgc gtg gaa tgc 355
Asn Gly Asn Val Thr Gly Met Thr Val Leu Glu Gly Arg Val Glu Cys
70 75 80 85

act gtc gcg ggc tcc caa aac gag ccg ttt gtt acc aca gtg acc ttc 403
Thr Val Ala Gly Ser Gln Asn Glu Pro Phe Val Thr Thr Val Thr Phe
90 95 100

cca tac cga agc tcg gaa aaa ctc cgc gaa gcc tac gca gct att gcg 451
Pro Tyr Arg Ser Ser Glu Lys Leu Arg Glu Ala Tyr Ala Ala Ile Ala
105 110 115

gat act ccc aat ggc ctg cgg ctt gtg cgt gat ggc cat ctg acc tcc 499
Asp Thr Pro Asn Gly Leu Arg Leu Val Arg Asp Gly His Leu Thr Ser
120 125 130

tcc atg ctg gat cac ttg gtg gga agt cct gat gag tcg att tat ttt 547
Ser Met Leu Asp His Leu Val Gly Ser Pro Asp Glu Ser Ile Tyr Phe
135 140 145

gac tgc acc tgc ccc gac cga tcg ctt gtg tgt aaa cat gcc gtt gcc 595
Asp Cys Thr Cys Pro Asp Arg Ser Leu Val Cys Lys His Ala Val Ala
150 155 160 165

agc gcg tat cac gtt gcc gag aag atg acc gcg aac ccc ggt ctg atc 643
 Ser Ala Tyr His Val Ala Glu Lys Met Thr Ala Asn Pro Gly Leu Ile 180
 170 175

ttg gat att cgt ggt caa ggg atg gct gga tta gaa gca ctg att cgg 691
 Leu Asp Ile Arg Gly Gln Gly Met Ala Gly Leu Glu Ala Leu Ile Arg 195
 185 190

acc tat cac acc aag gtt gaa act gaa cct gaa gac aat gac agt ttt 739
 Thr Tyr His Thr Lys Val Glu Thr Glu Pro Glu Asp Asn Asp Ser Phe 210
 200 205

tgg aac ggc agg gaa ctt cct gct ttg cct gat cca aag att gcc cct 787
 Trp Asn Gly Arg Glu Leu Pro Ala Leu Pro Asp Pro Lys Ile Ala Pro 225
 215 220

gct atc gac gat tcc gat atc aac tac ctc cac aag gct tta agg atg 835
 Ala Ile Asp Asp Ser Asp Ile Asn Tyr Leu His Lys Ala Leu Arg Met 245
 230 235 240

gtc tca tac acc tcc ctg gag cag ctt cgt gcg gtc agt gat att gaa 883
 Val Ser Tyr Thr Ser Leu Glu Gln Leu Arg Ala Val Ser Asp Ile Glu 260
 250 255

gat atg tac gag att ttg gta gcc aac cac cct gat aac cag caa gtg 931
 Asp Met Tyr Glu Ile Leu Val Ala Asn His Pro Asp Asn Gln Val 275
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tat gag gaa gaa gac act gat taaccagggc ttatggtgtt ggt 975
 Tyr Glu Glu Glu Asp Thr Asp 280

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Phe Gly Ser Lys Gln Arg Val Ser Thr Pro Asp Asp Arg Thr Gln Val 30
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Ile Asn Lys Ser Arg His Lys Gln Phe Ser Pro Ala Gly Thr Arg Thr 45
 35 40

Val Met Leu Thr Glu Lys Asn Ala Asp Ser Gly Arg Arg Ser Arg Gly 60
 50 55

Glu Gln Tyr Tyr Arg Asn Gly Asn Val Thr Gly Met Thr Val Leu Glu 80
 65 70 75

Gly Arg Val Glu Cys Thr Val Ala Gly Ser Gln Asn Glu Pro Phe Val 95
 85 90

Thr Thr Val Thr Phe Pro Tyr Arg Ser Glu Lys Leu Arg Glu Ala 110
 100 105

Tyr Ala Ala Ile Ala Asp Thr Pro Asn Gly Leu Arg Leu Val Arg Asp
115 120

Gly His Leu Thr Ser Ser Met Leu Asp His Leu Val Gly Ser Pro Asp
130 135 140

Glu Ser Ile Tyr Phe Asp Cys Thr Cys Pro Asp Arg Ser Leu Val Cys
145 150 155 160

Lys His Ala Val Ala Ser Ala Tyr His Val Ala Glu Lys Met Thr Ala
165 170 175

Asn Pro Gly Leu Ile Leu Asp Ile Arg Gly Gln Gly Met Ala Gly Leu
180 185 190

Glu Ala Leu Ile Arg Thr Tyr His Thr Lys Val Glu Thr Glu Pro Glu
195 200 205

Asp Asn Asp Ser Phe Trp Asn Gly Arg Glu Leu Pro Ala Leu Pro Asp
210 215 220

Pro Lys Ile Ala Pro Ala Ile Asp Asp Ser Asp Ile Asn Tyr Leu His
225 230 235 240

Lys Ala Leu Arg Met Val Ser Tyr Thr Ser Leu Glu Gln Leu Arg Ala
245 250 255

Val Ser Asp Ile Glu Asp Met Tyr Glu Ile Leu Val Ala Asn His Pro
260 265 270

Asp Asn Gln Gln Val Tyr Glu Glu Glu Asp Thr Asp
275 280

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<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(2728)

<223> RXA00185

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gctcaacctta ttgttccgac taagcccgga ggtctaagac atg cgt att cat gaa 115
Met Arg Ile His Glu
1 5

atc atc att gac aat ttc cga gcc atc gaa cat cta gaa ctt cgt gac 163
Ile Ile Ile Asp Asn Phe Arg Ala Ile Glu His Leu Glu Leu Arg Asp
10 15 20

att cct gac cag ggc gtt atc gtg atc cac ggt gac aat gag caa ggc 211
Ile Pro Asp Gln Gly Val Ile Val Ile His Gly Asp Asn Glu Gln Gly
25 30 35

aaa tct tca atc ctt gaa gcc ata aaa aca gtt ctg aat agt aaa cac 259
Lys Ser Ser Ile Leu Glu Ala Ile Lys Thr Val Leu Asn Ser Lys His

40	45	50	
aga acc acc agc aag acg atc aag gcc att cag cct gtt gac cgt gat Arg Thr Thr Ser Lys Thr Ile Lys Ala Ile Gln Pro Val Asp Arg Asp 55 60			307
gtt ccc atc agc atc acc ctc gag gca acc gta ggc acg gtt cga ttc Val Pro Ile Ser Ile Thr Leu Glu Ala Thr Val Gly Thr Val Arg Phe 70 75 80 85			355
cgc ata cac aaa cgc ttc cta aaa tcc aca gcc gca gaa ctg caa gtc Arg Ile His Lys Arg Phe Leu Lys Ser Thr Ala Ala Glu Leu Gln Val 90 95 100			403
atc gag cca cgt cca tcc aac cac cgt gga cta gaa gcc gaa gct gca Ile Glu Pro Arg Pro Ser Asn His Arg Gly Leu Glu Ala Glu Ala Ala 105 110 115			451
ctg gca gaa ata ctg gaa agc cat ttg gac acc tct ttg ctt gac gca Leu Ala Glu Ile Leu Glu Ser His Leu Asp Thr Ser Leu Leu Asp Ala 120 125 130			499
ttg ttt atg aaa cag ggt gaa gta gaa gca ggt atc agc gct gta gga Leu Phe Met Lys Gln Gly Glu Val Glu Ala Gly Ile Ser Ala Val Gly 135 140 145			547
att cct acc ctg acc agc gct ttg aac gct caa aat ggc aat acc gaa Ile Pro Thr Leu Thr Ser Ala Leu Asn Ala Gln Asn Gly Asn Thr Glu 150 155 160 165			595
gat gcc acc gaa gac acc gca ctc atg gag gct gta gaa aag gaa tac Asp Ala Thr Glu Asp Thr Ala Leu Met Glu Ala Val Glu Lys Glu Tyr 170 175 180			643
cta aag ttc tac acc aac tcc gga aag gcg aat acg agg ttc cta cag Leu Lys Phe Thr Asn Ser Gly Lys Ala Asn Thr Arg Phe Leu Gln 185 190 195			691
ttt tcc aaa cag gtg gaa acc ctt cgt act gat ttg gat gag gct aac Phe Ser Lys Gln Val Glu Thr Leu Arg Thr Asp Leu Asp Glu Ala Asn 200 205 210			739
gct gaa gta gca aag ctc tcc tcc cat gtt gac cga gtt aaa cga ttg Ala Glu Val Ala Lys Leu Ser Ser His Val Asp Arg Val Lys Arg Leu 215 220 225			787
gaa att gat cgg gat cag gcc aca gca cag tta ccc aag gca gag gaa Glu Ile Asp Arg Asp Gln Ala Thr Ala Gln Leu Pro Lys Ala Glu Glu 230 235 240 245			835
gaa ctc gca ggg agg aaa gca gaa ctg gag gaa gcc caa aag gtt aag Glu Leu Ala Gly Arg Lys Ala Glu Leu Glu Glu Ala Gln Lys Val Lys 250 255 260			883
gct caa gcc acg gaa atc ctt gcg cag ttt tcc cgg gcg gaa gaa cag Ala Gln Ala Thr Glu Ile Leu Ala Gln Phe Ser Arg Ala Glu Glu Gln 265 270 275			931
tta gag cag gca aca gga gct cag aaa cga cgt aaa gaa ctc cgc aat Leu Glu Gln Ala Thr Gly Ala Gln Lys Arg Arg Lys Glu Leu Arg Asn 280 285 290			979

aag ctg gaa tta gca cag aca gaa gtc gaa aag gct gaa gca ggg caa	1027
Lys Leu Glu Leu Ala Gln Thr Glu Val Glu Lys Ala Glu Ala Gly Gln	
295 300 305	
gag aac ctg gcg caa gaa gct tcc cgt gaa gca gaa ttc cta gcc	1075
Glu Asn Leu Ala Gln Glu Ala Ser Arg Glu Glu Phe Leu Ala	
310 315 320 325	
tta agt gaa aag ttc gag gca gcg cgc gca gct gaa act ctg gcc gtt	1123
Leu Ser Glu Lys Phe Glu Ala Ala Arg Ala Ala Glu Thr Leu Ala Val	
330 335 340	
gaa aag gtg aaa gca gca cgt caa tcg gtt gct gga atc aaa aac cgt	1171
Glu Lys Val Lys Ala Ala Arg Gln Ser Val Ala Gly Ile Lys Asn Arg	
345 350 355	
gac cgt aaa gaa cac ctc acg gtt atg ctt ggt gaa ctt gat cga att	1219
Asp Arg Lys Glu His Leu Thr Met Leu Gly Glu Leu Asp Arg Ile	
360 365 370	
ggg cag cgc ctc tac gaa ttg cgc agc gtc cag cac tca tcg gtg cgt	1267
Gly Gln Arg Leu Tyr Glu Leu Arg Ser Val Gln His Ser Ser Val Arg	
375 380 385	
gtg agc cag cgt gat att gat gct ctg caa aag gcg atc acc gag gtc	1315
Val Ser Gln Arg Asp Ile Asp Ala Leu Gln Lys Ala Ile Thr Glu Val	
390 395 400 405	
gat atc caa agg acg ctc gtt gaa gcg cag cag gga agt att acc ctc	1363
Asp Ile Gln Arg Thr Leu Val Glu Ala Gln Gln Gly Ser Ile Thr Leu	
410 415 420	
agt gct tcc aca ccc acc gac att caa cta ggt gat gac acc gtt tca	1411
Ser Ala Ser Thr Pro Thr Asp Ile Gln Leu Gly Asp Asp Thr Val Ser	
425 430 435	
gct acc gac gct gga acc aca gtt gcc ctc gac cga gaa ctc acc gtc	1459
Ala Thr Asp Ala Gly Thr Thr Val Ala Leu Asp Arg Glu Leu Thr Val	
440 445 450	
gtg gtc ggc gat gtc acc ttg gtg att aac cca gga aaa aca gca gcg	1507
Val Val Gly Asp Val Thr Leu Val Ile Asn Pro Gly Lys Thr Ala Ala	
455 460 465	
gaa agt cgc acc gat ttt gaa tcc gcc gag gca gca ttg gcg gag ctg	1555
Glu Ser Arg Thr Asp Phe Glu Ser Ala Glu Ala Leu Ala Glu Leu	
470 475 480 485	
ctt gat caa ctc gac gtc tca gac ttg gac cag ctc agg gaa cgt ttc	1603
Leu Asp Gln Leu Asp Val Ser Asp Leu Asp Gln Leu Arg Glu Arg Phe	
490 495 500	
act gcc caa gag caa cga gac gcg gat att gca gaa ctg gtt cgc gaa	1651
Thr Ala Gln Glu Gln Arg Asp Ala Asp Ile Ala Glu Leu Val Arg Glu	
505 510 515	
caa cag cgc atg agc ggt ggg aca gaa aca aca gtt tta cgt gcc gag	1699
Gln Gln Arg Met Ser Gly Gly Thr Glu Thr Thr Val Leu Arg Ala Glu	
520 525 530	

cta gaa ggc ctg cac gtc cca gag gat cta gac cca tca att tct gtg	1747
Leu Glu Gly Leu His Val Pro Glu Asp Leu Asp Pro Ser Ile Ser Val	
535 540 545	
gat gat gcg caa act cag ttg aat gag gca gaa gag tcc aga gag ctc	1795
Asp Asp Ala Gln Thr Gln Leu Asn Glu Ala Glu Ser Arg Glu Leu	
550 555 560 565	
gct gcg gag gcg cat aaa cac gca aat gca gca ctt gat gga ttg cgt	1843
Ala Ala Glu Ala His Lys His Ala Asn Ala Ala Leu Asp Gly Leu Arg	
570 575 580	
tcg cgt ccc gta gat aaa gct ctg aca gtt ttc aac gct cag ctc gca	1891
Ser Arg Pro Val Asp Lys Ala Leu Thr Val Phe Asn Ala Gln Leu Ala	
585 590 595	
gca ctg cag aga aac ctc tct tcc gca caa gtt gaa tta gac cgt gca	1939
Ala Leu Gln Arg Asn Leu Ser Ser Ala Gln Val Glu Leu Asp Arg Ala	
600 605 610	
gtg gca gaa acc tcg gat gac gaa gtt gat gct gct gta cag cgg tgc	1987
Val Ala Glu Thr Ser Asp Glu Val Asp Ala Ala Val Gln Arg Cys	
615 620 625	
gct gaa gct cta gct ggg gtg cgg gta cag aag cag gag att gaa cag	2035
Ala Glu Ala Leu Ala Gly Val Arg Val Gln Lys Gln Glu Ile Glu Gln	
630 635 640 645	
gtc ttg gca aaa acc aac cca gac atg gct caa cgc tta tgt gat gct	2083
Val Leu Ala Lys Thr Asn Pro Asp Met Ala Gln Arg Leu Cys Asp Ala	
650 655 660	
gct gaa gca aat gtg cga tcg tat aaa acg gca gtg tct gat gcc acc	2131
Ala Glu Ala Asn Val Arg Ser Tyr Lys Thr Ala Val Ser Asp Ala Thr	
665 670 675	
aca gag ttg gtg cgc ctg gaa ggc ctc atc ggt gta gct gca ggt gcg	2179
Thr Glu Leu Val Arg Leu Glu Gly Leu Ile Gly Val Ala Ala Gly Ala	
680 685 690	
aaa gaa cga cta gat aaa gtt aag tct gcg ctg aca gca gct gaa aac	2227
Lys Glu Arg Leu Asp Lys Val Lys Ser Ala Leu Thr Ala Ala Glu Asn	
695 700 705	
cgg ttt gaa tca gaa caa cgt cgc gcc cac gct gca cgt cgc ctc tat	2275
Arg Phe Glu Ser Glu Gln Arg Arg Ala His Ala Ala Arg Arg Leu Tyr	
710 715 720 725	
gcc ctc atg gtg ttc tac cgt gat gaa tcc cga aag cgc tac gca gca	2323
Ala Leu Met Val Phe Tyr Arg Asp Glu Ser Arg Lys Arg Tyr Ala Ala	
730 735 740	
ccc ttc gcg gac aaa cta tcc agg ctg gca gca tcc gta ttt gga gaa	2371
Pro Phe Ala Asp Lys Leu Ser Arg Leu Ala Ala Ser Val Phe Gly Glu	
745 750 755	
tca gca gac ttt gat ctt gat gat gag ctg aag atc tcc agt cgt tcc	2419
Ser Ala Asp Phe Asp Leu Asp Asp Glu Leu Lys Ile Ser Ser Arg Ser	
760 765 770	
ata gga cca cga aca gtg gac ctt gcc aat ctt tct gcc gcc gca aag	2467

Ile Gly Pro Arg Thr Val Asp Leu Ala Asn Leu Ser Gly Gly Ala Lys
 775 780 785
 gaa cag ctg gca atc ctc acc cgc ttt gct atc gca gaa ttg gta gca 2515
 Glu Gln Leu Ala Ile Leu Thr Arg Phe Ala Ile Ala Glu Leu Val Ala
 790 795 800 805
 gaa tcc tcc gcg caa ggt gct gtg cct gtg ttt att gat gat gca ttg 2563
 Glu Ser Ser Ala Gln Gly Ala Val Pro Val Phe Ile Asp Asp Ala Leu
 810 815 820
 ggg agc aca gac cca gag cga ctg acc cgc ata tct act ctg ttt agt 2611
 Gly Ser Thr Asp Pro Glu Arg Leu Thr Arg Ile Ser Thr Leu Phe Ser
 825 830 835
 gat gca ggc aag gac tct cag gtg ttt gtt ctc acc tgt gtt cca gac 2659
 Asp Ala Gly Lys Asp Ser Gln Val Phe Val Leu Thr Cys Val Pro Asp
 840 845 850
 cgg tac aac tat gta gag gtc acc caa aag cac agc atc gag tca ttg 2707
 Arg Tyr Asn Tyr Val Glu Val Thr Gln Lys His Ser Ile Glu Ser Leu
 855 860 865
 aaa act gcc aac gct ctg ctg tagctgagca aaaagccaag caa 2751
 Lys Thr Ala Asn Ala Leu Leu
 870 875
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 Asp Asn Glu Gln Gly Lys Ser Ser Ile Leu Glu Ala Ile Lys Thr Val
 35 40 45
 Leu Asn Ser Lys His Arg Thr Thr Ser Lys Thr Ile Lys Ala Ile Gln
 50 55 60
 Pro Val Asp Arg Asp Val Pro Ile Ser Ile Thr Leu Glu Ala Thr Val
 65 70 75 80
 Gly Thr Val Arg Phe Arg Ile His Lys Arg Phe Leu Lys Ser Thr Ala
 85 90 95
 Ala Glu Leu Gln Val Ile Glu Pro Arg Pro Ser Asn His Arg Gly Leu
 100 105 110
 Glu Ala Glu Ala Ala Leu Ala Glu Ile Leu Glu Ser His Leu Asp Thr
 115 120 125
 Ser Leu Leu Asp Ala Leu Phe Met Lys Gln Gly Glu Val Glu Ala Gly
 130 135 140

Ile Ser Ala Val Gly Ile Pro Thr Leu Thr Ser Ala Leu Asn Ala Gln
 145 150 155 160
 Asn Gly Asn Thr Glu Asp Ala Thr Glu Asp Thr Ala Leu Met Glu Ala
 165 170 175
 Val Glu Lys Glu Tyr Leu Lys Phe Tyr Thr Asn Ser Gly Lys Ala Asn
 180 185 190
 Thr Arg Phe Leu Gln Phe Ser Lys Gln Val Glu Thr Leu Arg Thr Asp
 195 200 205
 Leu Asp Glu Ala Asn Ala Glu Val Ala Lys Leu Ser Ser His Val Asp
 210 215 220
 Arg Val Lys Arg Leu Glu Ile Asp Arg Asp Gln Ala Thr Ala Gln Leu
 225 230 235 240
 Pro Lys Ala Glu Glu Leu Ala Gly Arg Lys Ala Glu Leu Glu Glu
 245 250 255
 Ala Gln Lys Val Lys Ala Gln Ala Thr Glu Ile Leu Ala Gln Phe Ser
 260 265 270
 Arg Ala Glu Glu Gln Leu Glu Gln Ala Thr Gly Ala Gln Lys Arg Arg
 275 280 285
 Lys Glu Leu Arg Asn Lys Leu Glu Leu Ala Gln Thr Glu Val Glu Lys
 290 295 300
 Ala Glu Ala Gly Gln Glu Asn Leu Ala Gln Glu Ala Ser Arg Glu Ala
 305 310 315 320
 Glu Glu Phe Leu Ala Leu Ser Glu Lys Phe Glu Ala Ala Arg Ala Ala
 325 330 335
 Glu Thr Leu Ala Val Glu Lys Val Lys Ala Ala Arg Gln Ser Val Ala
 340 345 350
 Gly Ile Lys Asn Arg Asp Arg Lys Glu His Leu Thr Val Met Leu Gly
 355 360 365
 Glu Leu Asp Arg Ile Gly Gln Arg Leu Tyr Glu Leu Arg Ser Val Gln
 370 375 380
 His Ser Ser Val Arg Val Ser Gln Arg Asp Ile Asp Ala Leu Gln Lys
 385 390 395 400
 Ala Ile Thr Glu Val Asp Ile Gln Arg Thr Leu Val Glu Ala Gln Gln
 405 410 415
 Gly Ser Ile Thr Leu Ser Ala Ser Thr Pro Thr Asp Ile Gln Leu Gly
 420 425 430
 Asp Asp Thr Val Ser Ala Thr Asp Ala Gly Thr Thr Val Ala Leu Asp
 435 440 445
 Arg Glu Leu Thr Val Val Val Gly Asp Val Thr Leu Val Ile Asn Pro
 450 455 460
 Gly Lys Thr Ala Ala Glu Ser Arg Thr Asp Phe Glu Ser Ala Glu Ala

465 470 475 480
 Ala Leu Ala Glu Leu Leu Asp Gln Leu Asp Val Ser Asp Leu Asp Gln
 485 490 495
 Leu Arg Glu Arg Phe Thr Ala Gln Glu Gln Arg Asp Ala Asp Ile Ala
 500 505 510
 Glu Leu Val Arg Glu Gln Gln Arg Met Ser Gly Gly Thr Glu Thr Thr
 515 520 525
 Val Leu Arg Ala Glu Leu Glu Gly Leu His Val Pro Glu Asp Leu Asp
 530 535 540
 Pro Ser Ile Ser Val Asp Asp Ala Gln Thr Gln Leu Asn Glu Ala Glu
 545 550 555 560
 Glu Ser Arg Glu Leu Ala Ala Glu Ala His Lys His Ala Asn Ala Ala
 565 570 575
 Leu Asp Gly Leu Arg Ser Arg Pro Val Asp Lys Ala Leu Thr Val Phe
 580 585 590
 Asn Ala Gln Leu Ala Ala Leu Gln Arg Asn Leu Ser Ser Ala Gln Val
 595 600 605
 Glu Leu Asp Arg Ala Val Ala Glu Thr Ser Asp Asp Glu Val Asp Ala
 610 615 620
 Ala Val Gln Arg Cys Ala Glu Ala Leu Ala Gly Val Arg Val Gln Lys
 625 630 635 640
 Gln Glu Ile Glu Gln Val Leu Ala Lys Thr Asn Pro Asp Met Ala Gln
 645 650 655
 Arg Leu Cys Asp Ala Ala Glu Ala Asn Val Arg Ser Tyr Lys Thr Ala
 660 665 670
 Val Ser Asp Ala Thr Thr Glu Leu Val Arg Leu Glu Gly Leu Ile Gly
 675 680 685
 Val Ala Ala Gly Ala Lys Glu Arg Leu Asp Lys Val Lys Ser Ala Leu
 690 695 700
 Thr Ala Ala Glu Asn Arg Phe Glu Ser Glu Gln Arg Arg Ala His Ala
 705 710 715 720
 Ala Arg Arg Leu Tyr Ala Leu Met Val Phe Tyr Arg Asp Glu Ser Arg
 725 730 735
 Lys Arg Tyr Ala Ala Pro Phe Ala Asp Lys Leu Ser Arg Leu Ala Ala
 740 745 750
 Ser Val Phe Gly Glu Ser Ala Asp Phe Asp Leu Asp Asp Glu Leu Lys
 755 760 765
 Ile Ser Ser Arg Ser Ile Gly Pro Arg Thr Val Asp Leu Ala Asn Leu
 770 775 780
 Ser Gly Gly Ala Lys Glu Gln Leu Ala Ile Leu Thr Arg Phe Ala Ile
 785 790 795 800

Ala Glu Leu Val Ala Glu Ser Ser Ala Gln Gly Ala Val Pro Val Phe
805 810 815

Ile Asp Asp Ala Leu Gly Ser Thr Asp Pro Glu Arg Leu Thr Arg Ile
820 825 830

Ser Thr Leu Phe Ser Asp Ala Gly Lys Asp Ser Gln Val Phe Val Leu
835 840 845

Thr Cys Val Pro Asp Arg Tyr Asn Tyr Val Glu Val Thr Gln Lys His
850 855 860

Ser Ile Glu Ser Leu Lys Thr Ala Asn Ala Leu Leu
865 870 875

<210> 1641

<211> 1542

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1519)

<223> RXA00199

<400> 1641

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Met Glu Asp Leu Glu
1 5

att ttt gat cgg cat ttg cag cat tcc gat ttt gag gat cag ggt tcc 163
Ile Phe Asp Arg His Leu Gln His Ser Asp Phe Glu Asp Gln Gly Ser
10 15 20

atc ggc ctc gag ttg gaa ctc aac ctc gtg gat aag cat atg caa cct 211
Ile Gly Leu Glu Leu Glu Leu Asn Leu Val Asp Lys His Met Gln Pro
25 30 35

gct ttg gca ggc cac gcg gtg ctt tcc cat tta gac gat gag tac cag 259
Ala Leu Ala Gly His Ala Val Leu Ser His Leu Asp Glu Tyr Gln
40 45 50

tcg gag atc ggt aac ttt aat gtt gaa atg aac cac ccg cca cta tcc 307
Ser Glu Ile Gly Asn Phe Asn Val Glu Met Asn His Pro Pro Leu Ser
55 60 65

gtt aaa ggc gat gct tta cga cgc ctc gag caa ggc atc acc tcg cgt 355
Val Lys Gly Asp Ala Leu Arg Arg Leu Glu Gln Gly Ile Thr Ser Arg
70 75 80 85

cta ggt cgc gtg cgc gcg gcc gcc aca tcg gag aac gtg aac gtg gcg 403
Leu Gly Arg Val Arg Ala Ala Ala Thr Ser Glu Asn Val Asn Val Ala
90 95 100

atg atc ggc acg ctg ccc acc atc acc cca gaa ttc ctc gaa gat ccg 451
Met Ile Gly Thr Leu Pro Thr Ile Thr Pro Glu Phe Leu Glu Asp Pro
105 110 115

gca tgg atg acc caa gaa aac cgc tac cgt gcg ctg agc aat gcg gtg Ala Trp Met Thr Gln Glu Asn Arg Tyr Arg Ala Leu Ser Asn Ala Val 120 125 130	499
atg gaa tgg cgt ggc gag tta gtg cac atc aac atc gcc gac cgt gaa Met Glu Ser Arg Gly Glu Leu Val His Ile Asn Ile Ala Asp Arg Glu 135 140 145	547
caa atc atc cac gat ttc act gat ctc gcc ccc gaa tca act tgc acg Gln Ile Ile His Asp Phe Thr Asp Leu Ala Pro Glu Ser Thr Cys Thr 150 155 160 165	595
tct att cag ttg cac ctg caa tta gca ccc aat aag ttt gct gca gcg Ser Ile Gln Leu His Leu Gln Leu Ala Pro Asn Lys Phe Ala Ala Ala 170 175 180	643
tgg aat gcg tgg caa gca ata gct ggt gtt caa gca gct ctt tcc gcc Trp Asn Ala Ser Gln Ala Ile Ala Gly Val Gln Ala Ala Leu Ser Ala 185 190 195	691
aac tcc cca ctt ttc cta ggc cgt cgg gtg tgg cat gaa agc cgc att Asn Ser Pro Leu Phe Leu Gly Arg Arg Val Trp His Glu Ser Arg Ile 200 205 210	739
cca gtg ttt caa caa gct atc gat acg cgt act cct gaa ctt gtg aat Pro Val Phe Gln Gln Ala Ile Asp Thr Arg Thr Pro Glu Leu Val Asn 215 220 225	787
caa gga gtc cgc ccc aga gta tgg ttc ggc gaa cga tgg atc acc agt Gln Gly Val Arg Pro Arg Val Trp Phe Gly Glu Arg Trp Ile Thr Ser 230 235 240 245	835
gtt ttt gat ctt ttc gaa gaa aac gta cgc tac ttc tcc cct ctc atc Val Phe Asp Leu Phe Glu Glu Asn Val Arg Tyr Phe Ser Pro Leu Ile 250 255 260	883
gca gaa tcc cgc gcc ctg tct ggc aca cca atg atg aag gga aaa tcc Ala Glu Ser Arg Ala Leu Ser Gly Thr Pro Met Met Lys Gly Lys Ser 265 270 275	931
ccc gca ctc cac tac ctc aat ctc cac aac gga acg gtg tgg cgc tgg Pro Ala Leu His Tyr Leu Asn Leu His Asn Gly Thr Val Trp Arg Trp 280 285 290	979
aac cga ccc att tac gca cgg ggg gaa gag cgc tct cat ctg cgt ttg Asn Arg Pro Ile Tyr Ala Pro Gly Glu Glu Arg Ser His Leu Arg Leu 295 300 305	1027
gaa aac cgt ctc cta cct gca ggt ccc acc ccc atc gac atc acc gcc Glu Asn Arg Leu Leu Pro Ala Gly Pro Thr Pro Ile Asp Ile Thr Ala 310 315 320 325	1075
gat gcc get ttc tac tac ggt ttg gtt aaa tat ctg gcc gag gaa aac Asp Ala Ala Phe Tyr Tyr Gly Leu Val Lys Tyr Leu Ala Glu Glu Asn 330 335 340	1123
cgc cct gtc tgg tca cgt ctc cta ttc cct gat gcg gaa aag aac ttc Arg Pro Val Trp Ser Arg Leu Leu Phe Pro Asp Ala Glu Lys Asn Phe 345 350 355	1171

caa tcc ggt gca cgt tca ggg ctg ttc gcc cgc atg acc tgg cca acc 1219
 Gln Ser Gly Ala Arg Ser Gly Leu Phe Ala Arg Met Thr Trp Pro Thr
 360 365 370

ctc gga caa gtc aac gtt gcg aat ctg gtc caa gag cac ctc atc cct 1267
 Leu Gly Gln Val Asn Val Ala Asn Leu Val Gln His Leu Ile Pro
 375 380 385

caa gcc aga atc gga ctg gaa cga ctc gaa gta aac aaa gac ctt atc 1315
 Gln Ala Arg Ile Gly Leu Glu Arg Leu Glu Val Asn Lys Asp Leu Ile
 390 395 400 405

gac caa tac ctg gcc atc atc acc gaa cgc gcg aag tcc cgc caa aac 1363
 Asp Gln Tyr Leu Gly Ile Ile Thr Glu Arg Ala Lys Ser Arg Gln Asn
 410 415 420

ggt gcc acc tgg cag ttg cgt agc ctc aac aag ctg gaa gca cac gga 1411
 Gly Ala Thr Trp Gln Leu Arg Ser Leu Asn Lys Leu Glu Ala His Gly
 425 430 435

agc atg ccg ggt tcc gat gct cga aaa gca ggt ctt gca gca atg ttg 1459
 Ser Met Pro Gly Ser Asp Ala Arg Lys Ala Gly Leu Ala Ala Met Leu
 440 445 450

caa cag tat tta cag aat caa gaa agc gcc caa cct gtc cac aca tgg 1507
 Gln Gln Tyr Leu Gln Asn Gln Glu Ser Gly Gln Pro Val His Thr Trp
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gct att ggt tcg taaaacggca aggaagata ata 1542
 Ala Ile Gly Ser
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<210> 1642
 <211> 473
 <212> PRT
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<400> 1642
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 Lys His Met Gln Pro Ala Leu Ala Gly His Ala Val Leu Ser His Leu
 35 40 45
 Asp Asp Glu Tyr Gln Ser Glu Ile Gly Asn Phe Asn Val Glu Met Asn
 50 55 60
 His Pro Pro Leu Ser Val Lys Gly Asp Ala Leu Arg Arg Leu Glu Gln
 65 70 75 80
 Gly Ile Thr Ser Arg Leu Gly Arg Val Arg Ala Ala Ala Thr Ser Glu
 85 90 95
 Asn Val Asn Val Ala Met Ile Gly Thr Leu Pro Thr Ile Thr Pro Glu
 100 105 110
 Phe Leu Glu Asp Pro Ala Trp Met Thr Gln Glu Asn Arg Tyr Arg Ala

115					120					125					
Leu	Ser	Asn	Ala	Val	Met	Glu	Ser	Arg	Gly	Glu	Leu	Val	His	Ile	Asn
130					135					140					
Ile	Ala	Asp	Arg	Glu	Gln	Ile	Ile	His	Asp	Phe	Thr	Asp	Leu	Ala	Pro
145					150					155					160
Glu	Ser	Thr	Cys	Thr	Ser	Ile	Gln	Leu	His	Leu	Gln	Leu	Ala	Pro	Asn
				165					170					175	
Lys	Phe	Ala	Ala	Ala	Trp	Asn	Ala	Ser	Gln	Ala	Ile	Ala	Gly	Val	Gln
				180				185					190		
Ala	Ala	Leu	Ser	Ala	Asn	Ser	Pro	Leu	Phe	Leu	Gly	Arg	Arg	Val	Trp
				195			200					205			
His	Glu	Ser	Arg	Ile	Pro	Val	Phe	Gln	Gln	Ala	Ile	Asp	Thr	Arg	Thr
				210			215					220			
Pro	Glu	Leu	Val	Asn	Gln	Gly	Val	Arg	Pro	Arg	Val	Trp	Phe	Gly	Glu
225					230					235					240
Arg	Trp	Ile	Thr	Ser	Val	Phe	Asp	Leu	Phe	Glu	Glu	Asn	Val	Arg	Tyr
				245					250					255	
Phe	Ser	Pro	Leu	Ile	Ala	Glu	Ser	Arg	Ala	Leu	Ser	Gly	Thr	Pro	Met
				260					265					270	
Met	Lys	Gly	Lys	Ser	Pro	Ala	Leu	His	Tyr	Leu	Asn	Leu	His	Asn	Gly
				275				280				285			
Thr	Val	Trp	Arg	Trp	Asn	Arg	Pro	Ile	Tyr	Ala	Pro	Gly	Glu	Glu	Arg
				290			295				300				
Ser	His	Leu	Arg	Leu	Glu	Asn	Arg	Leu	Leu	Pro	Ala	Gly	Pro	Thr	Pro
305					310					315					320
Ile	Asp	Ile	Thr	Ala	Asp	Ala	Ala	Phe	Tyr	Tyr	Gly	Leu	Val	Lys	Tyr
				325					330					335	
Leu	Ala	Glu	Glu	Asn	Arg	Pro	Val	Trp	Ser	Arg	Leu	Leu	Phe	Pro	Asp
				340				345					350		
Ala	Glu	Lys	Asn	Phe	Gln	Ser	Gly	Ala	Arg	Ser	Gly	Leu	Phe	Ala	Arg
				355			360					365			
Met	Thr	Trp	Pro	Thr	Leu	Gly	Gln	Val	Asn	Val	Ala	Asn	Leu	Val	Gln
				370			375					380			
Glu	His	Leu	Ile	Pro	Gln	Ala	Arg	Ile	Gly	Leu	Glu	Arg	Leu	Glu	Val
385					390					395					400
Asn	Lys	Asp	Leu	Ile	Asp	Gln	Tyr	Leu	Gly	Ile	Ile	Thr	Glu	Arg	Ala
				405					410					415	
Lys	Ser	Arg	Gln	Asn	Gly	Ala	Thr	Trp	Gln	Leu	Arg	Ser	Leu	Asn	Lys
				420				425					430		
Leu	Glu	Ala	His	Gly	Ser	Met	Pro	Gly	Ser	Asp	Ala	Arg	Lys	Ala	Gly
				435			440					445			

Leu Ala Ala Met Leu Gln Gln Tyr Leu Gln Asn Gln Glu Ser Gly Gln
 450 455 460

Pro Val His Thr Trp Ala Ile Gly Ser
 465 470

<210> 1643

<211> 326

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(303)

<223> RKA00200

<400> 1643

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 His Tyr Ala Gly Val Thr Glu Ile Pro Glu Tyr Arg Ile Ser Pro Asp
 1 5 10 15

cac ggc gga aaa tcc acc ctc tcc cca ttc caa gac tgg gca ggc ggc 96
 His Gly Gly Lys Ser Thr Leu Ser Pro Phe Gln Asp Trp Ala Gly Gly
 20 25 30

gga tcc atg ggc acg gcc gaa gca gta aac aac gcc tac gaa atc ccg 144
 Gly Ser Met Gly Thr Ala Glu Ala Val Asn Asn Ala Tyr Glu Ile Pro
 35 40 45

tcc tac ctc cgc aac gac tgg ggc cgc gac tgg ggt tcc atc gaa cgc 192
 Ser Tyr Leu Arg Asn Asp Trp Gly Arg Asp Trp Gly Ser Ile Glu Arg
 50 55 60

tac tcg ctg cgc acc aac tcc aac ggc gat gca cct aag gtt gca gac 240
 Tyr Ser Leu Arg Thr Asn Ser Asn Gly Asp Ala Pro Lys Val Ala Asp
 65 70 75 80

atc aac ctt gaa acc atc caa cgt tcc gga ctc tgg aat cca ggg cat 288
 Ile Asn Leu Glu Thr Ile Gln Arg Ser Gly Leu Trp Asn Pro Gly His
 85 90 95

atg aag gta gat gaa taagaccttc agtactggaa gtt 326
 Met Lys Val Asp Glu
 100

<210> 1644

<211> 101

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1644

His Tyr Ala Gly Val Thr Glu Ile Pro Glu Tyr Arg Ile Ser Pro Asp
 1 5 10 15

His Gly Gly Lys Ser Thr Leu Ser Pro Phe Gln Asp Trp Ala Gly Gly
 20 25 30

Gly Ser Met Gly Thr Ala Glu Ala Val Asn Asn Ala Tyr Glu Ile Pro

	35		40		45										
Ser	Tyr	Leu	Arg	Asn	Asp	Trp	Gly	Arg	Asp	Trp	Gly	Ser	Ile	Glu	Arg
	50					55					60				
Tyr	Ser	Leu	Arg	Thr	Asn	Ser	Asn	Gly	Asp	Ala	Pro	Lys	Val	Ala	Asp
	65				70				75						80
Ile	Asn	Leu	Glu	Thr	Ile	Gln	Arg	Ser	Gly	Leu	Trp	Asn	Pro	Gly	His
			85						90					95	
Met	Lys	Val	Asp	Glu											
			100												

<210> 1645

<211> 441

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(418)

<223> RXA00207

<400> 1645

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aaacccccgc	ggaataattt	tgtctctaga	ctggctcacc	atg	gaa	atg	aaa	ttg	115
				Met	Glu	Met	Lys	Leu	
				1				5	

aaa	aag	gca	tcc	cag	gtc	agc	act	gcc	acc	gtc	gtc	gca	gca	ggg	ttg	163
Lys	Lys	Ala	Ser	Gln	Val	Ser	Thr	Ala	Thr	Val	Val	Ala	Ala	Gly	Leu	
			10						15					20		

atc	ggc	ggg	tgg	ttg	act	gcc	cgt	gaa	tcc	ggc	att	cgc	cca	ctg	ggc	211
Ile	Gly	Gly	Trp	Leu	Thr	Ala	Arg	Glu	Ser	Gly	Ile	Arg	Pro	Leu	Gly	
			25					30					35			

acc	att	cca	ttg	gca	gca	tcc	gga	gcg	ctt	gct	gca	cga	agc	tggt	aat	259
Thr	Ile	Pro	Leu	Ala	Ala	Ser	Gly	Ala	Leu	Ala	Ala	Arg	Ser	Trp	Asn	
		40				45						50				

gaa	aag	aag	ggg	cct	gca	gta	gct	act	ggc	ctg	ctg	gca	acc	tac	gtt	307
Glu	Lys	Lys	Gly	Pro	Ala	Val	Ala	Thr	Gly	Leu	Leu	Ala	Thr	Tyr	Val	
	55					60					65					

ggg	gca	ttt	ggc	ctg	tcc	cac	cca	ctt	gcc	aag	aag	att	ggc	gcg	tggt	355
Gly	Ala	Phe	Gly	Leu	Ser	His	Pro	Leu	Ala	Lys	Lys	Ile	Gly	Ala	Trp	
	70				75					80				85		

cct	gca	gtt	ctt	act	gtg	acc	gct	ggc	gct	gct	gcg	att	gct	tac	gca	403
Pro	Ala	Val	Leu	Thr	Val	Thr	Ala	Gly	Ala	Ala	Ala	Ile	Ala	Tyr	Ala	
				90				95					100			

gta	tct	gac	tcc	cag	taataattac	ggtaaaaaaa	ctt	441
Val	Ser	Asp	Ser	Gln				
			105					

<210> 1646

<211> 106

<212> PRT

<213> Corynebacterium glutamicum

<400> 1646

Met Glu Met Lys Leu Lys Lys Ala Ser Gln Val Ser Thr Ala Thr Val
 1 5 10 15

Val Ala Ala Gly Leu Ile Gly Gly Trp Leu Thr Ala Arg Glu Ser Gly
 20 25 30

Ile Arg Pro Leu Gly Thr Ile Pro Leu Ala Ala Ser Gly Ala Leu Ala
 35 40 45

Ala Arg Ser Trp Asn Glu Lys Lys Gly Pro Ala Val Ala Thr Gly Leu
 50 55 60

Leu Ala Thr Tyr Val Gly Ala Phe Gly Leu Ser His Pro Leu Ala Lys
 65 70 75 80

Lys Ile Gly Ala Trp Pro Ala Val Leu Thr Val Thr Ala Gly Ala Ala
 85 90 95

Ala Ile Ala Tyr Ala Val Ser Asp Ser Gln
 100 105

<210> 1647

<211> 786

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(763)

<223> RXA00211

<400> 1647

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accaatcatc ccctagtttt gaaaagaagg aagcgagcca atg tca ttc ctg atc 115
 Met Ser Phe Leu Ile
 1 5

cgc gtc ctg ttg tcc gac acc cca ggc agc ctc gcg tta ctc gct gaa 163
 Arg Val Leu Leu Ser Asp Thr Pro Gly Ser Leu Ala Leu Leu Ala Glu
 10 15 20

gcc ctt ggg att gta gag gcc aat att caa tcc gtg gac gtg gtg gaa 211
 Ala Leu Gly Ile Val Glu Ala Asn Ile Gln Ser Val Asp Val Val Glu
 25 30 35

cgc ttc ccc aat ggc acg gtc atg gac gat ctg gtg atc tcc atc cct 259
 Arg Phe Pro Asn Gly Thr Val Met Asp Asp Leu Val Ile Ser Ile Pro
 40 45 50

cgc gat gtc atg gca gac acc atc atc acc gca gct gaa gaa gtc gac 307
 Arg Asp Val Met Ala Asp Thr Ile Ile Thr Ala Ala Glu Glu Val Asp
 55 60 65

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ggc gtg gag att gat tcc atc cgc cca ttc tcc ggg act gtt gac cgc 355
Gly Val Glu Ile Asp Ser Ile Arg Pro Phe Ser Gly Thr Val Asp Arg 85
70 75 80

cgc gga cag atc caa atg ctg gct gct gtt gct cac caa cgc cgc gat 403
Arg Gly Gln Ile Gln Met Leu Ala Ala Val Ala His Gln Arg Arg Asp 100
90 95

atc acc gca gcg atg gaa gaa atg gtc gat gtc atc ccc cgc acc atg 451
Ile Thr Ala Ala Met Glu Glu Met Val Asp Val Ile Pro Arg Thr Met 115
105 110

acc tct ggt tgg gct ttg gtc att gat cta aaa gga ccc atc act cgc 499
Thr Ser Gly Trp Ala Leu Val Ile Asp Leu Lys Gly Pro Ile Thr Arg 130
120 125

atc gct ggt tcc cta gca gcg ccc gaa gat gac ggc acc gtt cgc gag 547
Ile Ala Gly Ser Leu Ala Ala Pro Glu Asp Asp Gly Thr Val Pro Glu 145
135 140

aac atc gtt ctc aaa gaa gct cgc atg ctc aac ccg gaa aac gat ccg 595
Asn Ile Val Leu Lys Glu Ala Arg Met Leu Asn Pro Glu Asn Asp Pro 165
150 155

tgg att cca gag tcc tgg aca ctg ctt gat tct tcc ctt gcc atc gct 643
Trp Ile Pro Glu Ser Trp Thr Leu Leu Asp Ser Ser Leu Ala Ile Ala 180
170 175

ccg atc ggc aag cac ggc ctg gct ctg att atc ggt cgc cct ggt ggc 691
Pro Ile Gly Lys His Gly Leu Ala Leu Ile Ile Gly Arg Pro Gly Gly 195
185 190

cct gat ttc ttg gcc agc gaa gtg gag cac tta ggc caa gtc ggt gac 739
Pro Asp Phe Leu Ala Ser Glu Val Glu His Leu Gly Gln Val Gly Asp 210
200 205

att atc gga gca atg ctt caa aaa taatctgagc tgtttaaaaa atg 786
Ile Ile Gly Ala Met Leu Gln Lys 220
215 220

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<210> 1648

<211> 221

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1648

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Met Ser Phe Leu Ile Arg Val Leu Leu Ser Asp Thr Pro Gly Ser Leu
1 5 10 15

Ala Leu Leu Ala Glu Ala Leu Gly Ile Val Glu Ala Asn Ile Gln Ser
20 25 30

Val Asp Val Val Glu Arg Phe Pro Asn Gly Thr Val Met Asp Asp Leu
35 40 45

Val Ile Ser Ile Pro Arg Asp Val Met Ala Asp Thr Ile Ile Thr Ala
50 55 60

Ala Glu Glu Val Asp Gly Val Glu Ile Asp Ser Ile Arg Pro Phe Ser
65 70 75 80

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Gly Thr Val Asp Arg Arg Gly Gln Ile Gln Met Leu Ala Ala Val Ala
85 90 95

His Gln Arg Arg Asp Ile Thr Ala Ala Met Glu Glu Met Val Asp Val
100 105 110

Ile Pro Arg Thr Met Thr Ser Gly Trp Ala Leu Val Ile Asp Leu Lys
115 120 125

Gly Pro Ile Thr Arg Ile Ala Gly Ser Leu Ala Ala Pro Glu Asp Asp
130 135 140

Gly Thr Val Pro Glu Asn Ile Val Leu Lys Glu Ala Arg Met Leu Asn
145 150 155 160

Pro Glu Asn Asp Pro Trp Ile Pro Glu Ser Trp Thr Leu Leu Asp Ser
165 170 175

Ser Leu Ala Ile Ala Pro Ile Gly Lys His Gly Leu Ala Leu Ile Ile
180 185 190

Gly Arg Pro Gly Gly Pro Asp Phe Leu Ala Ser Glu Val Glu His Leu
195 200 205

Gly Gln Val Gly Asp Ile Ile Gly Ala Met Leu Gln Lys
210 215 220

<210> 1649

<211> 1263

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1240)

<223> RXA00218

<400> 1649

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gcattccgca aaccgcacta gaccatccaa ggtgtcttct atg tca gct cgc aat 115
Met Ser Ala Arg Asn
1 5

ccg ttc cgc ccc act ttc gga gtt tcc ccc acc gta ctt gca ggc cga 163
Pro Phe Arg Pro Thr Phe Gly Val Ser Pro Thr Val Leu Ala Gly Arg
10 15 20

gac tca ctt cta cag tct ttc aaa ctt ggt ctc gcg gaa ggc ccc gga 211
Asp Ser Leu Leu Gln Ser Phe Lys Leu Gly Leu Ala Glu Gly Pro Gly
25 30 35

agc ccc ttt aga gca ttg ctg att tcg gga tct cgt ggc atg ggt aaa 259
Ser Pro Phe Arg Ala Leu Leu Ile Ser Gly Ser Arg Gly Met Gly Lys
40 45 50

act gtg ttg ctc aat gaa ttt gaa gat gca gct gcg tct caa ggg tgg 307
Thr Val Leu Leu Asn Glu Phe Glu Asp Ala Ala Ala Ser Gln Gly Trp
55 60 65

atc acg ctg cgc gcc tat ccg gat aat tcc atg gtg gat ggc tta gtt Ile Thr Leu Arg Ala Tyr Pro Asp Asn Ser Met Val Asp Gly Leu Val 70 75 80 85	355
aat tcc gcc atc ccg gag gcg cta cag aat ctt gac gga ccg cag tcc Asn Ser Ala Ile Pro Glu Ala Leu Gln Asn Leu Asp Gly Pro Gln Ser 90 95 100	403
aaa aga atg ctc agt ggt gtg gcc att cct ggt atc gct acg gtg acg Lys Arg Met Leu Ser Gly Val Ala Ile Pro Gly Ile Ala Thr Val Thr 105 110 115	451
gcc att gct gat cca acc aag aag gat ccc act ccc acg ctg att tcc Ala Ile Ala Asp Pro Thr Lys Lys Asp Pro Thr Pro Thr Leu Ile Ser 120 125 130	499
agg ctc cgc gag ttg gct act cgt ttg caa aag cac ggc tcc gga att Arg Leu Arg Glu Leu Ala Thr Arg Leu Gln Lys His Gly Ser Gly Ile 135 140 145	547
ttg atc acc ctt gat gaa ctc caa agc gcc aat gtg gat ctt ttg cat Leu Ile Thr Leu Asp Glu Leu Gln Ser Ala Asn Val Asp Leu Leu His 150 155 160 165	595
gtg ttg gcc act gcg gtc cag gat ctc cta ccg gat gat ttc gat atc Val Leu Ala Thr Ala Val Gln Asp Leu Leu Arg Asp Asp Phe Asp Ile 170 175 180	643
gca ttg gta gca gcg ggt ctg cca gag gga atc gat cgt ctt ctc cag Ala Leu Val Ala Ala Gly Leu Pro Glu Gly Ile Asp Arg Leu Leu Gln 185 190 195	691
cat gag gcc aca acc ttt atc cgc cga gcc gaa aga atc ctg ctc aat His Glu Gly Thr Thr Phe Ile Arg Arg Ala Glu Arg Ile Leu Leu Asn 200 205 210	739
cct gtc aac cat gaa gat tcg gtg gag atg ttc ctg gat acc gct gcg Pro Val Asn His Glu Asp Ser Val Glu Met Phe Leu Asp Thr Ala Ala 215 220 225	787
gaa ggc caa cgc cac atg act tcc gag gcc gcc gaa ctc gcg gcg cag Glu Gly Gln Arg His Met Thr Ser Glu Ala Ala Glu Leu Ala Ala Gln 230 235 240 245	835
atc agc aag gcc tac ccc tac tcc atg cag ctg act ggt tct ctg gca Ile Ser Lys Gly Tyr Pro Tyr Ser Met Gln Leu Thr Gly Ser Leu Ala 250 255 260	883
tgg gcg cga agt act ctt gac aac tcc gat acc atc cag gcc gaa caa Trp Ala Arg Ser Thr Leu Asp Asn Ser Asp Thr Ile Gln Ala Glu Gln 265 270 275	931
gta gat gct gtc cgc gac gag gtt gtg cgc cgc atg gcc atg caa gtc Val Asp Ala Val Arg Asp Glu Val Val Arg Arg Met Gly Met Gln Val 280 285 290	979
cac gag cca agc ctg cac cag gtc cct gat ggt gag ctg acc att ttg His Glu Pro Ser Leu His Gln Val Pro Asp Gly Glu Leu Thr Ile Leu 295 300 305	1027

tac gcg att gcc caa ctg tca aaa aac ggc gag atg gtg tct act gga 1075
 Tyr Ala Ile Ala Gln Leu Ser Lys Asn Gly Glu Met Val Ser Thr Gly
 310 315 320 325
 gat atc gca cac ctc atg ggc gtc aag ccc aac gcc ttg tgg atg cag 1123
 Asp Ile Ala His Leu Met Gly Val Lys Pro Asn Ala Leu Ser Met Gln
 330 335 340
 aga aag caa ctt ctc agc aga ggt ctc gta gag gtt ccc aag tac ggt 1171
 Arg Lys Gln Leu Leu Ser Arg Gly Leu Val Glu Val Pro Lys Tyr Gly
 345 350 355
 ttc ctc aat ttc act ttg cgg tac atg cgc gag cac ctc ctc aac agc 1219
 Phe Leu Asn Phe Thr Leu Pro Tyr Met Arg Glu His Leu Leu Asn Ser
 360 365 370
 ccg cac cac cga cca atc aca taagacacaa gcactaaaac agc 1263
 Pro His His Arg Pro Ile Thr
 375 380

<210> 1650

<211> 380

<212> PRT

<213> Corynebacterium glutamicum

<400> 1650

Met Ser Ala Arg Asn Pro Phe Arg Pro Thr Phe Gly Val Ser Pro Thr
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 Val Leu Ala Gly Arg Asp Ser Leu Leu Gln Ser Phe Lys Leu Gly Leu
 20 25 30
 Ala Glu Gly Pro Gly Ser Pro Phe Arg Ala Leu Leu Ile Ser Gly Ser
 35 40 45
 Arg Gly Met Gly Lys Thr Val Leu Leu Asn Glu Phe Glu Asp Ala Ala
 50 55 60
 Ala Ser Gln Gly Trp Ile Thr Leu Arg Ala Tyr Pro Asp Asn Ser Met
 65 70 75 80
 Val Asp Gly Leu Val Asn Ser Ala Ile Pro Glu Ala Leu Gln Asn Leu
 85 90 95
 Asp Gly Pro Gln Ser Lys Arg Met Leu Ser Gly Val Ala Ile Pro Gly
 100 105 110
 Ile Ala Thr Val Thr Ala Ile Ala Asp Pro Thr Lys Lys Asp Pro Thr
 115 120 125
 Pro Thr Leu Ile Ser Arg Leu Arg Glu Leu Ala Thr Arg Leu Gln Lys
 130 135 140
 His Gly Ser Gly Ile Leu Ile Thr Leu Asp Glu Leu Gln Ser Ala Asn
 145 150 155 160
 Val Asp Leu Leu His Val Leu Ala Thr Ala Val Gln Asp Leu Leu Arg
 165 170 175
 Asp Asp Phe Asp Ile Ala Leu Val Ala Ala Gly Leu Pro Glu Gly Ile

180										185										190									
Asp	Arg	Leu	Leu	Gln	His	Glu	Gly	Thr	Thr	Phe	Ile	Arg	Arg	Ala	Glu														
195										200										205									
Arg	Ile	Leu	Leu	Asn	Pro	Val	Asn	His	Glu	Asp	Ser	Val	Glu	Met	Phe														
210										215										220									
Leu	Asp	Thr	Ala	Ala	Glu	Gly	Gln	Arg	His	Met	Thr	Ser	Glu	Ala	Ala														
225										230										235									
Glu	Leu	Ala	Ala	Gln	Ile	Ser	Lys	Gly	Tyr	Pro	Tyr	Ser	Met	Gln	Leu														
240										245										250									
Thr	Gly	Ser	Leu	Ala	Trp	Ala	Arg	Ser	Thr	Leu	Asp	Asn	Ser	Asp	Thr														
255										260										265									
Ile	Gln	Ala	Glu	Gln	Val	Asp	Ala	Val	Arg	Asp	Glu	Val	Val	Arg	Arg														
270										275										280									
Met	Gly	Met	Gln	Val	His	Glu	Pro	Ser	Leu	His	Gln	Val	Pro	Asp	Gly														
285										290										295									
Glu	Leu	Thr	Ile	Leu	Tyr	Ala	Ile	Ala	Gln	Leu	Ser	Lys	Asn	Gly	Glu														
300										305										310									
Met	Val	Ser	Thr	Gly	Asp	Ile	Ala	His	Leu	Met	Gly	Val	Lys	Pro	Asn														
315										320										325									
Ala	Leu	Ser	Met	Gln	Arg	Lys	Gln	Leu	Leu	Ser	Arg	Gly	Leu	Val	Glu														
330										335										340									
Val	Pro	Lys	Tyr	Gly	Phe	Leu	Asn	Phe	Thr	Leu	Pro	Tyr	Met	Arg	Glu														
345										350										355									
His	Leu	Leu	Asn	Ser	Pro	His	His	Arg	Pro	Ile	Thr																		
360										365										370									
375										380																			
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tgatcggtgcc gggttttcctt gcgttggttag tcttggggct atg agc gca ttc cac 115																													
										Met Ser Ala Phe His																			
										1										5									
atc cga gcg gaa caa tcg cac gat atc agc gcg att cat gat gtt act 163																													
Ile Arg Ala Glu Gln Ser His Asp Ile Ser Ala Ile His Asp Val Thr																													
										10										15									
																				20									
gaa gcg gcc ttt aca gga att gag cat tca gat qga aca gag caa gat 211																													


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Glu Ala Ala Phe Thr Gly Ile Glu His Ser Asp Gly Thr Glu Gln Asp
      25                      30                      35
ctc gtc gat aag ctt cgt gct gca aag gcg ctg agc ctt tcg ctc gtc 259
Leu Val Asp Lys Leu Arg Ala Ala Lys Ala Leu Ser Leu Ser Leu Val
      40                      45                      50

gct gag gcg gat ggc gag gtc att ggg cat att gct gcc tct gag gtg 307
Ala Glu Ala Asp Gly Glu Val Ile Gly His Ile Ala Ala Ser Glu Val
      55                      60                      65

ctg att ggc ggt ggg gtg cag ggc tgg ttt ggc att ggg cct gtc agt 355
Leu Ile Gly Gly Gly Val Gln Gly Trp Phe Gly Ile Gly Pro Val Ser
      70                      75                      80                      85

gtt cgg ccc gat aag cag cag caa ggc gtg ggt att gcg ctg atg ggc 403
Val Arg Pro Asp Lys Gln Gln Gln Gly Val Gly Ile Ala Leu Met Gly
      90                      95                      100

agc gcg ctt gat cag ttg cgt gcg gag ggt gct ggc gcc atc gtg ttg 451
Ser Ala Leu Asp Gln Leu Arg Ala Glu Gly Ala Gly Gly Ile Val Leu
      105                      110                      115

ctg ggg gat ccg ggc tat tat cga cgc ttc ggt ttt gag gtc gtg ccc 499
Leu Gly Asp Pro Gly Tyr Tyr Arg Arg Phe Gly Phe Glu Val Val Pro
      120                      125                      130

ggg ctg gtc tat ccg gac gcg cca gcg gaa ttt ttt atg gct gtg tgt 547
Gly Leu Val Tyr Pro Asp Ala Pro Ala Glu Phe Phe Met Ala Val Cys
      135                      140                      145

ttg aat gct ccg gcg ttt ccg cag ggt gtt gtg gag tat cac tcg gca 595
Leu Asn Ala Pro Ala Phe Pro Gln Gly Val Val Glu Tyr His Ser Ala
      150                      155                      160                      165

ttt gga ggg tagagacccc atcgtggcgg gcc 627
Phe Gly Gly

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<210> 1652

<211> 168

<212> PRT

<213> Corynebacterium glutamicum

<400> 1652

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  1                      5                      10                      15

Ile His Asp Val Thr Glu Ala Ala Phe Thr Gly Ile Glu His Ser Asp
      20                      25                      30

Gly Thr Glu Gln Asp Leu Val Asp Lys Leu Arg Ala Ala Lys Ala Leu
      35                      40                      45

Ser Leu Ser Leu Val Ala Glu Ala Asp Gly Glu Val Ile Gly His Ile
      50                      55                      60

Ala Ala Ser Glu Val Leu Ile Gly Gly Gly Val Gln Gly Trp Phe Gly
      65                      70                      75                      80

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Ile Gly Pro Val Ser Val Arg Pro Asp Lys Gln Gln Gln Gly Val Gly
85 90 95

Ile Ala Leu Met Gly Ser Ala Leu Asp Gln Leu Arg Ala Glu Gly Ala
100 105 110

Gly Gly Ile Val Leu Leu Gly Asp Pro Gly Tyr Tyr Arg Arg Phe Gly
115 120 125

Phe Glu Val Val Pro Gly Leu Val Tyr Pro Asp Ala Pro Ala Glu Phe
130 135 140

Phe Met Ala Val Cys Leu Asn Ala Pro Ala Phe Pro Gln Gly Val Val
145 150 155 160

Glu Tyr His Ser Ala Phe Gly Gly
165

<210> 1653

<211> 843

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(820)

<223> RXA00230

<400> 1653

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tcctatctat ctgctccac tagcacagat aggaactccg ttg att cat gag caa 115
Leu Ile His Glu Gln
1 5

gac gtt cag aag ctg tta aac tac atc act tca cac ttt ggt gtt gac 163
Asp Val Gln Lys Leu Leu Asn Tyr Ile Thr Ser His Phe Gly Val Asp
10 15 20

cct gaa aga tgg ttt cat cct gaa ggc tac caa agc att gcc cta gcg 211
Pro Glu Arg Trp Phe His Pro Glu Gly Tyr Gln Ser Ile Ala Leu Ala
25 30 35

att ctt gac tcc att tac tcg act ggt aat cgc tat aca ggt gta etc 259
Ile Leu Asp Ser Ile Tyr Ser Thr Gly Asn Arg Tyr Thr Gly Val Leu
40 45 50

aac ctt gtc aat cga tac tgc ggg ctg cgc gca aat gaa gga tca cac 307
Asn Leu Val Asn Arg Tyr Cys Gly Leu Arg Ala Asn Glu Gly Ser His
55 60 65

cct gaa gcc gat act gcc act gat ctc atc gag aca ttc tac cgg tgg 355
Pro Glu Ala Asp Thr Ala Thr Asp Leu Ile Glu Thr Phe Tyr Arg Trp
70 75 80 85

gga ggg gtc gac gaa ttt gtt ctc aaa acg aat aat cgg tgg aga act 403
Gly Gly Val Asp Glu Phe Val Leu Lys Thr Asn Asn Arg Trp Arg Thr
90 95 100

tcc tcc aag att cac gca ccc tat aag gca tac gca gct ttg gaa gca 451

Ser Ser Lys Ile His Ala Pro Tyr Lys Ala Tyr Ala Ala Leu Glu Ala
 105 110 115
 gca aag gta ctt gcg ggt cat tcc atc gaa tcc atc agc gat gtt gtc 499
 Ala Lys Val Leu Ala Gly His Ser Ile Glu Ser Ile Ser Asp Val Val
 120 125 130
 ggc agg ttc gat tcg cgc gaa agc cgt gaa cac tca gat atc gcg aga 547
 Gly Arg Phe Asp Ser Arg Glu Ser Arg Glu His Ser Asp Ile Ala Arg
 135 140 145
 gaa tgg ttg atg ata acc ggc caa agt agt gcg ttg acc tgg agt tac 595
 Glu Trp Leu Met Ile Thr Gly Gln Ser Ser Ala Leu Thr Trp Ser Tyr
 150 155 160 165
 ttc ctt atg ctc gta ggt gtc cca gga gtg aaa gca gac cga atg atc 643
 Phe Leu Met Leu Val Gly Val Pro Gly Val Lys Ala Asp Arg Met Ile
 170 175 180
 gtc cgt ttc gtc act cac gtg ctc gag cgt ccg aaa gag att tcc agg 691
 Val Arg Phe Val Thr His Val Leu Glu Arg Pro Lys Glu Ile Ser Arg
 185 190 195
 cac gaa gct tca cgg ttg att gag gaa gtt gcg gac att atg tgc gtc 739
 His Glu Ala Ser Arg Leu Ile Glu Glu Val Ala Asp Ile Met Cys Val
 200 205 210
 aac tac atc tac ctc gac cac acc atc tgg cgg ttc caa tca ggg cgc 787
 Asn Tyr Ile Tyr Leu Asp His Thr Ile Trp Arg Phe Gln Ser Gly Arg
 215 220 225
 ccc tac ctc caa gaa gac tcc tcc cct ttc gaa taaatccatc acatttcaca 840
 Pro Tyr Leu Gln Glu Asp Ser Ser Pro Phe Glu
 230 235 240
 gtc 843
 <210> 1654
 <211> 240
 <212> PRT
 <213> *Corynebacterium glutamicum*
 <400> 1654
 Leu Ile His Glu Gln Asp Val Gln Lys Leu Leu Asn Tyr Ile Thr Ser
 1 5 10 15
 His Phe Gly Val Asp Pro Glu Arg Trp Phe His Pro Glu Gly Tyr Gln
 20 25 30
 Ser Ile Ala Leu Ala Ile Leu Asp Ser Ile Tyr Ser Thr Gly Asn Arg
 35 40 45
 Tyr Thr Gly Val Leu Asn Leu Val Asn Arg Tyr Cys Gly Leu Arg Ala
 50 55 60
 Asn Glu Gly Ser His Pro Glu Ala Asp Thr Ala Thr Asp Leu Ile Glu
 65 70 75 80
 Thr Phe Tyr Arg Trp Gly Gly Val Asp Glu Phe Val Leu Lys Thr Asn
 85 90 95

Asn Arg Trp Arg Thr Ser Ser Lys Ile His Ala Pro Tyr Lys Ala Tyr
100 105 110

Ala Ala Leu Glu Ala Ala Lys Val Leu Ala Gly His Ser Ile Glu Ser
115 120 125

Ile Ser Asp Val Val Gly Arg Phe Asp Ser Arg Glu Ser Arg Glu His
130 135 140

Ser Asp Ile Ala Arg Glu Trp Leu Met Ile Thr Gly Gln Ser Ser Ala
145 150 155 160

Leu Thr Trp Ser Tyr Phe Leu Met Leu Val Gly Val Pro Gly Val Lys
165 170 175

Ala Asp Arg Met Ile Val Arg Phe Val Thr His Val Leu Glu Arg Pro
180 185 190

Lys Glu Ile Ser Arg His Glu Ala Ser Arg Leu Ile Glu Glu Val Ala
195 200 205

Asp Ile Met Cys Val Asn Tyr Ile Tyr Leu Asp His Thr Ile Trp Arg
210 215 220

Phe Gln Ser Gly Arg Pro Tyr Leu Gln Glu Asp Ser Ser Pro Phe Glu
225 230 235 240

<210> 1655

<211> 517

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(517)

<223> RXA00233

<400> 1655

cgccctccagc agttgagggga gaagttccaa cacttgacacc aactgaggaa gcaactgtgc 60

aatagcgctt tagacacaga ctcatgacag aatagaagac atg agt gtg aat gaa 115
Met Ser Val Asn Glu
1 5

gca gat ctg aac gct gtc gaa gag caa ttg gga agg gcc cca cga ggt 163
Ala Asp Leu Asn Ala Val Glu Glu Gln Leu Gly Arg Ala Pro Arg Gly
10 15 20

gtc ctc gat att tct tac cgc agc cct gat gga gta ccc ggt gtg gtg 211
Val Leu Asp Ile Ser Tyr Arg Ser Pro Asp Gly Val Pro Gly Val Val
25 30 35

atg acc gca cca aaa ctg gat gac gga acc cca ttc cca acc ctg tac 259
Met Thr Ala Pro Lys Leu Asp Asp Gly Thr Pro Phe Pro Thr Leu Tyr
40 45 50

tac ttg aca gat cca cgc ctg acc acc gag gca tcc cgc ctc gag gtc 307
 Tyr Leu Thr Asp Pro Arg Leu Thr Thr Glu Ala Ser Arg Leu Glu Val
 55 60 65

gca ttg gta atg aag tgg atg act gat cgc ctt tcc acc gac gaa gag 355
 Ala Leu Val Met Lys Trp Met Thr Asp Arg Leu Ser Thr Asp Glu Glu
 70 75 80 85

ctt cgt gcc gac tac cag cgc gcc cac gag cac ttc ctg gca aag cgc 403
 Leu Arg Ala Asp Tyr Gln Arg Ala His Glu His Phe Leu Ala Lys Arg
 90 95 100

aac gca att gaa gat ctc ggc acg gat ttt tcc ggc ggt ggc atg cct 451
 Asn Ala Ile Glu Asp Leu Gly Thr Asp Phe Ser Gly Gly Gly Met Pro
 105 110 115

gac cga gtg aag tgc ctt cac gtc ctc att gac tat gca ctg gca gaa 499
 Asp Arg Val Lys Cys Leu His Val Leu Ile Asp Tyr Ala Leu Ala Glu
 120 125 130

ggc cca cac cat ttc ctt 517
 Gly Pro His His Phe Leu
 135

<210> 1656

<211> 139

<212> PRT

<213> Corynebacterium glutamicum

<400> 1656

Met Ser Val Asn Glu Ala Asp Leu Asn Ala Val Glu Glu Gln Leu Gly
 1 5 10 15

Arg Ala Pro Arg Gly Val Leu Asp Ile Ser Tyr Arg Ser Pro Asp Gly
 20 25 30

Val Pro Gly Val Val Met Thr Ala Pro Lys Leu Asp Asp Gly Thr Pro
 35 40 45

Phe Pro Thr Leu Tyr Tyr Leu Thr Asp Pro Arg Leu Thr Thr Glu Ala
 50 55 60

Ser Arg Leu Glu Val Ala Leu Val Met Lys Trp Met Thr Asp Arg Leu
 65 70 75 80

Ser Thr Asp Glu Glu Leu Arg Ala Asp Tyr Gln Arg Ala His Glu His
 85 90 95

Phe Leu Ala Lys Arg Asn Ala Ile Glu Asp Leu Gly Thr Asp Phe Ser
 100 105 110

Gly Gly Gly Met Pro Asp Arg Val Lys Cys Leu His Val Leu Ile Asp
 115 120 125

Tyr Ala Leu Ala Glu Gly Pro His His Phe Leu
 130 135

<210> 1657

<211> 663

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(640)

<223> RXA00234

<400> 1657

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ttcagggtcta aataaaagcg cttttcgacg cccggtaacc tcaagggtgc cgggcgtcgt 60
tgccttacta ctgttactgg tgtgactatg atcgaggatt atg gca aag cag aag 115
Met Ala Lys Gln Lys
1 5
aaa act cat aaa ggc ctt gtt cct gtc tca agc agg gaa cgt gct tca 163
Lys Thr His Lys Gly Leu Val Pro Val Ser Ser Arg Glu Arg Ala Ser
10 15 20
gag tca gtt tct gct acc cgc gcc cca ttt aga ttg ggt gcc gtc ggc 211
Glu Ser Val Ser Ala Thr Arg Ala Pro Phe Arg Leu Gly Ala Val Gly
25 30 35
atc ggt gca atc gca ctc gta gtt ctt ctc atc ctg ttt gtc atc gcg 259
Ile Gly Ala Ile Ala Leu Val Val Leu Leu Ile Leu Phe Val Ile Ala
40 45 50
att cct gtg cgt aac tat ttt cag ctg cgc tcc gac atc gcc caa aca 307
Ile Pro Val Arg Asn Tyr Phe Gln Leu Arg Ser Asp Ile Ala Gln Thr
55 60 65
gag gct tcc att gaa gcc aaa gaa caa cag atc aaa caa ctg gaa tct 355
Glu Ala Ser Ile Glu Ala Lys Glu Gln Gln Ile Lys Gln Leu Glu Ser
70 75 80 85
gac ctc aac agg tac caa tca gag gcg tac atc cgc gaa caa gca cgc 403
Asp Leu Asn Arg Tyr Gln Ser Glu Ala Tyr Ile Arg Glu Gln Ala Arg
90 95 100
ctg cgc cta ggc gtc att gaa cct gga gaa acc gcg ttc aga atc gtg 451
Leu Arg Leu Gly Val Ile Glu Pro Gly Glu Thr Ala Phe Arg Ile Val
105 110 115
gac cca gca cta gat acc gac acc tca gtc acc tct gac gcc aac gaa 499
Asp Pro Ala Leu Asp Thr Asp Thr Ser Val Thr Ser Asp Gly Asn Glu
120 125 130
gag aaa cca ctg gga gct tgg tat gaa aac ctc tgg gac tca gtc acc 547
Glu Lys Pro Leu Gly Ala Trp Tyr Glu Asn Leu Trp Asp Ser Val Thr
135 140 145
aag cca gaa gca ctc ggc gaa gag gaa att gcg cct cca gca gtt gag 595
Lys Pro Glu Ala Leu Gly Glu Glu Glu Ile Ala Pro Pro Ala Val Glu
150 155 160 165
gga gaa gtt cca aca ctt gca cca act gag gaa gca act gtg caa 640
Gly Glu Val Pro Thr Leu Ala Pro Thr Glu Glu Ala Thr Val Gln
170 175 180
tagcgcttta gacacagact cat 663

```

<210> 1658
 <211> 180
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1658
 Met Ala Lys Gln Lys Lys Thr His Lys Gly Leu Val Pro Val Ser Ser
 1 5 10 15
 Arg Glu Arg Ala Ser Glu Ser Val Ser Ala Thr Arg Ala Pro Phe Arg
 20 25 30
 Leu Gly Ala Val Gly Ile Gly Ala Ile Ala Leu Val Val Leu Leu Ile
 35 40 45
 Leu Phe Val Ile Ala Ile Pro Val Arg Asn Tyr Phe Gln Leu Arg Ser
 50 55 60
 Asp Ile Ala Gln Thr Glu Ala Ser Ile Glu Ala Lys Glu Gln Gln Ile
 65 70 75 80
 Lys Gln Leu Glu Ser Asp Leu Asn Arg Tyr Gln Ser Glu Ala Tyr Ile
 85 90 95
 Arg Glu Gln Ala Arg Leu Arg Leu Gly Val Ile Glu Pro Gly Glu Thr
 100 105 110
 Ala Phe Arg Ile Val Asp Pro Ala Leu Asp Thr Asp Thr Ser Val Thr
 115 120 125
 Ser Asp Gly Asn Glu Glu Lys Pro Leu Gly Ala Trp Tyr Glu Asn Leu
 130 135 140
 Trp Asp Ser Val Thr Lys Pro Glu Ala Leu Gly Glu Glu Ile Ala
 145 150 155 160
 Pro Pro Ala Val Glu Gly Glu Val Pro Thr Leu Ala Pro Thr Glu Glu
 165 170 175
 Ala Thr Val Gln
 180

<210> 1659
 <211> 501
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(478)
 <223> RXA00237

<400> 1659
 actggtagaa gctttgatga tctacatcac aaatttacaa tgtgtggtga gttattcata 60
 ttacccaag acttaaacct taaaaggagc cctaaaaatc atg aag ctt tca cac 115
 Met Lys Leu Ser His
 1 5

cgc atc gca gca atg gca gca acc gca ggc atc aca gtg gca gca ttc 163
 Arg Ile Ala Ala Met Ala Ala Thr Ala Gly Ile Thr Val Ala Ala Phe
 10 15 20

gca gca cct gct tcc gca tcc gac ttc gca aac cta tcc tcc acc aac 211
 Ala Ala Pro Ala Ser Ala Ser Asp Phe Ala Asn Leu Ser Ser Thr Asn
 25 30 35

aaa gaa ctg tcc cct cag tac aac tgg gtt gct tgc ggc atc ctt gag 259
 Lys Glu Leu Ser Pro Gln Tyr Asn Trp Val Ala Cys Gly Ile Leu Glu
 40 45 50

ggt ggc ctc aaa gca gct ggc gtc ctt gaa gaa ggc cag tac aac cgc 307
 Gly Gly Leu Lys Ala Ala Gly Val Leu Glu Glu Gly Gln Tyr Asn Arg
 55 60 65

gag ctc gca gaa gca atc gcc gca aag ggt gaa ggc ttc tgg acc act 355
 Glu Leu Ala Glu Ala Ile Ala Ala Lys Gly Glu Gly Phe Trp Thr Thr
 70 75 80 85

cag ttc cca caa atc ggt gat tgg aac gaa gat cag gca gca gca ctt 403
 Gln Phe Pro Gln Ile Gly Asp Trp Asn Glu Asp Gln Ala Ala Ala Leu
 90 95 100

gcc gac cgc gca caa acc tgt ggc cta gtt aag gct gac acc tac ctt 451
 Ala Asp Arg Ala Gln Thr Cys Gly Leu Val Lys Ala Asp Thr Tyr Leu
 105 110 115

tct gag ctg tcc tcc aac ttc tct tcc taaaagggttc gggggtaacc 498
 Ser Glu Leu Ser Ser Asn Phe Ser Ser
 120 125

cca 501

<210> 1660
 <211> 126
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 1660
 Met Lys Leu Ser His Arg Ile Ala Ala Met Ala Ala Thr Ala Gly Ile
 1 5 10 15

Thr Val Ala Ala Phe Ala Ala Pro Ala Ser Ala Ser Asp Phe Ala Asn
 20 25 30

Leu Ser Ser Thr Asn Lys Glu Leu Ser Pro Gln Tyr Asn Trp Val Ala
 35 40 45

Cys Gly Ile Leu Glu Gly Gly Leu Lys Ala Ala Gly Val Leu Glu Glu
 50 55 60

Gly Gln Tyr Asn Arg Glu Leu Ala Glu Ala Ile Ala Ala Lys Gly Glu
 65 70 75 80

Gly Phe Trp Thr Thr Gln Phe Pro Gln Ile Gly Asp Trp Asn Glu Asp
 85 90 95

Gln Ala Ala Ala Leu Ala Asp Arg Ala Gln Thr Cys Gly Leu Val Lys
 100 105 110

Ala Asp Thr Tyr Leu Ser Glu Leu Ser Ser Asn Phe Ser Ser
 115 120 125

<210> 1661

<211> 492

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(469)

<223> RXA00238

<400> 1661

aacagtcaca taaatcactt cagtaacgta tgattttgga ctgttgtggc ttttgccata 60

ttttatttoat ttccatctca gtgatctctt aaggaaaccc atg aag aaa cta cgt 115
 Met Lys Lys Leu Arg
 1 5

ttc gcc acc atc gct gcc gct acc gtt gcc ctg act gcg agc ctt acc 163
 Phe Ala Thr Ile Ala Ala Thr Val Ala Leu Thr Ala Ser Leu Thr
 10 15 20

ccc tca gct tcc gca cag gat ttc aac caa atc atc gac aac ttt gat 211
 Pro Ser Ala Ser Ala Gln Asp Phe Asn Gln Ile Ile Asp Asn Phe Asp
 25 30 35

tgc ggc atc ctt cag acc gct atc tac acc acc ggc ctg gct cac gag 259
 Cys Gly Ile Leu Gln Thr Ala Ile Tyr Thr Thr Gly Leu Ala His Glu
 40 45 50

aac tcc act cgc tca gag ctg gcc gct aat ctg cgc aac tcc gca gct 307
 Asn Ser Thr Arg Ser Glu Leu Ala Ala Asn Leu Arg Asn Ser Ala Ala
 55 60 65

gtc ggc caa cta gac ttc cca ttg aat atc gcg gct acc ggc tac tcc 355
 Val Gly Gln Leu Asp Phe Pro Leu Asn Ile Ala Ala Thr Gly Tyr Ser
 70 75 80 85

gag cgc atc gct aac cgc gca ctg acc tgc gga atc gtg aag gaa gat 403
 Glu Arg Ile Ala Asn Arg Ala Leu Thr Cys Gly Ile Val Lys Glu Asp
 90 95 100

cca cag gac ttc ctg tcc cag ctg cag ctt ctg tcc tct aac cta tct 451
 Pro Gln Asp Phe Leu Ser Gln Leu Gln Leu Ser Ser Asn Leu Ser
 105 110 115

tct tcc ttc ttc act gct tagttttctt tgggcttttc ctt 492
 Ser Ser Phe Phe Thr Ala
 120

<210> 1662

<211> 123

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1662

```

Met Lys Lys Leu Arg Phe Ala Thr Ile Ala Ala Ala Thr Val Ala Leu
 1          5          10          15

Thr Ala Ser Leu Thr Pro Ser Ala Ser Ala Gln Asp Phe Asn Gln Ile
          20          25          30

Ile Asp Asn Phe Asp Cys Gly Ile Leu Gln Thr Ala Ile Tyr Thr Thr
          35          40          45

Gly Leu Ala His Glu Asn Ser Thr Arg Ser Glu Leu Ala Ala Asn Leu
 50          55          60

Arg Asn Ser Ala Ala Val Gly Gln Leu Asp Phe Pro Leu Asn Ile Ala
 65          70          75          80

Ala Thr Gly Tyr Ser Glu Arg Ile Ala Asn Arg Ala Leu Thr Cys Gly
          85          90          95

Ile Val Lys Glu Asp Pro Gln Asp Phe Leu Ser Gln Leu Gln Leu Leu
100          105          110

Ser Ser Asn Leu Ser Ser Ser Phe Phe Thr Ala
115          120

```

<210> 1663

<211> 708

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(685)

<223> RXA00239

<400> 1663

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acaaagcgga tcagattaac aaggtccgtg acgctgtcga tgagcgcatt gcaaaaaaca 60

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```

acggcggcga agagaatcca gccaaactagt attaggcgtc atg cgc gtc gta gtt 115
                                     Met Arg Val Val Val
                                     1          5

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```

gtt gat cct aaa cac ccc gtc ctt cca gtc tct ttc ctc gag gct gtt 163
Val Asp Pro Lys His Pro Val Leu Pro Val Ser Phe Leu Glu Ala Val
          10          15          20

```

```

ctt ggg cgg ggt gaa cct gtt tct atc gat ccc gat ttt cca ttt gat 211
Leu Gly Arg Gly Glu Pro Val Ser Ile Asp Pro Asp Phe Pro Phe Asp
          25          30          35

```

```

att gaa aaa tgg ggg atc aag acg tcg aca agc gcc tcc tgg ttt atc 259
Ile Glu Lys Trp Gly Ile Lys Thr Ser Thr Ser Ala Ser Trp Phe Ile
          40          45          50

```

```

atc gca aaa ccg caa agc acg ctg ctt atc gac gcg ccc ctc aac cct 307
Ile Ala Lys Pro Gln Ser Thr Leu Leu Ile Asp Ala Pro Leu Asn Pro
          55          60          65

```

```

ttg cat gag gcc gtc ggc gtc atg cgg gcg gcc gtg ggc cgc ggc gag 355
Leu His Glu Ala Val Gly Val Met Arg Ala Ala Val Gly Arg Gly Glu
 70          75          80          85

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tgg gaa cgc acg caa acc cat gag agt ttg att ccg tat ctg gaa gaa 403
 Trp Glu Arg Thr Gln Thr His Glu Ser Leu Ile Pro Tyr Leu Glu Glu
 90 95 100

gaa tcg cag gag ttt att gaa gcg att cat ggt ggc gat gat gag cac 451
 Glu Ser Gln Glu Phe Ile Glu Ala Ile His Gly Gly Asp Asp Glu His
 105 110 115

atg aaa agc gaa ctg ggg gat gtt ttg ctg cag gtg ctt ttt cat gca 499
 Met Lys Ser Glu Leu Gly Asp Val Leu Leu Gln Val Leu Phe His Ala
 120 125 130

gaa atc gcc gcc cgt cag ggt cga ttc gac att ttt gac gtg gcg gcg 547
 Glu Ile Ala Ala Arg Gln Gly Arg Phe Asp Ile Phe Asp Val Ala Ala
 135 140 145

agt ttc gta gcc aag atg caa tct cgt tcg ccg tac ctg ttc gac ggc 595
 Ser Phe Val Ala Lys Met Gln Ser Arg Ser Pro Tyr Leu Phe Asp Gly
 150 155 160 165

tct acc gga att gtg gac acc gac gag cag cag cgg ctg tgg gct caa 643
 Ser Thr Gly Ile Val Asp Thr Asp Glu Gln Gln Arg Leu Trp Ala Gln
 170 175 180

gga aaa gcc caa gag aaa cta agc agt gaa gaa gga aga aga 685
 Gly Lys Ala Gln Glu Lys Leu Ser Ser Glu Glu Gly Arg Arg
 185 190 195

taggttagag gacagaagct gca 708

<210> 1664
 <211> 195
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1664
 Met Arg Val Val Val Val Asp Pro Lys His Pro Val Leu Pro Val Ser
 1 5 10 15
 Phe Leu Glu Ala Val Leu Gly Arg Gly Glu Pro Val Ser Ile Asp Pro
 20 25 30
 Asp Phe Pro Phe Asp Ile Glu Lys Trp Gly Ile Lys Thr Ser Thr Ser
 35 40 45
 Ala Ser Trp Phe Ile Ile Ala Lys Pro Gln Ser Thr Leu Leu Ile Asp
 50 55 60
 Ala Pro Leu Asn Pro Leu His Glu Ala Val Gly Val Met Arg Ala Ala
 65 70 75 80
 Val Gly Arg Gly Glu Trp Glu Arg Thr Gln Thr His Glu Ser Leu Ile
 85 90 95
 Pro Tyr Leu Glu Glu Glu Ser Gln Glu Phe Ile Glu Ala Ile His Gly
 100 105 110
 Gly Asp Asp Glu His Met Lys Ser Glu Leu Gly Asp Val Leu Leu Gln
 115 120 125

Val Leu Phe His Ala Glu Ile Ala Ala Arg Gln Gly Arg Phe Asp Ile
130 135 140

Phe Asp Val Ala Ala Ser Phe Val Ala Lys Met Gln Ser Arg Ser Pro
145 150 155 160

Tyr Leu Phe Asp Gly Ser Thr Gly Ile Val Asp Thr Asp Glu Gln Gln
165 170 175

Arg Leu Trp Ala Gln Gly Lys Ala Gln Glu Lys Leu Ser Ser Glu Glu
180 185 190

Gly Arg Arg
195

<210> 1665

<211> 333

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(310)

<223> RKA00240

<400> 1665

tcatttaacg tagttgacgt acggcggaagt cgctaaaactt cgcgtaattct tggggccaat 60

taatcaagtg cagatgaatt gttagaaaag gctggagacc atg ggt att ttt gac 115
Met Gly Ile Phe Asp
1 5

gaa gct aag aag aag gca acc gaa ttc ctc gac tct gat tca ggc gag 163
Glu Ala Lys Lys Lys Ala Thr Glu Phe Leu Asp Ser Asp Ser Gly Glu
10 15 20

cag aag tcc gat gga ctg ctg gat aag gcc gca gac aaa gct aag ggt 211
Gln Lys Ser Asp Gly Leu Leu Asp Lys Ala Ala Asp Lys Ala Lys Gly
25 30 35

ctc ctc ggt gaa gac aaa gcg gat cag att aac aag gtc cgt gac gct 259
Leu Leu Gly Glu Asp Lys Ala Asp Gln Ile Asn Lys Val Arg Asp Ala
40 45 50

gtc gat gag cgc att ggc aaa aac aac ggc ggc gaa gag aat cca gcc 307
Val Asp Glu Arg Ile Gly Lys Asn Asn Gly Gly Gln Glu Asn Pro Ala
55 60 65

aac tagtattagg cgtoatgcgc gtc 333
Asn
70

<210> 1666

<211> 70

<212> PRT

<213> Corynebacterium glutamicum

<400> 1666

Met Gly Ile Phe Asp Glu Ala Lys Lys Lys Ala Thr Glu Phe Leu Asp
 1 5 10 15
 Ser Asp Ser Gly Glu Gln Lys Ser Asp Gly Leu Leu Asp Lys Ala Ala
 20 25 30
 Asp Lys Ala Lys Gly Leu Leu Gly Glu Asp Lys Ala Asp Gln Ile Asn
 35 40 45
 Lys Val Arg Asp Ala Val Asp Glu Arg Ile Gly Lys Asn Asn Gly Gly
 50 55 60
 Glu Glu Asn Pro Ala Asn
 65 70

<210> 1667

<211> 759

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(736)

<223> RXA00244

<400> 1667

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gtttaaacag tgaagatttg gcagaaagcg agatggataa atg aat gat cag ctg 115
 Met Asn Asp Gln Leu
 1 5

tgg gaa ggc gac act gga acg ctg act ttt ggg tcc agg aaa gct ctg 163
 Trp Glu Gly Asp Thr Gly Thr Leu Thr Phe Gly Ser Arg Lys Ala Leu
 10 15 20

gtg caa tta ctc aaa ggt ccc atg gtg aat gct ttg cag cat gtt gaa 211
 Val Gln Leu Leu Lys Gly Pro Met Val Asn Ala Leu Gln His Val Glu
 25 30 35

gtg tgg cgg gct atc acc aca gat caa gat gcg ctc aat gct gtg ctt 259
 Val Trp Arg Ala Ile Thr Thr Asp Gln Asp Ala Leu Asn Ala Val Leu
 40 45 50

aac aat ttg ttc ctc gag ttg gtt ctt gat gag gat gcg ggt gtt gca 307
 Asn Asn Leu Phe Leu Glu Val Leu Asp Gly Ala Gly Val Ala
 55 60 65

ttt act cgg cct gcc aat ggt aga caa gaa gta ttg gtt gga aat aac 355
 Phe Thr Arg Pro Ala Asn Gly Arg Gln Glu Val Leu Val Gly Asn Asn
 70 75 80 85

aaa act gaa gcg atg ccc aaa gtg ctg cgc acg gag acg ctg tcg cat 403
 Lys Thr Glu Ala Met Pro Lys Val Leu Arg Thr Glu Thr Leu Ser His
 90 95 100

ttt gat acg ttg atc att ttg att ctg cgc caa gaa ctc acc atg gcg 451
 Phe Asp Thr Leu Ile Ile Leu Ile Leu Arg Gln Glu Leu Thr Met Ala
 105 110 115

cca ccg ggg gaa cga gtc att gtg gat cgt gaa gaa atc cgc gaa caa 499
 Pro Pro Gly Glu Arg Val Ile Val Asp Arg Glu Ile Arg Glu Gln
 120 125 130

gtg ttg ctc tac cgc gtt gat gaa gag cga gat gaa gcc aaa cta gct 547
 Val Leu Leu Tyr Arg Val Asp Glu Glu Arg Asp Glu Ala Lys Leu Ala
 135 140 145

aag cga ttc gac gct gca ttt agg cgc atc gtg gat tat tca tta gct 595
 Lys Arg Phe Asp Ala Ala Phe Arg Arg Ile Val Asp Tyr Ser Leu Ala
 150 155 160 165

aaa aag aca gag aca cct gaa cgt ttt gag gtc tca cca gca ctg cgc 643
 Lys Lys Thr Glu Thr Pro Glu Arg Phe Glu Val Ser Pro Ala Leu Arg
 170 175 180

cag att ttt gat gcc gac act gtg gca ggt gtg cgc gct gag tac gaa 691
 Gln Ile Phe Asp Ala Asp Thr Val Ala Gly Val Arg Ala Glu Tyr Glu
 185 190 195

aaa ttt aac aaa gca gcc cat gat gga aat gaa gag gaa cag aag 736
 Lys Phe Asn Lys Ala Ala His Asp Gly Asn Glu Glu Glu Gln Lys
 200 205 210

tgaccagcga acaagcttta gat 759

<210> 1668
 <211> 212
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1668
 Met Asn Asp Gln Leu Trp Glu Gly Asp Thr Gly Thr Leu Thr Phe Gly
 1 5 10 15

Ser Arg Lys Ala Leu Val Gln Leu Leu Lys Gly Pro Met Val Asn Ala
 20 25 30

Leu Gln His Val Glu Val Trp Arg Ala Ile Thr Thr Asp Gln Asp Ala
 35 40 45

Leu Asn Ala Val Leu Asn Asn Leu Phe Leu Glu Leu Val Leu Asp Glu
 50 55 60

Asp Ala Gly Val Ala Phe Thr Arg Pro Ala Asn Gly Arg Gln Glu Val
 65 70 75 80

Leu Val Gly Asn Asn Lys Thr Glu Ala Met Pro Lys Val Leu Arg Thr
 85 90 95

Glu Thr Leu Ser His Phe Asp Thr Leu Ile Ile Leu Ile Leu Arg Gln
 100 105 110

Glu Leu Thr Met Ala Pro Pro Gly Glu Arg Val Ile Val Asp Arg Glu
 115 120 125

Glu Ile Arg Glu Gln Val Leu Leu Tyr Arg Val Asp Glu Glu Arg Asp
 130 135 140

Glu Ala Lys Leu Ala Lys Arg Phe Asp Ala Ala Phe Arg Arg Ile Val

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<210> 1669
<211> 1608
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1585)
<223> BXA00245
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[illegible]

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ttg	cag	act	ttg	gcg	ttg	gaa	tcg	gac	ccc	agc	aca	gcg	aaa	cgt	tta	547
Leu	Gln	Thr	Leu	Ala	Leu	Glu	Ser	Asp	Pro	Ser	Thr	Ala	Lys	Arg	Leu	
	135				140				145							
gct	gag	tta	gag	cgt	gaa	cgc	gac	agg	att	gaa	cgc	cag	att	gaa	gcg	595
Ala	Glu	Leu	Glu	Arg	Glu	Arg	Asp	Arg	Ile	Glu	Arg	Gln	Ile	Glu	Ala	
	150				155				160					165		
gtc	cac	gct	ggc	gaa	ttt	gaa	gtc	ctc	acc	acc	gtg	cag	att	ggc	gat	643
Val	His	Ala	Gly	Glu	Phe	Glu	Val	Leu	Thr	Thr	Val	Gln	Ile	Gly	Asp	
				170				175						180		
cgg	gta	gca	gat	att	ttg	gat	cta	gca	gca	tct	att	cct	gca	gat	ttc	691
Arg	Val	Ala	Asp	Ile	Leu	Asp	Leu	Ala	Ala	Ser	Ile	Pro	Ala	Asp	Phe	
			185				190						195			
gcc	agg	gta	agg	cat	gag	ctg	agc	gat	ctg	aac	cgg	aag	ctg	cgc	agg	739
Ala	Arg	Val	Arg	His	Glu	Leu	Ser	Asp	Leu	Asn	Arg	Lys	Leu	Arg	Arg	
	200						205				210					
cag	ttg	ctt	gat	cct	gaa	gat	tcc	cgt	ggc	gat	gtt	ttg	gaa	gag	atc	787
Gln	Leu	Leu	Asp	Pro	Glu	Asp	Ser	Arg	Gly	Asp	Val	Leu	Glu	Glu	Ile	
	215					220					225					
ttc	agg	gga	gtt	gat	ctg	att	ggg	gat	tcc	gat	gcg	ggg	cgc	agc	ttc	835
Phe	Arg	Gly	Val	Asp	Leu	Ile	Gly	Asp	Ser	Asp	Ala	Gly	Arg	Ser	Phe	
	230				235				240					245		
aat	agt	ttc	ttt	gat	gtt	ttg	ctc	gat	cgg	gaa	cgc	tca	agt	ctg	att	883
Asn	Ser	Phe	Phe	Asp	Val	Leu	Leu	Asp	Arg	Glu	Arg	Ser	Ser	Leu	Ile	
			250					255						260		
gat	cga	tgg	atc	aga	gaa	gtt	ctg	gga	cgc	gat	gag	gct	att	gat	ctg	931
Asp	Arg	Trp	Ile	Arg	Glu	Val	Leu	Gly	Arg	Asp	Glu	Ala	Ile	Asp	Leu	
			265				270						275			
gat	tca	aaa	tta	agg	aca	ggg	ctg	tac	cga	att	ttc	cgg	gat	atg	gag	979
Asp	Ser	Lys	Leu	Arg	Thr	Gly	Leu	Tyr	Arg	Ile	Phe	Arg	Asp	Met	Glu	
	280					285					290					
gat	gcc	agc	ttc	gag	gtc	aac	ggg	gaa	atg	aca	ggg	ctg	gct	cga	agt	1027
Asp	Ala	Ser	Phe	Glu	Val	Asn	Gly	Glu	Met	Thr	Gly	Leu	Ala	Arg	Ser	
	295					300					305					
ttg	cgt	cac	tat	gtc	act	acc	gag	gag	ttc	gca	gag	agc	cga	cgc	atg	1075
Leu	Arg	His	Tyr	Val	Thr	Thr	Glu	Glu	Phe	Ala	Glu	Ser	Arg	Arg	Met	
	310				315				320					325		
att	cag	ttg	ctt	cgc	gat	acc	cgc	agt	gcc	gct	gct	aag	gcc	gcc	gag	1123
Ile	Gln	Leu	Leu	Arg	Asp	Thr	Arg	Ser	Ala	Ala	Ala	Lys	Ala	Ala	Glu	
				330					335					340		
gct	ggc	gaa	gtg	acc	tca	ctc	aat	cac	atg	gac	aca	cca	ctc	gtg	cgc	1171
Ala	Gly	Glu	Val	Thr	Ser	Leu	Asn	His	Met	Asp	Thr	Pro	Leu	Val	Arg	
			345				350						355			
att	ggc	atg	gat	gtt	cgc	tcg	att	gcg	ggg	ttg	aaa	ctg	aag	aac	cca	1219
Ile	Gly	Met	Asp	Val	Arg	Ser	Ile	Ala	Gly	Leu	Lys	Leu	Lys	Asn	Pro	

360	365	370	
ggt gaa gaa cgc gtc gaa gat	ttg cct gag cca gtt gaa gaa caa gaa	1267	
Gly Glu Glu Arg Val Glu Asp	Leu Pro Glu Pro Val Glu Glu Gln Glu		
375	380	385	
cta gac act gaa gtc ttg atg gaa caa att cgg gca agc gag att gat	1315		
Leu Asp Thr Glu Val Leu Met Glu Gln Ile Arg Ala Ser Glu Ile Asp			
390	395	400	405
ttt gag gaa ttg gaa gag gct gtt tct tta gtt ctt gcc gag caa tcg	1363		
Phe Glu Glu Leu Glu Glu Ala Val Ser Leu Val Leu Ala Glu Gln Ser			
410	415	420	
cac gcc acg atc acc gag gta cta gaa cat ttc cgg gca acg caa ggt	1411		
His Ala Thr Ile Thr Glu Val Leu Glu His Phe Pro Ala Thr Gln Gly			
425	430	435	
ctc gcc agc att gtt gga ttg tta tac ctg gcg atg cgt gat ggt gtt	1459		
Leu Ala Ser Ile Val Gly Leu Leu Tyr Leu Ala Met Arg Asp Gly Val			
440	445	450	
ccc aca ggt cgc gcg caa ata gtg gag tgg gaa agt gat gat gcc aca	1507		
Pro Thr Gly Arg Ala Gln Ile Val Glu Trp Glu Ser Asp Asp Ala Thr			
455	460	465	
cac cgc cgg cgg att aca gga tgg cag ttc atc agg ggt tta aac agt	1555		
His Arg Arg Arg Ile Thr Gly Trp Gln Phe Ile Arg Gly Leu Asn Ser			
470	475	480	485
gaa gat ttg gca gaa agc gag atg gat aaa tgaatgatca gctgtgggaa	1605		
Glu Asp Leu Ala Glu Ser Glu Met Asp Lys			
490	495		
ggc			1608
<210> 1670			
<211> 495			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 1670			
Met Thr Val Val Ser His Ala Leu Gly Phe Lys Arg Phe Arg Gln Glu			
1 5 10 15			
Ser Leu Glu Leu Ser Leu Leu Arg Ser Asp Asn Phe Pro Val Val Leu			
20 25 30			
Ala Val Val Ala Gln Tyr Phe Pro Gln Gly Ala Ile Ala Lys Pro Ala			
35 40 45			
Ser Glu Leu Tyr Gln Leu Leu Ser Asp Asp Phe Arg Val Leu Arg Glu			
50 55 60			
Glu Gly Phe Glu Leu Pro Lys Ser Pro Ser Asp Tyr Val Ser Asp Trp			
65 70 75 80			
Val Lys Ser Arg Trp Phe Val Arg Arg Pro Gly Ser Ser Gln Thr Gly			
85 90 95			

Glu Thr Val Glu Pro Ser Glu Glu Leu Leu Ala Val Leu Asp Ser Val
 100 105 110
 Gln Arg Trp Asp Asn Pro His Arg Ser Ile Ser Ala Ser Arg Ile Glu
 115 120 125
 Ser Leu Thr Gln Ala Leu Gln Thr Leu Ala Leu Glu Ser Asp Pro Ser
 130 135 140
 Thr Ala Lys Arg Leu Ala Glu Leu Glu Arg Glu Arg Asp Arg Ile Glu
 145 150 155 160
 Arg Gln Ile Glu Ala Val His Ala Gly Glu Phe Glu Val Leu Thr Thr
 165 170 175
 Val Gln Ile Gly Asp Arg Val Ala Asp Ile Leu Asp Leu Ala Ala Ser
 180 185 190
 Ile Pro Ala Asp Phe Ala Arg Val Arg His Glu Leu Ser Asp Leu Asn
 195 200 205
 Arg Lys Leu Arg Arg Gln Leu Leu Asp Pro Glu Asp Ser Arg Gly Asp
 210 215 220
 Val Leu Glu Glu Ile Phe Arg Gly Val Asp Leu Ile Gly Asp Ser Asp
 225 230 235 240
 Ala Gly Arg Ser Phe Asn Ser Phe Phe Asp Val Leu Leu Asp Arg Glu
 245 250 255
 Arg Ser Ser Leu Ile Asp Arg Trp Ile Arg Glu Val Leu Gly Arg Asp
 260 265 270
 Glu Ala Ile Asp Leu Asp Ser Lys Leu Arg Thr Gly Leu Tyr Arg Ile
 275 280 285
 Phe Arg Asp Met Glu Asp Ala Ser Phe Glu Val Asn Gly Glu Met Thr
 290 295 300
 Gly Leu Ala Arg Ser Leu Arg His Tyr Val Thr Thr Glu Glu Phe Ala
 305 310 315 320
 Glu Ser Arg Arg Met Ile Gln Leu Leu Arg Asp Thr Arg Ser Ala Ala
 325 330 335
 Ala Lys Ala Ala Glu Ala Gly Glu Val Thr Ser Leu Asn His Met Asp
 340 345 350
 Thr Pro Leu Val Arg Ile Gly Met Asp Val Arg Ser Ile Ala Gly Leu
 355 360 365
 Lys Leu Lys Asn Pro Gly Glu Glu Arg Val Glu Asp Leu Pro Glu Pro
 370 375 380
 Val Glu Glu Gln Glu Leu Asp Thr Glu Val Leu Met Glu Gln Ile Arg
 385 390 395 400
 Ala Ser Glu Ile Asp Phe Glu Glu Leu Glu Glu Ala Val Ser Leu Val
 405 410 415
 Leu Ala Glu Gln Ser His Ala Thr Ile Thr Glu Val Leu Glu His Phe

420 425 430
 Pro Ala Thr Gln Gly Leu Ala Ser Ile Val Gly Leu Leu Tyr Leu Ala
 435 440 445
 Met Arg Asp Gly Val Pro Thr Gly Arg Ala Gln Ile Val Glu Trp Glu
 450 455 460
 Ser Asp Asp Ala Thr His Arg Arg Arg Ile Thr Gly Trp Gln Phe Ile
 465 470 475 480
 Arg Gly Leu Asn Ser Glu Asp Leu Ala Glu Ser Glu Met Asp Lys
 485 490 495

 <210> 1671
 <211> 846
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (101)..(823)
 <223> RXA00248

 <400> 1671
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 tagaccagtg tcttaggcaa gacccattt aggacacctc atg att ccc ctg att 115
 Met Ile Pro Leu Ile
 1 5

 acg ctt tcc cac ggt tcc cgc aaa aag tcc gca gct gca ggc att act 163
 Thr Leu Ser His Gly Ser Arg Lys Lys Ser Ala Ala Ala Gly Ile Thr
 10 15 20

 gcg ctg act cat gag gcc gga cga atg ctg gaa aca cca gcc gtg gaa 211
 Ala Leu Thr His Glu Ala Gly Arg Met Leu Glu Thr Pro Ala Val Glu
 25 30 35

 gcg cat tta gag ctt gct gaa cct tcc ctt gat cag gtt gtg gca acg 259
 Ala His Leu Glu Leu Ala Glu Pro Ser Leu Asp Gln Val Val Ala Thr
 40 45 50

 ctg agt gcg gaa ggt gta acc agg gca gcg ttg gtt cct ttg ctg ttt 307
 Leu Ser Ala Glu Gly Val Thr Arg Ala Ala Leu Val Pro Leu Leu Phe
 55 60 65

 agc aat gcg tat cac gca aag att gac gtt cct gag gca gta aaa gat 355
 Ser Asn Ala Tyr His Ala Lys Ile Asp Val Pro Glu Ala Val Lys Asp
 70 75 80 85

 gct tca gaa aag tat ggt gtg gaa ctt ctg gtg ggt ccg cat ttg gcc 403
 Ala Ser Glu Lys Tyr Gly Val Glu Leu Leu Val Gly Pro His Leu Gly
 90 95 100

 act gcc tcc gat gta gcc agc gtg ctt gcg cag cgg ttg agt gcg gac 451
 Thr Gly Ser Asp Val Ala Ser Val Leu Ala Gln Arg Leu Ser Ala Asp
 105 110 115

 gcc ccc aca gat gcc cat gtg att ttg tat tcc gtt gcc agc tca cac 499

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Ala Pro Thr Asp Ala His Val Ile Leu Tyr Ser Val Gly Ser Ser His
120                               125                               130

gtg tcc gcc aat gaa tca gtc atc gat ctt gcc cac acc att gct ctc 547
Val Ser Ala Asn Glu Ser Val Ile Asp Leu Ala His Thr Ile Ala Leu
135                               140                               145

ctc act ggc ttt tgc gtt gag gtg gtg ccc gct acc ggt ggg cca ggt 595
Leu Thr Gly Phe Ser Val Glu Val Val Pro Ala Thr Gly Gly Pro Gly
150                               155                               160

gcc ggc ggc gcc gga gta ata gag gtg gcc tgc aaa cac aag gcc gtc 643
Ala Gly Gly Ala Gly Val Ile Glu Val Ala Ser Lys His Lys Ala Val
170                               175                               180

cac atc ctg ccg ctg ttt gtt acg gaa ggt ttg ctg ctg gat cgg gct 691
His Ile Leu Pro Leu Phe Val Thr Glu Gly Leu Leu Leu Asp Arg Ala
185                               190                               195

att gat caa tcc gcc aac atc gca gct gcc acc ggc aca aac ttc acc 739
Ile Asp Gln Ser Ala Asn Ile Ala Ala Ala Thr Gly Thr Asn Phe Thr
200                               205                               210

tat tcc gaa ccc cta act act gac ctg gca cca ctt gtt gca gcc cgt 787
Tyr Ser Glu Pro Leu Thr Thr Asp Leu Ala Pro Leu Val Ala Ala Arg
215                               220                               225

tac cac gct gca ttg agc gca ctg ctg gca cat atc taagaccgct 833
Tyr His Ala Ala Leu Ser Ala Leu Leu Ala His Ile
230                               235                               240

aaggaaatca gct 846

<210> 1672
<211> 241
<212> PRT
<213> Corynebacterium glutamicum

<400> 1672
Met Ile Pro Leu Ile Thr Leu Ser His Gly Ser Arg Lys Lys Ser Ala
1 5 10 15

Ala Ala Gly Ile Thr Ala Leu Thr His Glu Ala Gly Arg Met Leu Glu
20 25 30

Thr Pro Ala Val Glu Ala His Leu Glu Leu Ala Glu Pro Ser Leu Asp
35 40 45

Gln Val Val Ala Thr Leu Ser Ala Glu Gly Val Thr Arg Ala Ala Leu
50 55 60

Val Pro Leu Leu Phe Ser Asn Ala Tyr His Ala Lys Ile Asp Val Pro
65 70 75 80

Glu Ala Val Lys Asp Ala Ser Glu Lys Tyr Gly Val Glu Leu Leu Val
85 90 95

Gly Pro His Leu Gly Thr Gly Ser Asp Val Ala Ser Val Leu Ala Gln
100 105 110

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Arg Leu Ser Ala Asp Ala Pro Thr Asp Ala His Val Ile Leu Tyr Ser
   115                               120
Val Gly Ser Ser His Val Ser Ala Asn Glu Ser Val Ile Asp Leu Ala
   130                               135
His Thr Ile Ala Leu Leu Thr Gly Phe Ser Val Glu Val Val Pro Ala
   145                               150                               155                               160
Thr Gly Gly Pro Gly Ala Gly Gly Ala Gly Val Ile Glu Val Ala Ser
   165                               170                               175
Lys His Lys Ala Val His Ile Leu Pro Leu Phe Val Thr Glu Gly Leu
   180                               185                               190
Leu Leu Asp Arg Ala Ile Asp Gln Ser Ala Asn Ile Ala Ala Ala Thr
   195                               200                               205
Gly Thr Asn Phe Thr Tyr Ser Glu Pro Leu Thr Thr Asp Leu Ala Pro
   210                               215                               220
Leu Val Ala Ala Arg Tyr His Ala Ala Leu Ser Ala Leu Leu Ala His
   225                               230                               235                               240

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Ile

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<210> 1673
<211> 239
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (1)..(216)
<223> RXA00250

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<400> 1673
gct ttg ggt gct gcg ttg ggt cag ttc gat ttc gtc cgc aac aat att   48
Ala Leu Gly Ala Ala Leu Gly Gln Phe Asp Phe Val Arg Asn Asn Ile
   1                               5                               10                               15

gat ctg att ttc ttg ctg atc gtg ttc att tcg gtg gtt cct ggt ttg   96
Asp Leu Ile Phe Leu Leu Ile Val Phe Ile Ser Val Val Pro Gly Leu
   20                               25                               30

gtc ggc atg gcc cgc aag ctg gct gac ggc cac aag caa gcc aac acc   144
Val Gly Met Ala Arg Lys Leu Ala Asp Gly His Lys Gln Ala Asn Thr
   35                               40                               45

gag cca caa gaa aac ccc gca gtc cag aca gcc cca gta aaa acc cag   192
Glu Pro Gln Glu Asn Pro Ala Val Gln Thr Ala Pro Val Lys Thr Gln
   50                               55                               60

gaa gcc cag gaa gcc ccc cag aac taatctttcc ggtccgccag ttc   239
Glu Ala Gln Glu Ala Pro Gln Asn
   65                               70

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<210> 1674

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400> 1674
Ala Leu Gly Ala Ala Leu Gly Gln Phe Asp Phe Val Arg Asn Ile
  1             5             10             15
Asp Leu Ile Phe Leu Leu Ile Val Phe Ile Ser Val Val Pro Gly Leu
          20             25             30
Val Gly Met Ala Arg Lys Leu Ala Asp Gly His Lys Gln Ala Asn Thr
      35             40             45
Glu Pro Gln Glu Asn Pro Ala Val Gln Thr Ala Pro Val Lys Thr Gln
      50             55             60
Glu Ala Gln Glu Ala Pro Gln Asn
  65             70

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<220>  
<221> CDS  
<222> (101)..(343)  
<223> RXA00252
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400> 1675																															
gcagcatggg	ggtgttggtg	gggcggggc	tgacagtgct	gacgcggatg	ccgttgttgg	60																									
cttctctttt gcggaaggcg tcggcgagtc cgcggagggc						gtg ttt gct ggc ggc	115																								
						Val Phe Ala Gly Gly	5																								
						1																									
gta gat ggt gtt gcc ggg gtg tgg tcc gtt gcc ggc gcc gga gtt gat																163															
Val Asp Gly Val Ala Gly Val Trp Ser Val Ala Gly Ala Gly Val Asp																20															
						10																									
						15																									
gta gat gac gca gcc gga tgc cgc gcg gag ggc ggg caa gag ttg gcg																211															
Val Asp Asp Ala Ala Gly Cys Arg Ala Glu Gly Gly Gln Glu Leu Ala																35															
						25																									
						30																									
act caa ctg ggc cgg gac aat gac gtt gag atc aag gtg tgc gtg cca																259															
Thr Gln Leu Gly Arg Asp Asn Asp Val Glu Ile Lys Val Cys Val Pro																40															
						45																									
						50																									
ttc ggc cac act gcc ggc ttc gat ggt cgt gtc acg cgc cac cgc cgc																307															
Phe Gly His Thr Ala Gly Phe Asp Gly Arg Val Thr Arg His Arg Arg																65															
						55																									
						60																									
						65																									
ggc gtg cac cag cgt atc cac gtg gtc gag gtt ttt tagcttgtcg																353															
Gly Val His Gln Arg Ile His Val Val Glu Val Phe																70															
						75																									
						80																									
acgcctccct ctt																					366										

<210> 1676

<211> 81

<212> PRT

<213> Corynebacterium glutamicum

<400> 1676

Val Phe Ala Gly Gly Val Asp Gly Val Ala Gly Val Trp Ser Val Ala
 1 5 10 15

Gly Ala Gly Val Asp Val Asp Asp Ala Gly Cys Arg Ala Glu Gly
 20 25 30

Gly Gln Glu Leu Ala Thr Gln Leu Gly Arg Asp Asn Asp Val Glu Ile
 35 40 45

Lys Val Cys Val Pro Phe Gly His Thr Ala Gly Phe Asp Gly Arg Val
 50 55 60

Thr Arg His Arg Arg Gly Val His Gln Arg Ile His Val Val Glu Val
 65 70 75 80

Phe

<210> 1677

<211> 579

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(556)

<223> RXA00257

<400> 1677

catcatcaat ggcatgaaa cgggtgcgct cagtacttgt gtatccatgg ctaatatcgg 60

gctacttcat actctgttgt aaacaaagga agtttctatc atg aaa atc aag aaa 115
 Met Lys Ile Lys Lys
 1 5

ttc agc atc aca gcg cta gcc tca gtt cta atg ctc acg ggt tgc gcg 163
 Phe Ser Ile Thr Ala Leu Ala Ser Val Leu Met Leu Thr Gly Cys Ala
 10 15 20

acc aat cac agc tca cct ctg tac agt tat ctg aat gcg tca aca tca 211
 Thr Asn His Ser Ser Pro Leu Tyr Ser Tyr Leu Asn Ala Ser Thr Ser
 25 30 35

acc act gtt gaa caa gta cgt ctc agc gat ctt tac ggt gag cag tgg 259
 Thr Thr Val Glu Gln Val Arg Leu Ser Asp Leu Tyr Gly Glu Gln Trp
 40 45 50

acc gag ttc gct ctt gtc tgc ccc tac acc aca aaa gac gag gta aaa 307
 Thr Glu Phe Ala Leu Val Cys Pro Tyr Thr Thr Lys Asp Glu Val Lys
 55 60 65

gaa gag ctt ggt ata aaa ata aac acc tac ctc acc gat tgg acc gat 355
 Glu Glu Leu Gly Ile Lys Ile Asn Thr Tyr Leu Thr Asp Ser Thr Asp
 70 75 80 85

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gac agt agt aac gat att gtg ctc agg gat aaa gac ggt tca tat gat 403
Asp Ser Ser Asn Asp Ile Val Leu Arg Asp Lys Asp Gly Ser Tyr Asp
          90          95          100

tgg atc tat ttc aac aga ttc gac att gtg tac ctc tgc aac ggc tca 451
Trp Ile Tyr Phe Asn Arg Phe Asp Ile Val Tyr Leu Cys Asn Gly Ser
          105          110          115

gcg gaa aat cta aaa atc tac ccc att gat tca gtt cta gaa ttt gag 499
Ala Glu Asn Leu Lys Ile Tyr Pro Ile Asp Ser Val Leu Glu Phe Glu
          120          125          130

cat aga gac gac tac ggt acc tgg aaa ctg agc gct atc aca gag ccg 547
His Arg Asp Asp Tyr Gly Thr Trp Lys Leu Ser Ala Ile Thr Glu Pro
          135          140          145

ggt aat caa taataacgcg gacacttaag tac 579
Gly Asn Gln
150

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<210> 1678
<211> 152
<212> PRT
<213> Corynebacterium glutamicum

<400> 1678
Met Lys Ile Lys Lys Phe Ser Ile Thr Ala Leu Ala Ser Val Leu Met
  1              5              10              15

Leu Thr Gly Cys Ala Thr Asn His Ser Ser Pro Leu Tyr Ser Tyr Leu
      20              25              30

Asn Ala Ser Thr Ser Thr Thr Val Glu Gln Val Arg Leu Ser Asp Leu
  35              40              45

Tyr Gly Glu Gln Trp Thr Glu Phe Ala Leu Val Cys Pro Tyr Thr Thr
  50              55              60

Lys Asp Glu Val Lys Glu Glu Leu Gly Ile Lys Ile Asn Thr Tyr Leu
  65              70              75              80

Thr Asp Ser Thr Asp Asp Ser Ser Asn Asp Ile Val Leu Arg Asp Lys
      85              90              95

Asp Gly Ser Tyr Asp Trp Ile Tyr Phe Asn Arg Phe Asp Ile Val Tyr
  100              105              110

Leu Cys Asn Gly Ser Ala Glu Asn Leu Lys Ile Tyr Pro Ile Asp Ser
  115              120

Val Leu Glu Phe Glu His Arg Asp Asp Tyr Gly Thr Trp Lys Leu Ser
  130              135              140

Ala Ile Thr Glu Pro Gly Asn Gln
  145              150

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<210> 1679
<211> 795

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<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(772)

<223> RXA00258

<400> 1679

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accacgtcac aacattctct cagatcacag aggttcgctc atg cgc cac acc acg 115
 Met Arg His Thr Thr
 1 5

tca gcc aca tca act aca tct att att aag cgt gct atg acc att agt 163
 Ser Ala Thr Ser Thr Thr Ser Ile Ile Lys Arg Ala Met Thr Ile Ser
 10 15 20

gcc gct gtt ctt att gcc agc gct gtt ggt ctc aca acc agc gca agt 211
 Ala Ala Val Leu Ile Ala Ser Ala Val Gly Leu Thr Thr Ser Ala Ser
 25 30 35

tgc ctc aat act ctc agc gct aca tca cct gaa tca ccc gat cag gca 259
 Ser Leu Asn Thr Leu Ser Ala Thr Ser Pro Glu Ser Pro Asp Gln Ala
 40 45 50

gcc act gtg tca cag gct gaa tca gat agt gaa tta gat gac ggc atg 307
 Ala Thr Val Ser Gln Ala Glu Ser Asp Ser Glu Leu Asp Asp Gly Met
 55 60 65

aaa aag ctt gca acc aag atc ctt aat cgc gct gac aac gct gaa aat 355
 Lys Lys Leu Ala Thr Lys Ile Leu Asn Arg Ala Asp Asn Ala Glu Asn
 70 75 80 85

aat gat gac acc ggc aaa aac ctc aac aat gat gat aag aag ctc aac 403
 Asn Asp Asp Thr Gly Lys Asn Leu Asn Asn Asp Asp Lys Lys Leu Asn
 90 95 100

acg aag cag ccg cag cgc cct gct gaa aaa gtt gcc cag gcg atc gag 451
 Thr Lys Gln Pro Gln Arg Pro Ala Glu Lys Val Ala Gln Ala Ile Glu
 105 110 115

cta agc ctt gat acc acc acg aat gca gaa aag cct gat aaa agt ttt 499
 Leu Ser Leu Asp Thr Thr Asn Ala Glu Lys Pro Asp Lys Ser Phe
 120 125 130

cac cat gaa aaa ccc gta aac gcc tat gtc aca agt gtc agc tac aac 547
 His His Glu Lys Pro Val Asn Ala Tyr Val Thr Ser Val Ser Tyr Asn
 135 140 145

aaa agc aat gac acc tgg act atc aaa cca tca gac agc gcg gtg aat 595
 Lys Ser Asn Asp Thr Trp Thr Ile Lys Pro Ser Asp Ser Ala Val Asn
 150 155 160 165

aca ccg acc aat gat gct gag cgc atc agc aat atc atc caa gaa gct 643
 Thr Pro Thr Asn Asp Ala Glu Arg Ile Ser Asn Ile Ile Gln Glu Ala
 170 175 180

cgc gac ctc ggt ctc agc gac gat gaa tcc ttg acg caa cag atc gca 691
 Arg Asp Leu Gly Leu Ser Asp Asp Glu Ser Leu Thr Gln Gln Ile Ala

185

190

195

ttt cac gct cat gct gct aat tat tta gtc acc gaa tgg gta ctt cgc 739
 Phe His Ala His Ala Ala Asn Tyr Leu Val Thr Glu Trp Val Leu Arg
 200 205 210

ggc tat cag ctt gct aac ccg aag gtg ctt cca tgagaaaaca acgacgcatg 792
 Gly Tyr Gln Leu Ala Asn Pro Lys Val Leu Pro
 215 220

atg 795

<210> 1680

<211> 224

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1680

Met Arg His Thr Thr Ser Ala Thr Ser Thr Thr Ser Ile Ile Lys Arg
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Ala Met Thr Ile Ser Ala Ala Val Leu Ile Ala Ser Ala Val Gly Leu
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Thr Thr Ser Ala Ser Ser Leu Asn Thr Leu Ser Ala Thr Ser Pro Glu
 35 40 45

Ser Pro Asp Gln Ala Ala Thr Val Ser Gln Ala Glu Ser Asp Ser Glu
 50 55 60

Leu Asp Asp Gly Met Lys Lys Leu Ala Thr Lys Ile Leu Asn Arg Ala
 65 70 75 80

Asp Asn Ala Glu Asn Asn Asp Asp Thr Gly Lys Asn Leu Asn Asn Asp
 85 90 95

Asp Lys Lys Leu Asn Thr Lys Gln Pro Gln Arg Pro Ala Glu Lys Val
 100 105 110

Ala Gln Ala Ile Glu Leu Ser Leu Asp Thr Thr Thr Asn Ala Glu Lys
 115 120 125

Pro Asp Lys Ser Phe His His Glu Lys Pro Val Asn Ala Tyr Val Thr
 130 135 140

Ser Val Ser Tyr Asn Lys Ser Asn Asp Thr Trp Thr Ile Lys Pro Ser
 145 150 155 160

Asp Ser Ala Val Asn Thr Pro Thr Asn Asp Ala Glu Arg Ile Ser Asn
 165 170 175

Ile Ile Gln Glu Ala Arg Asp Leu Gly Leu Ser Asp Asp Glu Ser Leu
 180 185 190

Thr Gln Gln Ile Ala Phe His Ala His Ala Ala Asn Tyr Leu Val Thr
 195 200 205

Glu Trp Val Leu Arg Gly Tyr Gln Leu Ala Asn Pro Lys Val Leu Pro
 210 215 220

<210> 1681

<211> 1299

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1276)

<223> RXA00260

<400> 1681

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tcagcagggt	attgcagatc	gctatgggcc	gttggtgaat	atg	cat	agc	gac	gct	115
				Met	His	Ser	Asp	Ala	
				1				5	

gtg	cta	gcg	ggt	gct	tca	ata	aga	gca	aaa	ata	ggt	gct	ctc	gca	act	163
Val	Leu	Ala	Gly	Ala	Ser	Ile	Arg	Ala	Lys	Ile	Gly	Ala	Leu	Ala	Thr	
			10						15				20			

att	tac	ggt	gct	caa	aac	tta	gag	aat	gtc	att	cac	tca	ggt	agt	ttt	211
Ile	Tyr	Gly	Ala	Gln	Asn	Leu	Glu	Asn	Val	Ile	His	Ser	Val	Ser	Phe	
			25					30					35			

act	gac	aga	cgt	att	tct	ccc	gat	gga	caa	ctg	tcg	aaa	gaa	tta	ttt	259
Thr	Asp	Arg	Arg	Ile	Ser	Pro	Asp	Gly	Gln	Leu	Ser	Lys	Glu	Leu	Phe	
			40				45					50				

cgc	gaa	gct	tggt	agc	gca	aac	ctt	ctt	atc	cct	gat	cca	tct	tct	gat	307
Arg	Glu	Ala	Trp	Ser	Ala	Asn	Leu	Leu	Ile	Pro	Asp	Pro	Ser	Ser	Asp	
			55			60					65					

gtg	gaa	gcg	ttt	gcg	tggt	agc	gaa	aag	aat	tcc	act	gag	cta	gcg	gga	355
Val	Glu	Ala	Phe	Ala	Trp	Ser	Glu	Lys	Asn	Ser	Thr	Glu	Leu	Ala	Gly	
			70		75					80					85	

ggc	ata	ttc	ggt	gag	aaa	atg	cta	ttt	act	gtc	ccg	gac	aca	ggc	cgc	403
Gly	Ile	Phe	Val	Glu	Lys	Met	Leu	Phe	Thr	Val	Pro	Asp	Thr	Gly	Arg	
			90						95					100		

tcc	aat	aac	cgt	gtc	cag	agc	ttc	tca	gaa	gaa	ctt	cgt	aac	cac	att	451
Ser	Asn	Asn	Arg	Val	Gln	Ser	Phe	Ser	Glu	Glu	Leu	Arg	Asn	His	Ile	
			105				110					115				

tct	ttg	aaa	gat	atg	tat	tct	aca	caa	cgt	gaa	gag	cta	tta	gac	ctt	499
Ser	Leu	Lys	Asp	Met	Tyr	Ser	Thr	Gln	Arg	Glu	Glu	Leu	Leu	Asp	Leu	
			120				125					130				

gcc	tac	gag	ctc	atg	gtg	ggg	gaa	gca	gta	cgt	ttt	gct	aac	ttc	cgc	547
Ala	Tyr	Glu	Leu	Met	Val	Gly	Glu	Ala	Val	Arg	Phe	Ala	Asn	Phe	Arg	
			135			140				145						

ctt	tat	gat	cag	aat	ctc	cca	cca	ctt	act	gaa	gca	aat	ata	gac	aaa	595
Leu	Tyr	Asp	Gln	Asn	Leu	Pro	Pro	Leu	Thr	Glu	Ala	Asn	Ile	Asp	Lys	
					150				155				160		165	

ttg aga gcc cat cta cgt gag gcc gca gct agt gcg tca cta gga gtg	643
Leu Arg Ala His Leu Arg Glu Ala Ala Ser Ala Ser Leu Gly Val	
170 175 180	
tta tat cta atg gtg tgg cga tct gta aaa gac gca gct gca gcg cac	691
Leu Tyr Leu Met Val Trp Arg Ser Val Lys Asp Ala Ala Ala His	
185 190 195	
act aaa cat aca aga atg agc aaa gaa aat gcg aca acg cat agt gtt	739
Thr Lys His Thr Arg Met Ser Lys Glu Asn Ala Thr Thr His Ser Val	
200 205 210	
aca aaa gtt tct atc ttt gtt gac caa tta tta agc gga aca ttc cct	787
Thr Lys Val Ser Ile Phe Val Asp Gln Leu Leu Ser Gly Thr Phe Pro	
215 220 225	
tgt tca aag cct ttt cac gaa tct tca caa gtc cca ctg agt gaa gcc	835
Cys Ser Lys Pro Phe His Glu Ser Ser Gln Val Val Ser Glu Ala	
230 235 240 245	
acc aag ata gtt ttt aat ttg att atg gag tca ccg ccg atg gaa act	883
Thr Lys Ile Val Phe Asn Leu Ile Met Glu Ser Pro Pro Met Glu Thr	
250 255 260	
gag ccg agt gtg ctg cga aat tcc ctc caa gaa cac tcg gat tgg gag	931
Glu Pro Ser Val Leu Arg Asn Ser Leu Gln Glu His Ser Asp Trp Glu	
265 270 275	
cta ttg caa cag tgt gat gag aag att cct gat cgg gag ttt ctg atg	979
Leu Leu Gln Gln Cys Asp Glu Lys Ile Pro Asp Arg Glu Phe Leu Met	
280 285 290	
gag tgg tta tat caa gaa cag acg tgg act gca gag caa ttt ttt gat	1027
Glu Trp Leu Tyr Gln Glu Gln Thr Trp Thr Ala Glu Gln Phe Phe Asp	
295 300 305	
gct cta gct atg gtt tct tct agc gag ttt cgt ata tgt gca cct gga	1075
Ala Leu Ala Met Val Ser Ser Ser Glu Phe Arg Ile Cys Ala Pro Gly	
310 315 320 325	
tgt gcg cat caa gta agt gca gac atc gct aca caa gtc tta gaa ttc	1123
Cys Ala His Gln Val Ser Ala Asp Ile Ala Thr Gln Val Leu Glu Phe	
330 335 340	
cac gat cga gtg tct ttc cat gac gat cgt aaa agc gcc atg ctt gct	1171
His Asp Arg Val Ser Phe His Asp Asp Arg Lys Ser Ala Met Leu Ala	
345 350 355	
gct gaa gca act att att ggt aac aaa att ggt tca caa gca cgg gcc	1219
Ala Glu Ala Thr Ile Ile Gly Asn Lys Ile Gly Ser Gln Ala Arg Ala	
360 365 370	
gga gac ttt gtt tta ggt gaa gta atc acc aag ctg cag aac ata cct	1267
Gly Asp Phe Val Leu Gly Glu Val Ile Thr Lys Leu Gln Asn Ile Pro	
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ggt gag gta taacttctgc gtggtccaat tag	1299
Gly Glu Val	
390	

<210> 1682

<211> 392

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1682

Met His Ser Asp Ala Val Leu Ala Gly Ala Ser Ile Arg Ala Lys Ile
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20 25 30His Ser Val Ser Phe Thr Asp Arg Arg Ile Ser Pro Asp Gly Gln Leu
35 40 45Ser Lys Glu Leu Phe Arg Glu Ala Trp Ser Ala Asn Leu Leu Ile Pro
50 55 60Asp Pro Ser Ser Asp Val Glu Ala Phe Ala Trp Ser Glu Lys Asn Ser
65 70 75 80Thr Glu Leu Ala Gly Gly Ile Phe Val Glu Lys Met Leu Phe Thr Val
85 90 95Pro Asp Thr Gly Arg Ser Asn Asn Arg Val Gln Ser Phe Ser Glu Glu
100 105 110Leu Arg Asn His Ile Ser Leu Lys Asp Met Tyr Ser Thr Gln Arg Glu
115 120 125Glu Leu Leu Asp Leu Ala Tyr Glu Leu Met Val Gly Glu Ala Val Arg
130 135 140Phe Ala Asn Phe Arg Leu Tyr Asp Gln Asn Leu Pro Pro Leu Thr Glu
145 150 155 160Ala Asn Ile Asp Lys Leu Arg Ala His Leu Arg Glu Ala Ala Ser
165 170 175Ala Ser Leu Gly Val Leu Tyr Leu Met Val Trp Arg Ser Val Lys Asp
180 185 190Ala Ala Ala Ala His Thr Lys His Thr Arg Met Ser Lys Glu Asn Ala
195 200 205Thr Thr His Ser Val Thr Lys Val Ser Ile Phe Val Asp Gln Leu Leu
210 215 220Ser Gly Thr Phe Pro Cys Ser Lys Pro Phe His Glu Ser Ser Gln Val
225 230 235 240Pro Leu Ser Glu Ala Thr Lys Ile Val Phe Asn Leu Ile Met Glu Ser
245 250 255Pro Pro Met Glu Thr Glu Pro Ser Val Leu Arg Asn Ser Leu Gln Glu
260 265 270His Ser Asp Trp Glu Leu Leu Gln Gln Cys Asp Glu Lys Ile Pro Asp
275 280 285

Arg Glu Phe Leu Met Glu Trp Leu Tyr Gln Glu Gln Thr Trp Thr Ala

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290                295                300
Glu Gln Phe Phe Asp Ala Leu Ala Met Val Ser Ser Ser Glu Phe Arg
305                310                315                320
Ile Cys Ala Pro Gly Cys Ala His Gln Val Ser Ala Asp Ile Ala Thr
325                330                335
Gln Val Leu Glu Phe His Asp Arg Val Ser Phe His Asp Asp Arg Lys
340                345                350
Ser Ala Met Leu Ala Ala Glu Ala Thr Ile Ile Gly Asn Lys Ile Gly
355                360                365
Ser Gln Ala Arg Ala Gly Asp Phe Val Leu Gly Glu Val Ile Thr Lys
370                375                380
Leu Gln Asn Ile Pro Gly Glu Val
385                390

<210> 1683
<211> 1236
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1213)
<223> RXA00273

<400> 1683
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                                         Met Ser Leu Lys Leu
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aat tct cgt cgt ctt gca tcc att gct gtc gct gtt gca gtc ggt gtc 163
Asn Ser Arg Arg Leu Ala Ser Ile Ala Val Ala Val Ala Val Gly Val
                10                15                20

tct ggt gtt gct gct gtt ggt gcg gca cca gct acg gct cag cag gta 211
Ser Gly Val Ala Ala Val Gly Ala Ala Pro Ala Thr Ala Gln Gln Val
                25                30                35

ggt gct ggt acc ccg att cac gtt gtc aac ctt gat cgc acc gtt gtt 259
Gly Ala Gly Thr Pro Ile His Val Val Asn Leu Asp Arg Thr Val Val
                40                45                50

gat cca gtg act ggt gac atc acc ttc cac ttc acc gac ggc act ttt 307
Asp Pro Val Thr Gly Asp Ile Thr Phe His Phe Thr Asp Gly Thr Phe
                55                60                65

gtc acc ctc aag gcg ggt gtt gat ggc aag gat ggt acc gat ggc caa 355
Val Thr Leu Lys Ala Gly Val Asp Gly Lys Asp Gly Thr Asp Gly Gln
                70                75                80                85

gat ggt gtg atc ggc aag gac gca acc att gtt gat gtc gct acg gag 403
Asp Gly Val Ile Gly Lys Asp Ala Thr Ile Val Asp Val Ala Thr Glu
                90                95                100

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tcc aat ggt gat gtc aag ctc acc ttc tct gat ggc acc gtc gtc acc	451
Ser Asn Gly Asp Val Lys Leu Thr Phe Ser Asp Gly Thr Val Val Thr	
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att cct gca gct aag gac ggt gtg gat ggt gaa gat ggc aag gat ggc	499
Ile Pro Ala Ala Lys Asp Gly Val Asp Gly Glu Asp Gly Lys Asp Gly	
120 125 130	
gag gac gct act gtg gtg tct act gcg act gac gcc aac ggc aat atc	547
Glu Asp Ala Thr Val Val Ser Thr Ala Thr Asp Ala Asn Gly Asn Ile	
135 140 145	
gtc att acg ttc tct gat ggc tct gtg ctt gtt gtt gct aac ggt aag	595
Val Ile Thr Phe Ser Asp Gly Ser Val Leu Val Val Ala Asn Gly Lys	
150 155 160 165	
gac ggc aac gat ggc tca gac ggc cag gat ggt gct gat ggt gaa aat	643
Asp Gly Asn Asp Gly Ser Ser Asp Gly Gln Asp Gly Ala Asp Gly Glu Asn	
170 175 180	
ggc aag gat ggt gag aac ggc gct aac gcg acc att gtc gat cag att	691
Gly Lys Asp Gly Glu Asn Gly Ala Asn Ala Thr Ile Val Asp Gln Ile	
185 190 195	
gcc aat gac gat ggt tcc att acc att gtg ttc tcc gat ggt tct gag	739
Ala Asn Asp Asp Gly Ser Ile Thr Ile Val Phe Ser Asp Gly Ser Glu	
200 205 210	
gtc act atc cca gcg cca gct aag ggt gcc acc gat gag ctg gca cag	787
Val Thr Ile Pro Ala Pro Ala Lys Gly Ala Thr Asp Glu Leu Ala Gln	
215 220 225	
tgt ctg ctg aac ccg aag atg ttg ctg ctg gca gca att cct gct gca	835
Cys Leu Leu Asn Pro Lys Met Leu Leu Leu Ala Ala Ile Pro Ala Ala	
230 235 240 245	
ggt gct att gct aac gct gtg gca ccg gcg atc cca cgt gtt gtt gaa	883
Gly Ala Ile Ala Asn Ala Val Ala Pro Ala Ile Pro Arg Val Val Glu	
250 255 260	
gat gtg cgt gca cag ttc aat ctt cca agc ctc aac ccc cag ttt gat	931
Asp Val Arg Ala Gln Phe Asn Leu Pro Ser Leu Asn Pro Gln Phe Asp	
265 270 275	
cag tgg ctc tac aac gcg acc aag gat att gat gca ggg ttg ttg atc	979
Gln Trp Leu Tyr Asn Ala Thr Lys Asp Ile Asp Ala Gly Leu Leu Ile	
280 285 290	
tct ggt gct acc ggc ctt gct gtg ctg tgg gtg ctc gct gat gat ttc	1027
Ser Gly Ala Thr Gly Leu Ala Val Leu Ser Val Leu Ala Asp Asp Phe	
295 300 305	
tgt ggc gac att gat gcc gat gac aac gca gat ggt gac gtg gcg gca	1075
Cys Gly Asp Ile Asp Ala Asp Asn Ala Asp Gly Asp Val Ala Ala	
310 315 320 325	
gaa aag cca act ggc tct tct ggg ctt gga tca tct gaa cag agt gaa	1123
Glu Lys Pro Thr Gly Ser Ser Gly Leu Gly Ser Ser Glu Gln Ser Glu	
330 335 340	

aag gtt gat ggt gac gac gat agt gtg atc gac act gaa act gat gca 1171
 Lys Val Asp Gly Asp Asp Ser Val Ile Asp Thr Glu Thr Asp Ala
 345 350 355

gat ctc gaa gta gaa gaa gac cct gag ctt gtt aac gca ggt 1213
 Asp Leu Glu Val Glu Glu Asp Pro Glu Leu Val Asn Ala Gly
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taacgccagt gtaatgctgg att 1236

<210> 1684

<211> 371

<212> PRT

<213> Corynebacterium glutamicum

<400> 1684

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Val Ala Val Gly Val Ser Gly Val Ala Ala Val Gly Ala Ala Pro Ala
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Thr Ala Gln Val Gly Ala Gly Thr Pro Ile His Val Val Asn Leu
 35 40 45

Asp Arg Thr Val Val Asp Pro Val Thr Gly Asp Ile Thr Phe His Phe
 50 55 60

Thr Asp Gly Thr Phe Val Thr Leu Lys Ala Gly Val Asp Gly Lys Asp
 65 70 75 80

Gly Thr Asp Gly Gln Asp Gly Val Ile Gly Lys Asp Ala Thr Ile Val
 85 90 95

Asp Val Ala Thr Glu Ser Asn Gly Asp Val Lys Leu Thr Phe Ser Asp
 100 105 110

Gly Thr Val Val Thr Ile Pro Ala Ala Lys Asp Gly Val Asp Gly Glu
 115 120 125

Asp Gly Lys Asp Gly Glu Asp Ala Thr Val Val Ser Thr Ala Thr Asp
 130 135 140

Ala Asn Gly Asn Ile Val Ile Thr Phe Ser Asp Gly Ser Val Leu Val
 145 150 155 160

Val Ala Asn Gly Lys Asp Gly Asn Asp Gly Ser Asp Gly Gln Asp Gly
 165 170 175

Ala Asp Gly Glu Asn Gly Lys Asp Gly Glu Asn Gly Ala Asn Ala Thr
 180 185 190

Ile Val Asp Gln Ile Ala Asn Asp Asp Gly Ser Ile Thr Ile Val Phe
 195 200 205

Ser Asp Gly Ser Glu Val Thr Ile Pro Ala Pro Ala Lys Gly Ala Thr
 210 215 220

Asp Glu Leu Ala Gln Cys Leu Leu Asn Pro Lys Met Leu Leu Leu Ala
 225 230 235 240

Ala Ile Pro Ala Ala Gly Ala Ile Ala Asn Ala Val Ala Pro Ala Ile
245 250 255

Pro Arg Val Val Glu Asp Val Arg Ala Gln Phe Asn Leu Pro Ser Leu
260 265 270

Asn Pro Gln Phe Asp Gln Trp Leu Tyr Asn Ala Thr Lys Asp Ile Asp
275 280 285

Ala Gly Leu Leu Ile Ser Gly Ala Thr Gly Leu Ala Val Leu Ser Val
290 295 300

Leu Ala Asp Asp Phe Cys Gly Asp Ile Asp Ala Asp Asp Asn Ala Asp
305 310 315 320

Gly Asp Val Ala Ala Glu Lys Pro Thr Gly Ser Ser Gly Leu Gly Ser
325 330 335

Ser Glu Gln Ser Glu Lys Val Asp Gly Asp Asp Asp Ser Val Ile Asp
340 345 350

Thr Glu Thr Asp Ala Asp Leu Glu Val Glu Glu Asp Pro Glu Leu Val
355 360 365

Asn Ala Gly
370

<210> 1685
<211> 2733
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (101)..(2710)
<223> RXA00274

<400> 1685
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Leu Ser Leu Asn Leu
1 5

aag aag aat tct gcg cgt tct att acc gcg ctg act gtt gct ggt ctg 163
Lys Lys Asn Ser Ala Arg Ser Ile Thr Ala Leu Thr Val Ala Gly Leu
10 15 20

ggt ctg tct att gtt cct gcg gca tct gca cag gat gtt gcg gat gac 211
Gly Leu Ser Ile Val Pro Ala Ala Ser Ala Gln Asp Val Ala Asp Asp
25 30 35

act acc aac tcc gat tcc acc cgt gat gcc att tgt gct gct gca ccg 259
Thr Thr Asn Ser Asp Ser Thr Arg Asp Ala Ile Cys Ala Ala Ala Pro
40 45 50

ctt gtt gca ggc gca gca gtg ggt gtt ggt ctg ctg tct cag cag cca 307
Leu Val Ala Gly Ala Ala Val Gly Val Gly Leu Leu Ser Gln Gln Pro
55 60 65

gaa ttc cag cat atg gtg tcc cag att cag tct gac gca cag cgc att 355
 Glu Phe Gln His Met Val Ser Gln Ile Gln Ser Asp Ala Gln Arg Ile
 70 75 80 85

ggg cag gat ctc agc aat cag ttc aac aac tct ctt gaa tcg ctc aac 403
 Gly Gln Asp Leu Ser Asn Gln Phe Asn Asn Ser Leu Glu Ser Leu Asn
 90 95 100

att ggc ctc ggt aac ggc gtg cac ggc cca cag cag aac gct gtg cag 451
 Ile Gly Leu Gly Asn Gly Val His Gly Pro Gln Gln Asn Ala Val Gln
 105 110 115

ggt att gat ctc act gaa gca gca cga acc atg gct gga tgg aat gac 499
 Gly Ile Asp Leu Thr Glu Ala Ala Arg Thr Met Ala Gly Trp Asn Asp
 120 125 130

ctg cgc gca cag gtg ggc cag act gca ggc cct gct atc ggc gct gtt 547
 Leu Ala Ala Gln Val Gly Gln Thr Ala Gly Pro Ala Ile Gly Ala Val
 135 140 145

gct ggt act gcc ggc ctg atc gca ctg gtt gac tac tgc tgg ctg gaa 595
 Ala Gly Thr Ala Gly Leu Ile Ala Leu Val Asp Tyr Cys Trp Leu Glu
 150 155 160 165

ggc ttc gac ttc cgc ggt ggc tcc agt ggc act gat ggt gaa aat ggt 643
 Gly Phe Asp Phe Ala Gly Gly Ser Ser Gly Thr Asp Gly Glu Asn Gly
 170 175 180

gtt gat ggt caa gat ggt acc tcg atc acc att act gag att aag act 691
 Val Asp Gly Gln Asp Gly Thr Ser Ile Thr Ile Thr Glu Ile Lys Thr
 185 190 195

gat gat gac ggc aat acc att gtt gtc ttt tcc gat ggt tct gaa atc 739
 Asp Asp Asp Gly Asn Thr Ile Val Val Phe Ser Asp Gly Ser Glu Ile
 200 205 210

acc atc acc aat ggt aaa gac ggc gct gct atc acc att gtt aat act 787
 Thr Ile Thr Asn Gly Lys Asp Gly Ala Ala Ile Thr Ile Val Asn Thr
 215 220 225

tac cgc gac gat gaa ggt aat act gtt gtt gag ttc tct gac ggt tcc 835
 Tyr Arg Asp Asp Glu Gly Asn Thr Val Val Glu Phe Ser Asp Gly Ser
 230 235 240 245

acc att gtt atc gac aag ggt gaa gac ggt aaa gat gga gaa gac ggc 883
 Thr Ile Val Ile Asp Lys Gly Glu Asp Gly Lys Asp Gly Glu Asp Gly
 250 255 260

aag gac ggc gaa gac ggt aag gac ctt acc gta act gat acc tac atc 931
 Lys Asp Gly Glu Asp Gly Lys Asp Leu Thr Val Thr Asp Thr Tyr Ile
 265 270 275

aac gat gat gga gac acc gtt gtt gag ctt tcc gat ggt tcc acg atc 979
 Asn Asp Asp Gly Asp Thr Val Val Glu Leu Ser Asp Gly Ser Thr Ile
 280 285 290

att gta aag aag ggt acc gat ggt aag gac ggt gct gac ggc tct gac 1027
 Ile Val Lys Lys Gly Thr Asp Gly Lys Asp Gly Ala Asp Gly Ser Asp
 295 300 305

ggt gct gat gga gtc agc atc act gtg gag aac tct tat gtt gat gcg Gly Ala Asp Gly Val Ser Ile Thr Val Glu Asn Ser Tyr Val Asp Ala 310 315 320 325	1075
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gat gcg gac ggc aac act gtt gtg gtg ttc tcg aac ggc act gaa atc Asp Ala Asp Gly Asn Thr Val Val Val Phe Ser Asn Gly Thr Glu Ile 425 430 435	1411
acc atc aac aag ggt gag aag ggc gac aag gga gat acc ggc gaa gac Thr Ile Asn Lys Gly Glu Lys Gly Asp Lys Gly Asp Thr Gly Glu Asp 440 445 450	1459
ggt aag gac gga ctg acc ccg tac atc ggc cca gat ggt aac tgg tgg Gly Lys Asp Gly Leu Thr Pro Tyr Ile Gly Pro Asp Gly Asn Trp Trp 455 460 465	1507
atc ggt gag aac aac acc tgt act gct gca cgt ggc aat gac ggt aaa Ile Gly Glu Asn Asn Thr Cys Thr Ala Ala Arg Gly Asn Asp Gly Lys 470 475 480 485	1555
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atc gtt gat acc ggc gtt cct gct cgt ggt cag gat ggc gcc aac gga Ile Val Asp Thr Gly Val Pro Ala Arg Gly Gln Asp Gly Ala Asn Gly 505 510 515	1651
gcc gat ggt gct aac acc gtt gag atc att aat ggc tac tgg tac atc Ala Asp Gly Ala Asn Thr Val Glu Ile Ile Asn Gly Tyr Trp Tyr Ile 520 525 530	1699
aat ggt gaa aat acc ggt gtc aag gca gtt ggt gaa aat ggc acc aac Asn Gly Glu Asn Thr Gly Val Lys Ala Val Gly Glu Asn Gly Thr Asn 535 540 545	1747
gga gcc gat gga caa gac ggt gaa aat gga acc aac ggt gct aac acc	1795

Gly Ala Asp Gly Gln Asp Gly Glu Asn Gly Thr Asn Gly Ala Asn Thr	
550 555 560 565	
gtt gag atc att aat ggc tac tgg tac atc aat ggt gaa aat acc ggt	1843
Val Glu Ile Ile Asn Gly Tyr Trp Tyr Ile Asn Gly Glu Asn Thr Gly	
570 575 580	
gtc aag gcg cag ggt cca aag ggc gat aag ggt gac act ggt gac acg	1891
Val Lys Ala Gln Gly Pro Lys Gly Asp Lys Gly Asp Thr Gly Asp Thr	
585 590 595	
ggc gct ccg ggc gag ggt tcc ggt aat gtg gac att gag atc cga gaa	1939
Gly Ala Pro Gly Glu Gly Ser Gly Asn Val Asp Ile Glu Ile Arg Glu	
600 605 610	
tcg agt tat cca ggt ggt ggc cag gcc acc atc atc att ctt gat caa	1987
Ser Ser Tyr Pro Gly Gly Glu Gln Ala Thr Ile Ile Leu Asp Gln	
615 620 625	
ttt gaa tat gaa atc ccg cac act gtt att ggt gac aac ggt aac tgg	2035
Phe Glu Tyr Glu Ile Pro His Thr Val Ile Gly Asp Asn Gly Asn Trp	
630 635 640 645	
tac atc ggt gaa aag gat act ggt atc cca gct cag ggt ggc act gga	2083
Tyr Ile Gly Glu Lys Asp Thr Gly Ile Pro Ala Gln Gly Thr Gly	
650 655 660	
aca cct ggt gag gat ggc ctc aca cca cac att ggc gac aac ggt aac	2131
Thr Pro Gly Glu Asp Gly Leu Thr Pro His Ile Gly Asp Asn Gly Asn	
665 670 675	
tgg tgg atc ggt gat acc gat aca ggt gtc tct gca agc ccg acc ccc	2179
Trp Trp Ile Gly Asp Thr Asp Thr Gly Val Ser Ala Ser Pro Thr Pro	
680 685 690	
gtt ggt gag gcg gta gcg ggt gtc act gat gtg gtc ttc aac act agt	2227
Val Gly Glu Ala Val Ala Gly Val Thr Asp Val Val Phe Asn Thr Ser	
695 700 705	
gat gaa ccc aag acc att act gca acg atc aat ggt gaa gaa tat gat	2275
Asp Glu Pro Lys Thr Ile Thr Ala Thr Ile Asn Gly Glu Glu Tyr Asp	
710 715 720 725	
tac acc ctt cca cca cat agt gct gtt gtg ttc tac gct aca ggt tca	2323
Tyr Thr Leu Pro Pro His Ser Ala Val Val Phe Tyr Ala Thr Gly Ser	
730 735 740	
cca atg gca tat tct cta ccg aat gca tcg ggc ctc act gtt ata ggt	2371
Pro Met Ala Tyr Ser Leu Pro Asn Ala Ser Gly Leu Thr Val Ile Gly	
745 750 755	
act gaa gag act cct ggt ttc acc act att cga ttc agt gac cat tcc	2419
Thr Glu Glu Thr Pro Gly Phe Thr Thr Ile Arg Phe Ser Asp His Ser	
760 765 770	
act gtg acc att cca cat gga cga gat ggc acc aac ggt act aac gaa	2467
Thr Val Thr Ile Pro His Gly Arg Asp Gly Thr Asn Gly Thr Asn Glu	
775 780 785	
ctg acg gta agg atg gtc tca ccc cgc aca tcg gtg aga acg gaa act	2515
Leu Thr Val Arg Met Val Ser Pro Arg Thr Ser Val Arg Thr Glu Thr	

790	795	800	805	
ggc gga tgc ggc aaa agg aca ctg gta ttt cga caa cct ttg gcg gtg				2563
Gly Gly Ser Ala Lys Arg Thr Leu Val Phe Arg Gln Pro Leu Ala Val				
810		815	820	
gcg gca acc ctg gta ccg gca atg act gca tca cgg tcc cag gtg atg				2611
Ala Ala Thr Leu Val Pro Ala Met Thr Ala Ser Arg Ser Gln Val Met				
825	830		835	
atc ttg gat tcc cag atg atg ctg agg ccg gtg cag aga ccg gtg cag				2659
Ile Leu Asp Ser Gln Met Met Leu Arg Pro Val Gln Arg Pro Val Gln				
840	845		850	
atg ccg aag gta cta ttg act aaa ggt cat aga gca acg acc atg act				2707
Met Pro Lys Val Leu Leu Thr Lys Gly His Arg Ala Thr Thr Met Thr				
855	860		865	
gat taaagtggga acacaacccc tag				2733
Asp				
870				

<210> 1686

<211> 870

<212> PRT

<213> Corynebacterium glutamicum

<400> 1686

Leu Ser Leu Asn Leu Lys Lys Asn Ser Ala Arg Ser Ile Thr Ala Leu	
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Thr Val Ala Gly Leu Gly Leu Ser Ile Val Pro Ala Ala Ser Ala Gln	
20 25 30	

Asp Val Ala Asp Asp Thr Thr Asn Ser Asp Ser Thr Arg Asp Ala Ile	
35 40 45	

Cys Ala Ala Ala Pro Leu Val Ala Gly Ala Ala Val Gly Val Gly Leu	
50 55 60	

Leu Ser Gln Gln Pro Glu Phe Gln His Met Val Ser Gln Ile Gln Ser	
65 70 75 80	

Asp Ala Gln Arg Ile Gly Gln Asp Leu Ser Asn Gln Phe Asn Asn Ser	
85 90 95	

Leu Glu Ser Leu Asn Ile Gly Leu Gly Asn Gly Val His Gly Pro Gln	
100 105 110	

Gln Asn Ala Val Gln Gly Ile Asp Leu Thr Glu Ala Ala Arg Thr Met	
115 120 125	

Ala Gly Trp Asn Asp Leu Ala Ala Gln Val Gly Gln Thr Ala Gly Pro	
130 135 140	

Ala Ile Gly Ala Val Ala Gly Thr Ala Gly Leu Ile Ala Leu Val Asp	
145 150 155 160	

Tyr Cys Trp Leu Glu Gly Phe Asp Phe Ala Gly Gly Ser Ser Gly Thr	
165 170 175	

Asp Gly Glu Asn Gly Val Asp Gly Gln Asp Gly Thr Ser Ile Thr Ile
 180 185 190
 Thr Glu Ile Lys Thr Asp Asp Asp Gly Asn Thr Ile Val Val Phe Ser
 195 200 205
 Asp Gly Ser Glu Ile Thr Ile Thr Asn Gly Lys Asp Gly Ala Ala Ile
 210 215 220
 Thr Ile Val Asn Thr Tyr Arg Asp Asp Glu Gly Asn Thr Val Val Glu
 225 230 235 240
 Phe Ser Asp Gly Ser Thr Ile Val Ile Asp Lys Gly Glu Asp Gly Lys
 245 250 255
 Asp Gly Glu Asp Gly Lys Asp Gly Glu Asp Gly Lys Asp Leu Thr Val
 260 265 270
 Thr Asp Thr Tyr Ile Asn Asp Asp Gly Asp Thr Val Val Glu Leu Ser
 275 280 285
 Asp Gly Ser Thr Ile Ile Val Lys Lys Gly Thr Asp Gly Lys Asp Gly
 290 295 300
 Ala Asp Gly Ser Asp Gly Ala Asp Gly Val Ser Ile Thr Val Glu Asn
 305 310 315 320
 Ser Tyr Val Asp Ala Asp Gly Asn Thr Val Val Glu Phe Ser Asp Gly
 325 330 335
 Ser Asn Val Thr Ile Asn Lys Gly Glu Lys Gly Asp Lys Gly Asp Ala
 340 345 350
 Gly Ala Asp Gly Glu Asp Gly Ala Asp Gly Glu Ser Ile Thr Val Val
 355 360 365
 Asn Thr Ser Asn Asp Ala Glu Gly Asn Thr Leu Val Glu Leu Ser Asp
 370 375 380
 Gly Thr Val Ile Thr Ile Asn Lys Gly Asp Lys Gly Asp Ala Gly Ala
 385 390 395 400
 Asp Gly Glu Asp Gly Ser Asn Gly Ala Asp Gly Glu Ser Ile Thr Val
 405 410 415
 Ile Glu Thr Arg Phe Asp Ala Asp Gly Asn Thr Val Val Val Phe Ser
 420 425 430
 Asn Gly Thr Glu Ile Thr Ile Asn Lys Gly Glu Lys Gly Asp Lys Gly
 435 440 445
 Asp Thr Gly Glu Asp Gly Lys Asp Gly Leu Thr Pro Tyr Ile Gly Pro
 450 455 460
 Asp Gly Asn Trp Trp Ile Gly Glu Asn Asn Thr Cys Thr Ala Ala Arg
 465 470 475 480
 Gly Asn Asp Gly Lys Asp Gly Asp Thr Pro Arg Ile Gly Asp Asn Gly
 485 490 495

Asn Trp Trp Ile Gly Ile Val Asp Thr Gly Val Pro Ala Arg Gly Gln
 500 505 510
 Asp Gly Ala Asn Gly Ala Asp Gly Ala Asn Thr Val Glu Ile Ile Asn
 515 520 525
 Gly Tyr Trp Tyr Ile Asn Gly Glu Asn Thr Gly Val Lys Ala Val Gly
 530 535 540
 Glu Asn Gly Thr Asn Gly Ala Asp Gly Gln Asp Gly Glu Asn Gly Thr
 545 550 555 560
 Asn Gly Ala Asn Thr Val Glu Ile Ile Asn Gly Tyr Trp Tyr Ile Asn
 565 570 575
 Gly Glu Asn Thr Gly Val Lys Ala Gln Gly Pro Lys Gly Asp Lys Gly
 580 585 590
 Asp Thr Gly Asp Thr Gly Ala Pro Gly Glu Gly Ser Gly Asn Val Asp
 595 600 605
 Ile Glu Ile Arg Glu Ser Ser Tyr Pro Gly Gly Gly Gln Ala Thr Ile
 610 615 620
 Ile Ile Leu Asp Gln Phe Glu Tyr Glu Ile Pro His Thr Val Ile Gly
 625 630 635 640
 Asp Asn Gly Asn Trp Tyr Ile Gly Glu Lys Asp Thr Gly Ile Pro Ala
 645 650 655
 Gln Gly Gly Thr Gly Thr Pro Gly Glu Asp Gly Leu Thr Pro His Ile
 660 665 670
 Gly Asp Asn Gly Asn Trp Trp Ile Gly Asp Thr Asp Thr Gly Val Ser
 675 680 685
 Ala Ser Pro Thr Pro Val Gly Glu Ala Val Ala Gly Val Thr Asp Val
 690 695 700
 Val Phe Asn Thr Ser Asp Glu Pro Lys Thr Ile Thr Ala Thr Ile Asn
 705 710 715 720
 Gly Glu Glu Tyr Asp Tyr Thr Leu Pro Pro His Ser Ala Val Val Phe
 725 730 735
 Tyr Ala Thr Gly Ser Pro Met Ala Tyr Ser Leu Pro Asn Ala Ser Gly
 740 745 750
 Leu Thr Val Ile Gly Thr Glu Glu Thr Pro Gly Phe Thr Thr Ile Arg
 755 760 765
 Phe Ser Asp His Ser Thr Val Thr Ile Pro His Gly Arg Asp Gly Thr
 770 775 780
 Asn Gly Thr Asn Glu Leu Thr Val Arg Met Val Ser Pro Arg Thr Ser
 785 790 795 800
 Val Arg Thr Glu Thr Gly Gly Ser Ala Lys Arg Thr Leu Val Phe Arg
 805 810 815
 Gln Pro Leu Ala Val Ala Ala Thr Leu Val Pro Ala Met Thr Ala Ser

	820		825		830
Arg Ser Gln Val Met Ile Leu Asp Ser Gln Met Met Leu Arg Pro Val					
835			840		845
Gln Arg Pro Val Gln Met Pro Lys Val Leu Leu Thr Lys Gly His Arg					
850			855		860
Ala Thr Thr Met Thr Asp					
865			870		

<210> 1687
 <211> 582
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(559)
 <223> RXA00275

<400> 1687
 ctgacgcaga cggtgcacag ctgcgaacccg ctattgcaga acagaaccgc cccacaaaga 60
 gctgttccct acggcagatc gcaaggaact attcgccctg ttg gat aag cgt cgc 115
 Leu Asp Lys Arg Arg
 1 5
 cca gaa tta agc gac gat ttc atc aaa gct ttt gat gat ttc ctt cat 163
 Pro Glu Leu Ser Asp Asp Phe Ile Lys Ala Phe Asp Asp Phe Leu His
 10 15 20
 tct ttt gcg tgc ctg gac aaa aca acg atc acc cta ttg gcg caa tca 211
 Ser Phe Ala Cys Leu Asp Lys Thr Thr Ile Thr Leu Leu Ala Gln Ser
 25 30 35
 ccg gtg cgc aca tcc act ggc tat aca ggt act ttt atc ggc atc ccc 259
 Pro Val Arg Thr Ser Thr Gly Tyr Thr Gly Thr Phe Ile Gly Ile Pro
 40 45 50
 aat aat gaa cca ctg tcc gaa gag ccc acc ccc acc att tac att gtg 307
 Asn Asn Glu Pro Leu Ser Glu Glu Pro Thr Pro Thr Ile Tyr Ile Val
 55 60 65
 cac gat aat cac aca ggg ata atc cac agt tac ccc gca cga atg att 355
 His Asp Asn His Thr Gly Ile Ile His Ser Tyr Pro Ala Arg Met Ile
 70 75 80 85
 aat ctt aaa tct gag ctc ggt tcc gct gag atg att cac gag gca atc 403
 Asn Leu Lys Ser Glu Leu Gly Ser Ala Glu Met Ile His Glu Ala Ile
 90 95 100
 tgg ggg tca ccc cat caa cag cag tta atc tca tgg tat gag act tac 451
 Trp Gly Ser Pro His Gln Gln Gln Leu Ile Ser Trp Tyr Glu Thr Tyr
 105 110 115
 tac acc aac atc tac tat ggt ttt aac cca ccc act gaa cca cat aag 499
 Tyr Thr Asn Ile Tyr Tyr Gly Phe Asn Pro Pro Thr Glu Pro His Lys
 120 125 130

agt ctt gag att ttt gct caa gac ttc tgt ctg acc cca cca gag aaa 547
 Ser Leu Glu Ile Phe Ala Gln Asp Phe Cys Leu Thr Pro Pro Glu Lys
 135 140 145

cct cct ttt ttc taaggcaagg cccgtggcac aca 582
 Pro Pro Phe Phe
 150

<210> 1688

<211> 153

<212> PRT

<213> Corynebacterium glutamicum

<400> 1688

Leu Asp Lys Arg Arg Pro Glu Leu Ser Asp Asp Phe Ile Lys Ala Phe
 1 5 10 15

Asp Asp Phe Leu His Ser Phe Ala Cys Leu Asp Lys Thr Thr Ile Thr
 20 25 30

Leu Leu Ala Gln Ser Pro Val Arg Thr Ser Thr Gly Tyr Thr Gly Thr
 35 40 45

Phe Ile Gly Ile Pro Asn Asn Glu Pro Leu Ser Glu Glu Pro Thr Pro
 50 55 60

Thr Ile Tyr Ile Val His Asp Asn His Thr Gly Ile Ile His Ser Tyr
 65 70 75 80

Pro Ala Arg Met Ile Asn Leu Lys Ser Glu Leu Gly Ser Ala Glu Met
 85 90 95

Ile His Glu Ala Ile Trp Gly Ser Pro His Gln Gln Gln Leu Ile Ser
 100 105 110

Trp Tyr Glu Thr Tyr Tyr Thr Asn Ile Tyr Tyr Gly Phe Asn Pro Pro
 115 120 125

Thr Glu Pro His Lys Ser Leu Glu Ile Phe Ala Gln Asp Phe Cys Leu
 130 135 140

Thr Pro Pro Glu Lys Pro Pro Phe Phe
 145 150

<210> 1689

<211> 465

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(442)

<223> RXA00276

<400> 1689

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taagtatcaa gccatcagca atgatgattt tgacaacccat atg gat gac ctc agc 115
 Met Asp Asp Leu Ser

1

5

agt cgc caa gac cat gaa gcc tac ggc acg tac aac ccc gat aac ggt 163
 Ser Arg Gln Asp His Glu Ala Tyr Gly Thr Tyr Asn Pro Asp Asn Gly
 10 15 20

gtc atg ccc gat cat gtc atc gtg cct tca ccc tat gaa cca tat gat 211
 Val Met Pro Asp His Val Ile Val Pro Ser Pro Tyr Glu Pro Tyr Asp
 25 30 35

gat gct gcg ccg att gat cct ttc gac tac gac gaa gat ctt ctc gat 259
 Asp Ala Ala Pro Ile Asp Pro Phe Asp Tyr Asp Glu Asp Leu Leu Asp
 40 45 50

gag att aaa gaa gag cgc gct gca cat gcg gtt gac gca caa gta aca 307
 Glu Ile Lys Glu Glu Arg Ala His Ala Val Asp Ala Gln Val Thr
 55 60 65

gaa aca act aaa gct gac gca gac gtt gca cag ctc gca acc gct att 355
 Glu Thr Thr Lys Ala Asp Ala Asp Val Ala Gln Leu Ala Thr Ala Ile
 70 75 80 85

gac gaa cag aac cgc ccc aca aag agc tgt tcc cta cgg cag atc gca 403
 Asp Glu Gln Asn Arg Pro Thr Lys Ser Cys Ser Leu Arg Gln Ile Ala
 90 95 100

agg aac tat tcg cct ggt tgg ata agc gtc gcc cag aat taagcgacga 452
 Arg Asn Tyr Ser Pro Gly Trp Ile Ser Val Ala Gln Asn
 105 110

tttcatcaaa gct 465

<210> 1690

<211> 114

<212> PRT

<213> Corynebacterium glutamicum

<400> 1690

Met Asp Asp Leu Ser Ser Arg Gln Asp His Glu Ala Tyr Gly Thr Tyr
 1 5 10 15

Asn Pro Asp Asn Gly Val Met Pro Asp His Val Ile Val Pro Ser Pro
 20 25 30

Tyr Glu Pro Tyr Asp Asp Ala Pro Ile Asp Pro Phe Asp Tyr Asp
 35 40 45

Glu Asp Leu Leu Asp Glu Ile Lys Glu Glu Arg Ala Ala His Ala Val
 50 55 60

Asp Ala Gln Val Thr Glu Thr Thr Lys Ala Asp Ala Asp Val Ala Gln
 65 70 75 80

Leu Ala Thr Ala Ile Asp Glu Gln Asn Arg Pro Thr Lys Ser Cys Ser
 85 90 95

Leu Arg Gln Ile Ala Arg Asn Tyr Ser Pro Gly Trp Ile Ser Val Ala
 100 105 110

Gln Asn

<210> 1691
 <211> 1509
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1486)
 <223> RXA00279

<400> 1691
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 acattcagcc ccacattcag ctccggaccgc gttggagttt ttg gat acc gat gac 115
 Leu Asp Thr Asp Asp
 1 5
 tcg cct gat cat tgg ctt gat ccg tta acg gag aag gat act tct aag 163
 Ser Pro Asp His Trp Leu Asp Pro Leu Thr Glu Lys Asp Thr Ser Lys
 10 15 20
 cgc act ctc gtt aat tcg att gtt cag gaa act ttc gcc cag cct att 211
 Arg Thr Leu Val Asn Ser Ile Val Gln Glu Thr Phe Gly Gln Pro Ile
 25 30 35
 ttt gtt gcc cgc aag att tgg gct ttc gtc aat acg tcg ccg gcc cgg 259
 Phe Val Ala Arg Lys Ile Trp Ala Phe Val Asn Thr Ser Pro Gly Arg
 40 45 50
 atg acg ttg atg acg att atc att tcg atc gcc att ttt gct gct ggt 307
 Met Thr Leu Met Thr Ile Ile Ile Ser Ile Ala Ile Phe Ala Ala Gly
 55 60 65
 tac gcc atg tcg gtg tct tcg gat act agg cag tcc aat ttg gat gat 355
 Tyr Ala Met Ser Val Ser Ser Asp Thr Arg Gln Ser Asn Leu Asp Asp
 70 75 80 85
 ttg atc act aat cgc gag cct gtt tcc tat aac cgc cat gtg ctg tat 403
 Leu Ile Thr Asn Ala Glu Pro Val Ser Tyr Asn Ala His Val Leu Tyr
 90 95 100
 aca tca ttg tcg gtt gct gat acc act gct acc act ggt ttt gtt cag 451
 Thr Ser Leu Ser Val Ala Asp Thr Thr Ala Thr Thr Gly Phe Val Gln
 105 110 115
 gct ggt gtg gag gcc cgc gtg aat cgg gtg aag tat cac act gct att 499
 Ala Gly Val Glu Gly Pro Val Asn Arg Val Lys Tyr His Thr Ala Ile
 120 125 130
 gat cgt gct cgc gtt gct gct act cat act cgc cgc tct cgc gat agt 547
 Asp Arg Ala Ala Val Ala Ala Thr His Thr Ala Ala Ser Ala Asp Ser
 135 140 145
 agt aat gag cat ttg atg gag ttg gtg ctg gag att cag cgt cag ttg 595
 Ser Asn Glu His Leu Met Glu Leu Val Leu Glu Ile Gln Arg Gln Leu
 150 155 160 165
 ccg gtg tat acg ggg ttg gtg gaa act gct cgg act aat aac cgt gcg 643

Pro	Val	Tyr	Thr	Gly	Leu	Val	Glu	Thr	Ala	Arg	Thr	Asn	Asn	Arg	Ala	
				170					175						180	
ggc	aat	ccc	gtg	ggc	gtg	gcc	tat	atg	tct	gag	gcc	agc	gcg	atg	atg	691
Gly	Asn	Pro	Val	Gly	Val	Ala	Tyr	Met	Ser	Glu	Ala	Ser	Ala	Met	Met	
		185					190						195			
cgt	aat	gaa	att	tgt	cgc	atg	gcg	tct	gag	ctt	tac	aac	ctg	acg	agt	739
Arg	Asn	Glu	Ile	Leu	Pro	Met	Ala	Ser	Glu	Leu	Tyr	Asn	Leu	Thr	Ser	
		200					205					210				
cgt	gcg	gtg	tct	gat	cag	cag	cgt	tgc	gtg	acg	ggc	cgc	cag	tgg	ttt	787
Arg	Ala	Val	Ser	Asp	Gln	Gln	Arg	Ser	Val	Thr	Gly	Pro	Gln	Trp	Phe	
	215					220					225					
cgc	ctg	tct	gga	tgt	ctt	gcg	gct	ctt	gcc	atg	tgt	att	ggt	gcg	cag	835
Pro	Leu	Ser	Gly	Leu	Leu	Ala	Ala	Leu	Ala	Met	Leu	Ile	Val	Ala	Gln	
	230					235				240					245	
tgg	tgg	tgt	atg	cgc	att	acg	cgc	agg	cgc	atc	aac	aag	ggg	ttt	gcc	883
Trp	Trp	Leu	Met	Arg	Ile	Thr	Arg	Arg	Arg	Ile	Asn	Lys	Gly	Phe	Ala	
				250					255					260		
ctg	gcc	acg	gtg	atg	atg	atg	acg	gca	acg	tta	tgg	gtg	tca	gct	gca	931
Leu	Ala	Thr	Val	Met	Met	Met	Thr	Ala	Thr	Leu	Trp	Val	Ser	Ala	Ala	
			265					270					275			
aac	tgg	gcg	acg	tgg	cag	gct	ggc	acg	aag	ggc	ttt	gag	gaa	gcg	tcg	979
Asn	Trp	Ala	Thr	Trp	Gln	Ala	Gly	Thr	Lys	Gly	Phe	Glu	Glu	Ala	Ser	
		280					285					290				
ggg	cgc	tgt	aat	tcc	atg	act	acg	gct	cgt	att	tat	gcg	cag	cag	acc	1027
Gly	Pro	Leu	Asn	Ser	Met	Thr	Thr	Ala	Arg	Ile	Tyr	Ala	Gln	Gln	Thr	
		295				300					305					
cgc	acg	acg	gag	acg	tgt	tgc	tgt	gtg	cgt	agg	cag	tgc	att	cag	ggc	1075
Arg	Thr	Thr	Glu	Thr	Leu	Ser	Leu	Val	Arg	Arg	Gln	Ser	Ile	Gln	Gly	
	310					315				320					325	
agt	ggc	act	ggt	ttt	acc	gca	acg	att	aat	cag	att	aag	cgt	gcg	ctg	1123
Ser	Gly	Thr	Gly	Phe	Thr	Ala	Thr	Ile	Asn	Gln	Ile	Lys	Arg	Ala	Leu	
				330					335					340		
gat	gag	tat	gaa	acc	act	gcg	cag	tca	cag	act	cgc	gag	cat	cag	cag	1171
Asp	Glu	Tyr	Glu	Thr	Thr	Ala	Gln	Ser	Gln	Thr	Pro	Glu	His	Gln	Gln	
			345					350					355			
tgt	att	acg	gcg	att	cgt	aat	gcg	att	gct	gca	tgg	act	gcc	gat	cac	1219
Leu	Ile	Thr	Ala	Ile	Arg	Asn	Ala	Ile	Ala	Ala	Trp	Thr	Ala	Asp	His	
		360					365					370				
gat	gag	ttc	acg	gtg	tgt	tgt	gcg	tct	ggt	gat	tac	aac	ggc	gcg	gtc	1267
Asp	Glu	Phe	Thr	Val	Leu	Leu	Ala	Ser	Gly	Asp	Tyr	Asn	Gly	Ala	Val	
		375				380					385					
aat	gcg	gtg	ctc	aac	aaa	gat	gag	gag	ggc	cag	acc	agc	ttt	gat	gag	1315
Asn	Ala	Val	Leu	Asn	Lys	Asp	Glu	Glu	Gly	Gln	Thr	Ser	Phe	Asp	Glu	
		390			395				400					405		
ctc	gat	act	gcg	ctg	gct	gag	ctg	atc	gcg	gat	tct	cgc	agc	tcc	atg	1363
Leu	Asp	Thr	Ala	Leu	Ala	Glu	Leu	Ile	Ala	Asp	Ser	Arg	Ser	Ser	Met	

	410	415	420	
cgt tcc tat atc cag tgc ggc ctg cag gcc acg gag ttg gtg tcc gtc				1411
Arg Ser Tyr Ile Gln Ser Gly Leu Gln Ala Thr Glu Leu Val Ser Val				
	425	430	435	
atg gtg atg att ctg tct gtc gtt tct gtg ttg gct ttg tgg gtc ggc				1459
Met Val Met Ile Leu Ser Val Val Ser Val Leu Ala Leu Trp Val Gly				
	440	445	450	
atc cgc ccc cgt ttg cag gag tac tta taaatgcacg cttttcgacg				1506
Ile Arg Pro Arg Leu Gln Glu Tyr Leu				
	455	460		
ccc				1509

<210> 1692

<211> 462

<212> PRT

<213> Corynebacterium glutamicum

<400> 1692

Leu Asp Thr Asp Ser Pro Asp His Trp Leu Asp Pro Leu Thr Glu				
1	5	10	15	
Lys Asp Thr Ser Lys Arg Thr Leu Val Asn Ser Ile Val Gln Glu Thr				
	20	25	30	
Phe Gly Gln Pro Ile Phe Val Ala Arg Lys Ile Trp Ala Phe Val Asn				
	35	40	45	
Thr Ser Pro Gly Arg Met Thr Leu Met Thr Ile Ile Ser Ile Ala				
	50	55	60	
Ile Phe Ala Ala Gly Tyr Ala Met Ser Val Ser Ser Asp Thr Arg Gln				
	65	70	75	80
Ser Asn Leu Asp Asp Leu Ile Thr Asn Ala Glu Pro Val Ser Tyr Asn				
	85	90	95	
Ala His Val Leu Tyr Thr Ser Leu Ser Val Ala Asp Thr Thr Ala Thr				
	100	105	110	
Thr Gly Phe Val Gln Ala Gly Val Glu Gly Pro Val Asn Arg Val Lys				
	115	120	125	
Tyr His Thr Ala Ile Asp Arg Ala Ala Val Ala Thr His Thr Ala				
	130	135	140	
Ala Ser Ala Asp Ser Ser Asn Glu His Leu Met Glu Leu Val Leu Glu				
	145	150	155	160
Ile Gln Arg Gln Leu Pro Val Tyr Thr Gly Leu Val Glu Thr Ala Arg				
	165	170	175	
Thr Asn Asn Arg Ala Gly Asn Pro Val Gly Val Ala Tyr Met Ser Glu				
	180	185	190	
Ala Ser Ala Met Met Arg Asn Glu Ile Leu Pro Met Ala Ser Glu Leu				
	195	200	205	

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Tyr Asn Leu Thr Ser Arg Ala Val Ser Asp Gln Gln Arg Ser Val Thr
  210                               215                               220

Gly Pro Gln Trp Phe Pro Leu Ser Gly Leu Leu Ala Ala Leu Ala Met
  225                               230                               235                               240

Leu Ile Val Ala Gln Trp Trp Leu Met Arg Ile Thr Arg Arg Arg Ile
                245                               250                               255

Asn Lys Gly Phe Ala Leu Ala Thr Val Met Met Met Thr Ala Thr Leu
                260                               265                               270

Trp Val Ser Ala Ala Asn Trp Ala Thr Trp Gln Ala Gly Thr Lys Gly
  275                               280                               285

Phe Glu Glu Ala Ser Gly Pro Leu Asn Ser Met Thr Thr Ala Arg Ile
  290                               295                               300

Tyr Ala Gln Gln Thr Arg Thr Thr Glu Thr Leu Ser Leu Val Arg Arg
  305                               310                               315                               320

Gln Ser Ile Gln Gly Ser Gly Thr Gly Phe Thr Ala Thr Ile Asn Gln
                325                               330                               335

Ile Lys Arg Ala Leu Asp Glu Tyr Glu Thr Thr Ala Gln Ser Gln Thr
                340                               345                               350

Pro Glu His Gln Gln Leu Ile Thr Ala Ile Arg Asn Ala Ile Ala Ala
                355                               360                               365

Trp Thr Ala Asp His Asp Glu Phe Thr Val Leu Leu Ala Ser Gly Asp
  370                               375                               380

Tyr Asn Gly Ala Val Asn Ala Val Leu Asn Lys Asp Glu Glu Gly Gln
  385                               390                               395                               400

Thr Ser Phe Asp Glu Leu Asp Thr Ala Leu Ala Glu Leu Ile Ala Asp
                405                               410                               415

Ser Arg Ser Ser Met Arg Ser Tyr Ile Gln Ser Gly Leu Gln Ala Thr
  420                               425                               430

Glu Leu Val Ser Val Met Val Met Ile Leu Ser Val Val Ser Val Leu
  435                               440                               445

Ala Leu Trp Val Gly Ile Arg Pro Arg Leu Gln Glu Tyr Leu
  450                               455                               460

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<210> 1693

<211> 789

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(789)

<223> RXA00282

<400> 1693

atg agc cgc gac gac cag acg aac aac aac ggt gag ggc gac gac aca	48
Met Ser Arg Asp Asp Gln Thr Asn Asn Asn Gly Glu Gly Asp Asp Thr	
1 5 10 15	
tgc cgc gag cag tcc tgg gat caa tcc tgg cag aac cta aat aag gat	96
Ser Arg Glu Gln Ser Trp Asp Gln Ser Trp Gln Asn Leu Asn Lys Asp	
20 25 30	
tcc cag tac ggt ccg acc tgc cat ccg gag gac gcg ccg gga gga ttc	144
Ser Gln Tyr Gly Pro Thr Ser His Pro Glu Asp Ala Pro Gly Gly Phe	
35 40 45	
cag gga aac ggc cag ggt aac agc cgg ggc aac gct cag ggc aat ggt	192
Gln Gly Asn Gly Gln Gly Asn Ser Arg Gly Asn Ala Gln Gly Asn Gly	
50 55 60	
cag ggc aat ggt cag ggc ttt ggc ccg ggt aat gct tgc gga tat gga	240
Gln Gly Asn Gly Gln Gly Phe Gly Pro Gly Asn Ala Ser Gly Tyr Gly	
65 70 75 80	
ggc tac ggt cag cca tac ccg cag act ccg tac cag aat tcc tac caa	288
Gly Tyr Gly Gln Pro Tyr Pro Gln Thr Pro Tyr Gln Asn Ser Tyr Gln	
85 90 95	
ggt tat ggc gct act tca ccg cag aac gac gtg gcg ctg gaa gcg agc	336
Gly Tyr Gly Ala Thr Ser Pro Gln Asn Asp Val Ala Leu Glu Ala Ser	
100 105 110	
aac ggc aaa gtc gac atc atg ccg gcg att ccg ttc gga ttc aaa gcc	384
Asn Gly Lys Val Asp Ile Met Arg Ala Ile Arg Phe Gly Phe Lys Ala	
115 120 125	
acg ttt gcc aat cca gca gtg tgg att ttg ggc acc gtc ggt ctt ggc	432
Thr Phe Ala Asn Pro Ala Val Trp Ile Leu Gly Thr Val Gly Leu Gly	
130 135 140	
ctt gcg ttc atg att gtg agt ggg ttg ctt ggc tac tta tca ttt ttg	480
Leu Ala Phe Met Ile Val Ser Gly Leu Leu Gly Tyr Leu Ser Phe Leu	
145 150 155 160	
atc gac cct aat gcg ggc acg acg act tct ggt ttt tgc gtt tcc gag	528
Ile Asp Pro Asn Ala Gly Thr Thr Thr Ser Gly Phe Ser Val Ser Glu	
165 170 175	
acc ctg ttg aac gta gct atc gga atc atc acc ttc gca ata acc att	576
Thr Leu Leu Asn Val Ala Ile Gly Ile Ile Thr Phe Ala Ile Thr Ile	
180 185 190	
tgc gtc atg ccg ggt gca ctg ctt tct gtt gat gga cac aaa gtt ccg	624
Cys Val Met Arg Gly Ala Leu Leu Ser Val Asp Gly His Lys Val Arg	
195 200 205	
ttc ggt gat ttc ttt aaa ccc atc aat gtt ggt caa aca gtg att ctg	672
Phe Gly Asp Phe Phe Lys Pro Ile Asn Val Gly Gln Thr Val Ile Leu	
210 215 220	
atg gtg ggg ctg ggt atc ttc ggc atc atc ctg ggc acc ttc acc act	720
Met Val Gly Leu Gly Ile Phe Gly Ile Ile Leu Gly Thr Phe Thr Thr	
225 230 235 240	
ttt ctc act caa aat ctg gtg tgc ttt aat gac gct gcc ggt acc gtt	768

Phe Leu Thr Gln Asn Leu Val Ser Phe Asn Asp Ala Ala Gly Thr Val
245 250 255

gag gtc aat aac agc ggt tta
Glu Val Asn Asn Ser Gly Leu
260

789

<210> 1694

<211> 263

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1694

Met Ser Arg Asp Asp Gln Thr Asn Asn Asn Gly Glu Gly Asp Asp Thr
1 5 10 15

Ser Arg Glu Gln Ser Trp Asp Gln Ser Trp Gln Asn Leu Asn Lys Asp
20 25 30

Ser Gln Tyr Gly Pro Thr Ser His Pro Glu Asp Ala Pro Gly Gly Phe
35 40 45

Gln Gly Asn Gly Gln Gly Asn Ser Arg Gly Asn Ala Gln Gly Asn Gly
50 55 60

Gln Gly Asn Gly Gln Gly Phe Gly Pro Gly Asn Ala Ser Gly Tyr Gly
65 70 75 80

Gly Tyr Gly Gln Pro Tyr Pro Gln Thr Pro Tyr Gln Asn Ser Tyr Gln
85 90 95

Gly Tyr Gly Ala Thr Ser Pro Gln Asn Asp Val Ala Leu Glu Ala Ser
100 105 110

Asn Gly Lys Val Asp Ile Met Arg Ala Ile Arg Phe Gly Phe Lys Ala
115 120 125

Thr Phe Ala Asn Pro Ala Val Trp Ile Leu Gly Thr Val Gly Leu Gly
130 135 140

Leu Ala Phe Met Ile Val Ser Gly Leu Leu Gly Tyr Leu Ser Phe Leu
145 150 155 160

Ile Asp Pro Asn Ala Gly Thr Thr Thr Ser Gly Phe Ser Val Ser Glu
165 170 175

Thr Leu Leu Asn Val Ala Ile Gly Ile Ile Thr Phe Ala Ile Thr Ile
180 185 190

Cys Val Met Arg Gly Ala Leu Leu Ser Val Asp Gly His Lys Val Arg
195 200 205

Phe Gly Asp Phe Phe Lys Pro Ile Asn Val Gly Gln Thr Val Ile Leu
210 215 220

Met Val Gly Leu Gly Ile Phe Gly Ile Ile Leu Gly Thr Phe Thr Thr
225 230 235 240

Phe Leu Thr Gln Asn Leu Val Ser Phe Asn Asp Ala Ala Gly Thr Val
245 250 255

Glu Val Asn Asn Ser Gly Leu
260

<210> 1695

<211> 536

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(513)

<223> RXA00285

<400> 1695

gga act gaa ttg ggc gca ttg tta ctg cgt gtc ctc aac agg gaa gaa 48
Gly Thr Glu Leu Gly Ala Leu Leu Leu Arg Val Leu Asn Arg Glu Glu
1 5 10 15

atg atg gac aga ttc gca cgg gag ctg ggt ttt ttc gtc gac aag cag 96
Met Met Asp Arg Phe Ala Arg Glu Leu Gly Phe Phe Val Asp Lys Gln
20 25 30

ctt gaa gag gtc gag cgc atc aac tgt cac cat aac tac acg gtc cag 144
Leu Glu Glu Val Glu Arg Ile Asn Cys His His Asn Tyr Thr Val Gln
35 40 45

gag gag cac tac ggc gag acc att tgg ctc acc cgt aag ggt gcc gtg 192
Glu Glu His Tyr Gly Glu Thr Ile Trp Leu Thr Arg Lys Gly Ala Val
50 55 60

ttg gcg gac gaa ggc acg cgg gcg ttg att cgg ggg tcg atg ggc acc 240
Leu Ala Asp Glu Gly Thr Pro Ala Leu Ile Pro Gly Ser Met Gly Thr
65 70 75 80

gcg tcg tac gtg ggc agt ggc aag ggc aac gcc gag gca ctg cgg tcg 288
Ala Ser Tyr Val Gly Ser Gly Lys Gly Asn Ala Glu Ala Leu Arg Ser
85 90 95

gcg ccg cat ggg gcg ggc cgg agg atg tac cgc aac cag gct aaa aag 336
Ala Pro His Gly Ala Gly Arg Arg Met Tyr Arg Asn Gln Ala Lys Lys
100 105 110

cgc ttc tcg acg gcc gac ctg gat tct cgg atg gcg ggc atc gtc tac 384
Arg Phe Ser Thr Ala Asp Leu Asp Ser Arg Met Ala Gly Ile Val Tyr
115 120 125

cgg ccc ggc aag gag tgg atc gat gaa att ccc gac gct tac aaa gac 432
Arg Pro Gly Lys Glu Trp Ile Asp Glu Ile Pro Asp Ala Tyr Lys Asp
130 135 140

atc gat cag gtg atg gcc gat gct gcc gat ttg gtg aca att cgc cat 480
Ile Asp Gln Val Met Ala Asp Ala Ala Asp Leu Val Thr Ile Arg His
145 150 155 160

aaa ttg cgc cag atc gtc aac gtg aaa ggc acc taaagcgcat tacggtaaag 533
Lys Leu Arg Gln Ile Val Asn Val Lys Gly Thr
165 170

tgc

536

<210> 1696
 <211> 171
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1696
 Gly Thr Glu Leu Gly Ala Leu Leu Arg Val Leu Asn Arg Glu Glu
 1 5 10 15
 Met Met Asp Arg Phe Ala Arg Glu Leu Gly Phe Phe Val Asp Lys Gln
 20 25 30
 Leu Glu Glu Val Glu Arg Ile Asn Cys His His Asn Tyr Thr Val Gln
 35 40 45
 Glu Glu His Tyr Gly Glu Thr Ile Trp Leu Thr Arg Lys Gly Ala Val
 50 55 60
 Leu Ala Asp Glu Gly Thr Pro Ala Leu Ile Pro Gly Ser Met Gly Thr
 65 70 75 80
 Ala Ser Tyr Val Gly Ser Gly Lys Gly Asn Ala Glu Ala Leu Arg Ser
 85 90 95
 Ala Pro His Gly Ala Gly Arg Arg Met Tyr Arg Asn Gln Ala Lys Lys
 100 105 110
 Arg Phe Ser Thr Ala Asp Leu Asp Ser Arg Met Ala Gly Ile Val Tyr
 115 120 125
 Arg Pro Gly Lys Glu Trp Ile Asp Glu Ile Pro Asp Ala Tyr Lys Asp
 130 135 140
 Ile Asp Gln Val Met Ala Asp Ala Ala Asp Leu Val Thr Ile Arg His
 145 150 155 160
 Lys Leu Arg Gln Ile Val Asn Val Lys Gly Thr
 165 170

<210> 1697
 <211> 687
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> {101}..(664)
 <223> RXA00286

<400> 1697
 ccataaattg cgccagatcg tcaacgtgaa aggcacctaag agcgattac ggtaaagtgc 60
 gagaggattt ttgacgggtt tagattgagg gatgtggata gtg ctg aaa atc cca 115
 Val Leu Lys Ile Pro
 1 5
 cgg ctg ctt cta cgc cgt gtg ctt ccg gta ctc atc acc ttg gcg ctc 163
 Arg Leu Leu Leu Arg Arg Val Leu Pro Val Leu Ile Thr Leu Ala Leu

	10	15	20	
ctg tgc gga ctg gtg ctt gcg tgg ttt atc tat cct gcg aag gct gag				211
Leu Cys Gly Leu Val Leu Ala Trp Phe Ile Tyr Pro Ala Lys Ala Glu	25	30	35	
ccc aaa aaa gat gat gta gtt ctg gtg ctg gcc ggt tcc agc gat ggt				259
Pro Lys Lys Asp Asp Val Val Leu Val Leu Ala Gly Ser Ser Asp Gly	40	45	50	
cga cac gaa tat ggt gcc gag ctt gtt gaa gaa ggc tac gcc agc aat				307
Arg His Glu Tyr Gly Ala Glu Leu Val Glu Glu Gly Tyr Ala Ser Asn	55	60	65	
tac gtc gtc tcc aac cgc agt ggc tcc aaa gac aaa gtg gga tat gcc				355
Tyr Val Val Ser Asn Pro Ser Gly Ser Lys Asp Lys Val Gly Tyr Ala	70	75	80	85
cac tgc gca gga aag tca cgg cca aaa aat gcg gaa agt ttc tgc atg				403
His Cys Ala Gly Lys Ser Arg Pro Lys Asn Ala Glu Ser Phe Cys Met	90	95	100	
gat cct tac ccc gtg atc acc tcc gcc gaa gcc cgc acg ttt aac gag				451
Asp Pro Tyr Pro Val Ile Thr Ser Gly Glu Ala Arg Thr Phe Asn Glu	105	110	115	
ctt gcc aaa aag gaa ggc tgg gaa agc gta ttg gta gtg acc agc cgc				499
Leu Ala Lys Lys Glu Gly Trp Glu Ser Val Leu Val Val Thr Ser Arg	120	125	130	
acg cac acc caa cgc gtt cgc acc atg ttt gac cag tgc tat acc ggt				547
Thr His Thr Gln Arg Val Arg Thr Met Phe Asp Gln Cys Tyr Thr Gly	135	140	145	
gat tcc aca gtg ctc aac gtc aac agc cta gga cgt acc ggg ctt cac				595
Asp Ser Thr Val Leu Asn Val Asn Ser Leu Gly Arg Thr Gly Leu His	150	155	160	165
aat gca gta ctc cac gag att ggc ggc ttc att aaa ttt tgg att acc				643
Asn Ala Val Leu His Glu Ile Gly Gly Phe Ile Lys Phe Trp Ile Thr	170	175	180	
gct cgc tgc gcg gac aca aac taaggacgtt ccagctccaa cag				687
Ala Pro Cys Ala Asp Thr Asn	185			

<210> 1698

<211> 188

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1698

Val	Leu	Lys	Ile	Pro	Arg	Leu	Leu	Leu	Arg	Val	Leu	Pro	Val	Leu
1				5					10				15	

Ile	Thr	Leu	Ala	Leu	Leu	Cys	Gly	Leu	Val	Leu	Ala	Trp	Phe	Ile	Tyr
		20					25						30		

Pro	Ala	Lys	Ala	Glu	Pro	Lys	Lys	Asp	Asp	Val	Val	Leu	Val	Leu	Ala
	35						40					45			

Gly Ser Ser Asp Gly Arg His Glu Tyr Gly Ala Glu Leu Val Glu Glu
50 55 60

Gly Tyr Ala Ser Asn Tyr Val Val Ser Asn Pro Ser Gly Ser Lys Asp
65 70 75 80

Lys Val Gly Tyr Ala His Cys Ala Gly Lys Ser Arg Pro Lys Asn Ala
85 90 95

Glu Ser Phe Cys Met Asp Pro Tyr Pro Val Ile Thr Ser Gly Glu Ala
100 105 110

Arg Thr Phe Asn Glu Leu Ala Lys Lys Glu Gly Trp Glu Ser Val Leu
115 120 125

Val Val Thr Ser Arg Thr His Thr Gln Arg Val Arg Thr Met Phe Asp
130 135 140

Gln Cys Tyr Thr Gly Asp Ser Thr Val Leu Asn Val Asn Ser Leu Gly
145 150 155 160

Arg Thr Gly Leu His Asn Ala Val Leu His Glu Ile Gly Gly Phe Ile
165 170 175

Lys Phe Trp Ile Thr Ala Pro Cys Ala Asp Thr Asn
180 185

<210> 1699

<211> 552

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(529)

<223> RXA00294

<400> 1699

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agttggtgcc gaatcaacaa totcttttgg aggaacttta atg agc att tcc aac 115
Met Ser Ile Ser Asn
1 5

gca atc ctg cgt ggt gtg tct ggc gct tat att ctg cag tcc ggc tac 163
Ala Ile Leu Arg Gly Val Ser Gly Ala Tyr Ile Leu Gln Ser Gly Tyr
10 15 20

gga aaa ctt gga ttg cct aat gag gcc gct gct ggc att cag ggt cta 211
Gly Lys Leu Gly Leu Pro Asn Glu Ala Ala Gly Ile Gln Gly Leu
25 30 35

gct gca acg ggt atc cca gcg gtg gct gat atg gat tca gat act ttc 259
Ala Ala Thr Gly Ile Pro Ala Val Ala Asp Met Asp Ser Asp Thr Phe
40 45 50

ggt aag ttt gtt gcc tac tcg gag ttg ggt atc ggt gga gct ttg ctt 307
Gly Lys Phe Val Ala Tyr Ser Glu Leu Gly Ile Gly Gly Ala Leu Leu
55 60 65

gct cca ttt atc cct agc cgt ctt gca ggt ttg ggt ctt ggt gct ttc 355
 Ala Pro Phe Ile Pro Ser Arg Leu Ala Gly Leu Gly Leu Gly Ala Phe
 70 75 80 85
 tct aca ggt ttg ttg gcc att tac ttc cgt aac cca gcg atg act caa 403
 Ser Thr Gly Leu Leu Ala Ile Tyr Phe Arg Asn Pro Ala Met Thr Gln
 90 95 100
 gac gac gga atc cgc cct tcc cag gat gga acc gga ttg tct aag gat 451
 Asp Asp Gly Ile Arg Pro Ser Gln Asp Gly Thr Gly Leu Ser Lys Asp
 105 110 115
 ctt ttc ctt gct gct att gcg ggt gct ttg gtg ttc gca cct gct aag 499
 Leu Phe Leu Ala Ala Ile Ala Gly Ala Leu Val Phe Ala Pro Ala Lys
 120 125 130
 aag cgt aag aag gcg aag aac aag tct aag taagcttgct tgaacggcgc 549
 Lys Arg Lys Lys Ala Lys Asn Lys Ser Lys
 135 140
 ttg 552

<210> 1700
 <211> 143
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1700
 Met Ser Ile Ser Asn Ala Ile Leu Arg Gly Val Ser Gly Ala Tyr Ile
 1 5 10 15
 Leu Gln Ser Gly Tyr Gly Lys Leu Gly Leu Pro Asn Glu Ala Ala Ala
 20 25 30
 Gly Ile Gln Gly Leu Ala Ala Thr Gly Ile Pro Ala Val Ala Asp Met
 35 40 45
 Asp Ser Asp Thr Phe Gly Lys Phe Val Ala Tyr Ser Glu Leu Gly Ile
 50 55 60
 Gly Gly Ala Leu Leu Ala Pro Phe Ile Pro Ser Arg Leu Ala Gly Leu
 65 70 75 80
 Gly Leu Gly Ala Phe Ser Thr Gly Leu Leu Ala Ile Tyr Phe Arg Asn
 85 90 95
 Pro Ala Met Thr Gln Asp Asp Gly Ile Arg Pro Ser Gln Asp Gly Thr
 100 105 110
 Gly Leu Ser Lys Asp Leu Phe Leu Ala Ala Ile Ala Gly Ala Leu Val
 115 120 125
 Phe Ala Pro Ala Lys Lys Arg Lys Lys Ala Lys Asn Lys Ser Lys
 130 135 140

<210> 1701
 <211> 1035
 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1012)

<223> RXA00297

<400> 1701

aacaaggcac cggaaaaacaa gcaacgcacc ttgcagaggt ggtcttaagc atcttggagc 60

aaaacaacat ggcacaataa cgatcatgca acaggtgctc atg ggt ttc acg gtg 115
 Met Gly Phe Thr Val
 1 5

gtg ttc atc gtc atc gga ata ggt tgg att ctc ggt aga aga gac acc 163
 Val Phe Ile Val Ile Gly Ile Gly Trp Ile Leu Gly Arg Arg Asp Thr
 10 15 20

ttg ggc aca cat gcc cag aaa cct ttg agc ctg ttt gtc tat tac gtg 211
 Leu Gly Thr His Ala Gln Lys Pro Leu Ser Leu Phe Val Tyr Tyr Val
 25 30 35

gcc acc cca gcg ttg ttg ttt gat cgg gtc acc aag tca gat acc tcg 259
 Ala Thr Pro Ala Leu Leu Phe Asp Arg Val Thr Lys Ser Asp Thr Ser
 40 45 50

acg att ttc tct ctg aac ttc gtg gtc att gca ctc tct gcg ttg atc 307
 Thr Ile Phe Ser Leu Asn Phe Val Val Ile Ala Leu Ser Ala Leu Ile
 55 60 65

gta ggt ttc ctg ttt ttc cta ctc atg cgg ttc gtg atc aaa aga act 355
 Val Gly Phe Leu Phe Phe Leu Leu Met Arg Phe Val Ile Lys Arg Thr
 70 75 80 85

gcc gca gta tcg gtg atc ggc atg cta gct gcg tcc tac gcc aac gcc 403
 Ala Ala Val Ser Val Ile Gly Met Leu Ala Ala Ser Tyr Ala Asn Ala
 90 95 100

ggt aac ctg ggt atc cct ttg gca gcc tat att ttg gat gat ttc acc 451
 Gly Asn Leu Gly Ile Pro Leu Ala Ala Tyr Ile Leu Asp Asp Phe Thr
 105 110 115

gtg gtg att ccc gtg att ttg ttc cag gtg gcg ttc tac gca ccg atc 499
 Val Val Ile Pro Val Ile Leu Phe Gln Val Ala Phe Tyr Ala Pro Ile
 120 125 130

acc atg acc atc atg gag atg ctg acc aac aag aaa tcc acc aac ttg 547
 Thr Met Thr Thr Ile Met Glu Met Leu Thr Asn Lys Lys Ser Thr Asn Leu
 135 140 145

gtg cgc aac ctc ctg gtc acg cca cta acc aac acc atg gtg ctc gca 595
 Val Arg Asn Leu Leu Val Thr Pro Leu Thr Asn Thr Met Val Leu Ala
 150 155 160 165

gcg att gcc ggt att gct gtg tct ttg act tcg atg agc gtg ccc gtg 643
 Ala Ile Ala Gly Ile Ala Val Ser Leu Thr Ser Met Ser Val Pro Val
 170 175 180

gtg att gct cag cca gtg gaa atg ttg gcg aat gct tca gtg cca ctg 691
 Val Ile Ala Gln Pro Val Glu Met Leu Ala Asn Ala Ser Val Pro Leu
 185 190 195

gct ttg gtg gtg ttc gga ctg tcc ttg tcc aag agc aag atc ctg gaa 739
 Ala Leu Val Val Phe Gly Leu Ser Leu Ser Lys Ser Lys Ile Leu Glu
 200 205 210

aag ggg cag gta tcc agg cgc gat gtg ttt acg gcg gca ctg ttc aag 787
 Lys Gly Gln Val Ser Arg Arg Asp Val Phe Thr Ala Ala Leu Phe Lys
 215 220 225

aat gtt ctg cac cca att gtt gcg gga ctt tta gcc tta gcc ttt ggt 835
 Asn Val Leu His Pro Ile Val Ala Gly Leu Leu Ala Leu Ala Phe Gly
 230 235 240 245

atg gaa ggt act gcc ttg ttg tgc gcg gtg att ctc ggt gca ctg cca 883
 Met Glu Gly Thr Ala Leu Leu Ser Ala Val Ile Leu Gly Ala Leu Pro
 250 255 260

aca gcg cag aat gtc tac acc tac gcg ttg cga ttt aga aca gct gaa 931
 Thr Ala Gln Asn Val Tyr Thr Tyr Ala Leu Arg Phe Arg Thr Ala Glu
 265 270 275

tgc atg gcg aga gac aca ggg gtg gtc acc aca ctc att tcc ttc ccc 979
 Ser Met Ala Arg Asp Thr Gly Val Val Thr Thr Leu Ile Ser Phe Pro
 280 285 290

gta ttg gtg gcg gtc tcc att atc ttt gga tct tagggtagc attagtggc 1032
 Val Leu Val Ala Val Ser Ile Ile Phe Gly Ser
 295 300

atg 1035

<210> 1702
 <211> 304
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1702
 Met Gly Phe Thr Val Val Phe Ile Val Ile Gly Ile Gly Trp Ile Leu
 1 5 10 15
 Gly Arg Arg Asp Thr Leu Gly Thr His Ala Gln Lys Pro Leu Ser Leu
 20 25 30
 Phe Val Tyr Tyr Val Ala Thr Pro Ala Leu Leu Phe Asp Arg Val Thr
 35 40 45
 Lys Ser Asp Thr Ser Thr Ile Phe Ser Leu Asn Phe Val Val Ile Ala
 50 55 60
 Leu Ser Ala Leu Ile Val Gly Phe Leu Phe Phe Leu Leu Met Arg Phe
 65 70 75 80
 Val Ile Lys Arg Thr Ala Ala Val Ser Val Ile Gly Met Leu Ala Ala
 85 90 95
 Ser Tyr Ala Asn Ala Gly Asn Leu Gly Ile Pro Leu Ala Ala Tyr Ile
 100 105 110
 Leu Asp Asp Phe Thr Val Val Ile Pro Val Ile Leu Phe Gln Val Ala
 115 120 125

Phe Tyr Ala Pro Ile Thr Met Thr Ile Met Glu Met Leu Thr Asn Lys
130 135 140

Lys Ser Thr Asn Leu Val Arg Asn Leu Leu Val Thr Pro Leu Thr Asn
145 150 155 160

Thr Met Val Leu Ala Ala Ile Ala Gly Ile Ala Val Ser Leu Thr Ser
165 170 175

Met Ser Val Pro Val Val Ile Ala Gln Pro Val Glu Met Leu Ala Asn
180 185 190

Ala Ser Val Pro Leu Ala Leu Val Val Phe Gly Leu Ser Leu Ser Lys
195 200 205

Ser Lys Ile Leu Glu Lys Gly Gln Val Ser Arg Asp Val Phe Thr
210 215 220

Ala Ala Leu Phe Lys Asn Val Leu His Pro Ile Val Ala Gly Leu Leu
225 230 235 240

Ala Leu Ala Phe Gly Met Glu Gly Thr Ala Leu Leu Ser Ala Val Ile
245 250 255

Leu Gly Ala Leu Pro Thr Ala Gln Asn Val Tyr Thr Tyr Ala Leu Arg
260 265 270

Phe Arg Thr Ala Glu Ser Met Ala Arg Asp Thr Gly Val Val Thr Thr
275 280 285

Leu Ile Ser Phe Pro Val Leu Val Ala Val Ser Ile Ile Phe Gly Ser
290 295 300

<210> 1703

<211> 303

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(280)

<223> RXA00320

<400> 1703

aacagaccga ctctagccgt tgcgggttct tattgaggtc tatagtgggg tgctacacac 60

tacaaaccgt gatttgtttc gtgattggag ctgagccac atg gct aaa gaa gat 115
Met Ala Lys Glu Asp
1 5

ttg aag tgg ttc tac gat ctg gca acc ggc aag gtt ttt caa ggc aag 163
Leu Lys Trp Phe Tyr Asp Leu Ala Thr Gly Lys Val Phe Gln Gly Lys
10 15 20

gtt tcc ggc ttt gaa acc cgc atg ggc cca tat gac act gaa gag gaa 211
Val Ser Gly Phe Glu Thr Arg Met Gly Pro Tyr Asp Thr Glu Glu Glu

25

30

35

gcc cat cac gcc atc tcc att gcg gca gcc cga acc aag gca gcc gaa 259
 Ala His His Ala Ile Ser Ile Ala Ala Arg Thr Lys Ala Ala Glu
 40 45 50

att tgg gac gac aag gaa gac taaaaaaaaac tggggtcaca ctt 303
 Ile Trp Asp Asp Lys Glu Asp
 55 60

<210> 1704

<211> 60

<212> PRT

<213> Corynebacterium glutamicum

<400> 1704

Met Ala Lys Glu Asp Leu Lys Trp Phe Tyr Asp Leu Ala Thr Gly Lys
 1 5 10 15

Val Phe Gln Gly Lys Val Ser Gly Phe Glu Thr Arg Met Gly Pro Tyr
 20 25 30

Asp Thr Glu Glu Ala His His Ala Ile Ser Ile Ala Ala Arg
 35 40 45

Thr Lys Ala Ala Glu Ile Trp Asp Asp Lys Glu Asp
 50 55 60

<210> 1705

<211> 1938

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1915)

<223> RXA00321

<400> 1705

caaaagacaac acaggttccc tatgaaaacg gggaacctgt ttacactact ttttaatcac 60

gcttcacaat cacataagtc tttaaaggat ggatacaaca atg ggc cag cat cta 115
 Met Gly Gln His Leu
 1 5

gaa gtg gaa act aag ttt tcc gtc agt gaa tca act cag att cca caa 163
 Glu Val Glu Thr Lys Phe Ser Val Ser Glu Ser Thr Gln Ile Pro Gln
 10 15 20

ctt gag gct atc gca gaa gtc gac cac att gat cgc acc gaa atc cac 211
 Leu Glu Ala Ile Ala Glu Val Asp His Ile Asp Arg Thr Glu Ile His
 25 30 35

caa cta agc gct gtt tac ttt gac acc gta gat ttg cgc ctc acc cgc 259
 Gln Leu Ser Ala Val Tyr Phe Asp Thr Val Asp Leu Arg Leu Thr Arg
 40 45 50

gca aaa att acc ctc cgt cgc cgc acc ggt gga aac gat gcc ggc tgg 307
 Ala Lys Ile Thr Leu Arg Arg Arg Thr Gly Gly Asn Asp Ala Gly Trp

55	60	65	
cac att aag ttc ccc gga acc atc ggt cgc cgt gaa gtc caa gcc cca			355
His Ile Lys Phe Pro Gly Thr Ile Gly Arg Arg Glu Val Gln Ala Pro			
70	75	80	85
ctt gat ggc gaa ggc gca aca gaa acc ctc cct cca cgt gag ctc ttg			403
Leu Asp Gly Glu Gly Ala Thr Glu Thr Leu Pro Pro Arg Glu Leu Leu			
	90	95	100
gga cac atc cga gcg ctg atc caa ggc cgt gag ctg acc cct atc gcc			451
Gly His Ile Arg Ala Leu Ile Gln Gly Arg Glu Leu Thr Pro Ile Ala			
105	110	115	
cag gtg gat aat gaa cgc cac atg tct tac ctc gcg gat gag gac ggc			499
Gln Val Asp Asn Glu Arg His Met Ser Tyr Leu Ala Asp Glu Asp Gly			
120	125	130	
gca gtc atc gca gaa ttc tgc gac gat cat gta tcc acc gtg tcc cac			547
Ala Val Ile Ala Glu Phe Cys Asp Asp His Val Ser Thr Val Ser His			
135	140	145	
ctt cca ggt ggc gtg cgc aag cag tgg cgt gag tgg gaa ttc gaa ctc			595
Leu Pro Gly Gly Val Arg Lys Gln Trp Arg Glu Trp Glu Phe Glu Leu			
150	155	160	165
gct gat ggc acc ctc gcc gaa gaa gcc atc tca gta ctg ctg caa tct			643
Ala Asp Gly Thr Leu Ala Glu Glu Ala Ile Ser Val Leu Leu Gln Ser			
	170	175	180
gca cag tca gtc ctg acc gca gct gga gct ttt gtc tcc aac agc cca			691
Ala Gln Ser Val Leu Thr Ala Ala Gly Ala Phe Val Ser Asn Ser Pro			
185	190	195	
tcc aaa ctt gtt tgc gcg ctg gac gaa tca gtc aac cac gcg cca aag			739
Ser Lys Leu Val Ser Ala Leu Asp Glu Ser Val Asn His Ala Pro Lys			
200	205	210	
cct cca cag atg gcg cag ctg gac aag aat gac cca gca cgt ggt gtt			787
Pro Pro Gln Met Ala Gln Leu Asp Lys Asn Asp Pro Ala Arg Gly Val			
215	220	225	
ctt gca gca atc gca gcc aac gcc tca aag atc gcc gaa tac gat cct			835
Leu Ala Ala Ile Ala Ala Asn Ala Ser Lys Ile Ala Glu Tyr Asp Pro			
230	235	240	245
cga gta cgc gcc gat gaa tat gat tca gtc cac cag atg cgc gta gct			883
Arg Val Arg Ala Asp Glu Tyr Asp Ser Val His Gln Met Arg Val Ala			
	250	255	260
acc cga gaa cta cgc agc cac ctc caa acc ttt gag ggc atc ctc ggc			931
Thr Arg Glu Leu Arg Ser His Leu Gln Thr Phe Glu Gly Ile Leu Gly			
265	270	275	
ggc gaa gac tac ctc aac ctg gaa aag gaa ctg aag gtt ctc gcc aac			979
Gly Glu Asp Tyr Leu Asn Leu Glu Lys Glu Leu Lys Val Leu Ala Asn			
280	285	290	
atc ttg ggt cgc gca cgc gat gct gaa gtt gtg gaa gag cgc ctc agc			1027
Ile Leu Gly Arg Ala Arg Asp Ala Glu Val Val Glu Glu Arg Leu Ser			
295	300	305	

aac ctg att aac act gag gtt ggc gac tcc atc gag gag gag act aag	1075
Asn Leu Ile Asn Thr Glu Val Gly Asp Ser Ile Glu Glu Glu Thr Lys	
310 315 320 325	
aag gaa ctg ctt gaa gat ctt ggt gca gaa tac cgt cgt gag cat gag	1123
Lys Glu Leu Leu Glu Asp Leu Gly Ala Glu Tyr Arg Arg Glu His Glu	
330 335 340	
cga gta gtt cgt gcg ctg gat aat gat cgc tac act gat ctt ctt cag	1171
Arg Val Val Arg Ala Leu Asp Asn Asp Arg Tyr Thr Asp Leu Leu Gln	
345 350 355	
gca ctg gaa aac ctc ctt gtt gat cca cgc ctg atc aca gaa gtc gaa	1219
Ala Leu Glu Asn Leu Leu Val Asp Pro Pro Leu Ile Thr Glu Val Glu	
360 365 370	
gaa ccc gaa gct acc gaa gcc cct gag tcc gct gag act acc gag tcc	1267
Glu Pro Glu Ala Thr Glu Ala Pro Glu Ser Ala Glu Thr Thr Glu Ser	
375 380 385	
act gac gtc tct gaa gca acc gaa gaa gca gac gca gaa gct gag tct	1315
Thr Asp Val Ser Glu Ala Thr Glu Glu Ala Asp Ala Glu Ala Glu Ser	
390 395 400 405	
gtc gaa gaa gct act gag cag gaa gaa tca gca gac gcg cct gaa tct	1363
Val Glu Glu Ala Thr Glu Gln Glu Ser Ala Asp Ala Pro Glu Ser	
410 415 420	
gca gat ctg gac gct ctc gat gag gag tac tcc cct ggt tcc caa gcg	1411
Ala Asp Leu Asp Ala Leu Asp Glu Glu Tyr Ser Pro Gly Ser Gln Ala	
425 430 435	
ccg gtg gag gag ccg aag gaa ccg aag aag gtt gat gct gct ctc gta	1459
Pro Val Glu Glu Pro Lys Glu Pro Lys Lys Val Asp Ala Ala Leu Val	
440 445 450	
ctt cta gag cac ctt gat aag gcg cac gtg aag ctc gtc aag ctg gaa	1507
Leu Leu Glu His Leu Asp Lys Ala His Val Lys Leu Val Lys Leu Glu	
455 460 465	
aag aag gct cgc tca cag tgg gat gat ctc agc att ccg atg ctg gag	1555
Lys Lys Ala Arg Ser Gln Trp Asp Asp Leu Ser Ile Pro Met Leu Glu	
470 475 480 485	
cgg gaa gaa aac ttc cac aac ctg cgc aag gct gcc aag aag ctt cgc	1603
Arg Glu Glu Asn Phe His Asn Leu Arg Lys Ala Ala Lys Lys Leu Arg	
490 495 500	
tac agt gca gag gca gtg ggc aaa gca acc acc gtt gag acg aag aaa	1651
Tyr Ser Ala Glu Ala Val Gly Lys Ala Thr Thr Val Glu Thr Lys Lys	
505 510 515	
ctg tac aag gcg tgc agt ggt ttg cag tca gtt ctt ggc gat tac caa	1699
Leu Tyr Lys Ala Cys Ser Gly Leu Gln Ser Val Leu Gly Asp Tyr Gln	
520 525 530	
gat gcc att act tcc cgt aat gag ctg ttg cgc cga gct cag gtt gcc	1747
Asp Ala Ile Thr Ser Arg Asn Glu Leu Leu Arg Arg Ala Gln Val Ala	
535 540 545	

cgc cgc caa ggc cgg gat acc ttc gca tac gga atc ctc tac cag cac 1795
 Arg Arg Gln Gly Arg Asp Thr Phe Ala Tyr Gly Ile Leu Tyr Gln His
 550 555 560 565

gaa caa acc ctg tcg agg gaa tac ctg act ggt tat tcc gat gcg ttc 1843
 Glu Gln Thr Leu Ser Arg Glu Tyr Leu Thr Gly Tyr Ser Asp Ala Phe
 570 575 580

aag agc gta gaa aaa gcc tat gca aag ctg gct gaa gat acc gcc aag 1891
 Lys Ser Val Glu Lys Ala Tyr Ala Lys Leu Ala Glu Asp Thr Ala Lys
 585 590 595

cgt tca aag aag aac aag cgt aag taaacgcagg caataaaaaa ctg 1938
 Arg Ser Lys Lys Asn Lys Arg Lys
 600 605

<210> 1706

<211> 605

<212> PRT

<213> Corynebacterium glutamicum

<400> 1706

Met Gly Gln His Leu Glu Val Glu Thr Lys Phe Ser Val Ser Glu Ser
 1 5 10 15

Thr Gln Ile Pro Gln Leu Glu Ala Ile Ala Glu Val Asp His Ile Asp
 20 25 30

Arg Thr Glu Ile His Gln Leu Ser Ala Val Tyr Phe Asp Thr Val Asp
 35 40 45

Leu Arg Leu Thr Arg Ala Lys Ile Thr Leu Arg Arg Arg Thr Gly Gly
 50 55 60

Asn Asp Ala Gly Trp His Ile Lys Phe Pro Gly Thr Ile Gly Arg Arg
 65 70 75 80

Glu Val Gln Ala Pro Leu Asp Gly Glu Glu Ala Thr Glu Thr Leu Pro
 85 90 95

Pro Arg Glu Leu Leu Gly His Ile Arg Ala Leu Ile Gln Gly Arg Glu
 100 105 110

Leu Thr Pro Ile Ala Gln Val Asp Asn Glu Arg His Met Ser Tyr Leu
 115 120 125

Ala Asp Glu Asp Gly Ala Val Ile Ala Glu Phe Cys Asp Asp His Val
 130 135 140

Ser Thr Val Ser His Leu Pro Gly Gly Val Arg Lys Gln Trp Arg Glu
 145 150 155 160

Trp Glu Phe Glu Leu Ala Asp Gly Thr Leu Ala Glu Glu Ala Ile Ser
 165 170 175

Val Leu Leu Gln Ser Ala Gln Ser Val Leu Thr Ala Ala Gly Ala Phe
 180 185 190

Val Ser Asn Ser Pro Ser Lys Leu Val Ser Ala Leu Asp Glu Ser Val
 195 200 205

Asn His Ala Pro Lys Pro Pro Gln Met Ala Gln Leu Asp Lys Asn Asp
 210 215 220
 Pro Ala Arg Gly Val Leu Ala Ala Ile Ala Ala Asn Ala Ser Lys Ile
 225 230 235 240
 Ala Glu Tyr Asp Pro Arg Val Arg Ala Asp Glu Tyr Asp Ser Val His
 245 250 255
 Gln Met Arg Val Ala Thr Arg Glu Leu Arg Ser His Leu Gln Thr Phe
 260 265 270
 Glu Gly Ile Leu Gly Gly Glu Asp Tyr Leu Asn Leu Glu Lys Glu Leu
 275 280 285
 Lys Val Leu Ala Asn Ile Leu Gly Arg Ala Arg Asp Ala Glu Val Val
 290 295 300
 Glu Glu Arg Leu Ser Asn Leu Ile Asn Thr Glu Val Gly Asp Ser Ile
 305 310 315 320
 Glu Glu Glu Thr Lys Lys Glu Leu Leu Glu Asp Leu Gly Ala Glu Tyr
 325 330 335
 Arg Arg Glu His Glu Arg Val Val Arg Ala Leu Asp Asn Asp Arg Tyr
 340 345 350
 Thr Asp Leu Leu Gln Ala Leu Glu Asn Leu Leu Val Asp Pro Pro Leu
 355 360 365
 Ile Thr Glu Val Glu Glu Pro Glu Ala Thr Glu Ala Pro Glu Ser Ala
 370 375 380
 Glu Thr Thr Glu Ser Thr Asp Val Ser Glu Ala Thr Glu Glu Ala Asp
 385 390 395 400
 Ala Glu Ala Glu Ser Val Glu Glu Ala Thr Glu Gln Glu Glu Ser Ala
 405 410 415
 Asp Ala Pro Glu Ser Ala Asp Leu Asp Ala Leu Asp Glu Glu Tyr Ser
 420 425 430
 Pro Gly Ser Gln Ala Pro Val Glu Glu Pro Lys Glu Pro Lys Lys Val
 435 440 445
 Asp Ala Ala Leu Val Leu Leu Glu His Leu Asp Lys Ala His Val Lys
 450 455 460
 Leu Val Lys Leu Glu Lys Lys Ala Arg Ser Gln Trp Asp Asp Leu Ser
 465 470 475 480
 Ile Pro Met Leu Glu Arg Glu Glu Asn Phe His Asn Leu Arg Lys Ala
 485 490 495
 Ala Lys Lys Leu Arg Tyr Ser Ala Glu Ala Val Gly Lys Ala Thr Thr
 500 505 510
 Val Glu Thr Lys Lys Leu Tyr Lys Ala Cys Ser Gly Leu Gln Ser Val
 515 520 525

Leu Gly Asp Tyr Gln Asp Ala Ile Thr Ser Arg Asn Glu Leu Leu Arg
 530 535 540
 Arg Ala Gln Val Ala Arg Arg Gln Gly Arg Asp Thr Phe Ala Tyr Gly
 545 550 555 560
 Ile Leu Tyr Gln His Glu Gln Thr Leu Ser Arg Glu Tyr Leu Thr Gly
 565 570 575
 Tyr Ser Asp Ala Phe Lys Ser Val Glu Lys Ala Tyr Ala Lys Leu Ala
 580 585 590
 Glu Asp Thr Ala Lys Arg Ser Lys Lys Asn Lys Arg Lys
 595 600 605

<210> 1707

<211> 1227

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1204)

<223> RKA00322

<400> 1707

cgcggttttt tgaatgacacg ggggtgggag gtgtccagct tgggtgggttc actgagaacc 60

gcaccgaaat tagaacactc ctacgaataa ggaaacgcga atg act ctc tcc cac 115
 Met Thr Leu Ser His
 1 5

ttc tcc gac aac gtc acc gac gca caa gac tct tac cgt cag att tta 163
 Phe Ser Asp Asn Val Thr Asp Ala Gln Asp Ser Tyr Arg Gln Ile Leu
 10 15 20

gaa gaa agc atc atc agc cac cta ggt ttc tgt gcg ctt cgt ggg tgg 211
 Glu Glu Ser Ile Ile Ser His Leu Gly Phe Cys Ala Leu Arg Gly Trp
 25 30 35

act ccc gcc gat ctc cgc cat gag ttt tcc gcc gat att gat cca ctc 259
 Thr Pro Ala Asp Leu Arg His Glu Phe Ser Ala Asp Ile Asp Pro Leu
 40 45 50

ctg ttt cac gcg cta cct gag att get tac tcc tgc tcc gat gag atg 307
 Leu Phe His Ala Leu Pro Glu Ile Ala Tyr Ser Cys Ser Asp Glu Met
 55 60 65

tac aca ctg tgg gtg aac gga acg cgt gcc gcc gaa act agc cac ttg 355
 Tyr Thr Leu Trp Val Asn Gly Thr Arg Ala Ala Glu Thr Ser His Leu
 70 75 80 85

cgg gtg atg acc ctg gag aag att ctc acc gag cta ccg aag cta agt 403
 Pro Val Met Thr Leu Glu Lys Ile Leu Thr Glu Leu Pro Lys Leu Ser
 90 95 100

acc ttg cct gac tgg gca atg ctc gca gag ctc cac gcc tta gac aat 451
 Thr Leu Pro Asp Trp Ala Met Leu Ala Glu Leu His Ala Leu Asp Asn
 105 110 115

caa gac acc agc cca atg acc ccg gca cag gcc aaa gcg cat cat cgt 499
 Gln Asp Thr Ser Pro Met Thr Pro Ala Gln Ala Lys Ala His His Arg
 120 125 130

atc acc gca ctt ttg aaa aag gca gag tcc acc aac ttc gaa gaa gaa 547
 Ile Thr Ala Leu Leu Lys Lys Ala Glu Ser Thr Asn Phe Glu Glu Glu
 135 140 145

gcc gaa gca ttg atc ctt aaa gca gag aca ctt cga cag cag tac cgg 595
 Ala Glu Ala Leu Ile Leu Lys Ala Glu Thr Leu Arg Gln Gln Tyr Arg
 150 155 160 165

att gaa tca ctg ctg att aat tcc tat gac caa gat gtc caa gct cga 643
 Ile Glu Ser Leu Leu Ile Asn Ser Tyr Asp Gln Asp Val Gln Ala Arg
 170 175 180

tct tct acg att cgt gca tct cgg gtg tat ctg gaa gct cca tgg atc 691
 Ser Ser Thr Ile Arg Ala Ser Arg Val Tyr Leu Glu Ala Pro Trp Ile
 185 190 195

cga cac caa tac aaa ctg ctc aat gcc att gct cgg gtg cat tcc agc 739
 Arg His Gln Tyr Lys Leu Leu Asn Ala Ile Ala Arg Val His Ser Ser
 200 205 210

gaa gcg ctg ctg atc acc aaa tct ggc atc tgc acc ctc ttc ggc gag 787
 Glu Ala Leu Leu Ile Thr Lys Ser Gly Ile Cys Thr Leu Phe Gly Glu
 215 220 225

caa gat gac gta gcc cac att att gat ctg ttc aac agt ctt aat cga 835
 Gln Asp Asp Val Ala His Ile Ile Asp Leu Phe Asn Ser Leu Asn Arg
 230 235 240 245

caa cgt gcc cac ttc atg aaa acg tca gca ggt gcc cga att gcc caa 883
 Gln Arg Ala His Phe Met Lys Thr Ser Ala Gly Ala Arg Ile Ala Gln
 250 255 260

tta aat ggc gaa aca agc tca tat cgc cgt agt ttt atg atc tcc tac 931
 Leu Asn Gly Glu Thr Ser Ser Tyr Arg Arg Ser Phe Met Ile Ser Tyr
 265 270 275

gcc agc caa atc tct aga ctt ctc atc tca gca aaa gag gat gca ttc 979
 Ala Ser Gln Ile Ser Arg Leu Leu Ile Ser Ala Lys Glu Asp Ala Phe
 280 285 290

aac gaa cta gct ggt cag gca cca cta gct cac agc gcc atc gtt cot 1027
 Asn Glu Leu Ala Gly Gln Ala Pro Leu Ala His Ser Ala Ile Val Pro
 295 300 305

gtc cta gag aac aga agt gtg agg tca aag gaa gca ctg aag gaa acc 1075
 Val Leu Glu Asn Arg Ser Val Arg Ser Lys Glu Ala Leu Lys Glu Thr
 310 315 320 325

ttc ccg aat atg cgg aca atg acc ttc aaa tcg acc aac cga cga ggc 1123
 Phe Pro Asn Met Arg Thr Met Thr Phe Lys Ser Thr Asn Arg Arg Gly
 330 335 340

att att gac gga ttt aat gct gcc aat gaa tcc cac ctt ggc ggg gaa 1171
 Ile Ile Asp Gly Phe Asn Ala Ala Asn Glu Ser His Leu Gly Gly Glu
 345 350 355

tct gcc agc ttg gaa gac tca aca ttc atg ttc tagagcgggt gaaagcccca 1224

Ser Ala Ser Leu Glu Asp Ser Thr Phe Met Phe
360 365

ttt

1227

<210> 1708

<211> 368

<212> PRT

<213> Corynebacterium glutamicum

<400> 1708

Met Thr Leu Ser His Phe Ser Asp Asn Val Thr Asp Ala Gln Asp Ser
1 5 10 15

Tyr Arg Gln Ile Leu Glu Glu Ser Ile Ile Ser His Leu Gly Phe Cys
20 25 30

Ala Leu Arg Gly Trp Thr Pro Ala Asp Leu Arg His Glu Phe Ser Ala
35 40 45

Asp Ile Asp Pro Leu Leu Phe His Ala Leu Pro Glu Ile Ala Tyr Ser
50 55 60

Cys Ser Asp Glu Met Tyr Thr Leu Trp Val Asn Gly Thr Arg Ala Ala
65 70 75 80

Glu Thr Ser His Leu Pro Val Met Thr Leu Glu Lys Ile Leu Thr Glu
85 90 95

Leu Pro Lys Leu Ser Thr Leu Pro Asp Trp Ala Met Leu Ala Glu Leu
100 105 110

His Ala Leu Asp Asn Gln Asp Thr Ser Pro Met Thr Pro Ala Gln Ala
115 120 125

Lys Ala His His Arg Ile Thr Ala Leu Leu Lys Lys Ala Glu Ser Thr
130 135 140

Asn Phe Glu Glu Glu Ala Glu Ala Leu Ile Leu Lys Ala Glu Thr Leu
145 150 155 160

Arg Gln Gln Tyr Arg Ile Glu Ser Leu Leu Ile Asn Ser Tyr Asp Gln
165 170 175

Asp Val Gln Ala Arg Ser Ser Thr Ile Arg Ala Ser Arg Val Tyr Leu
180 185 190

Glu Ala Pro Trp Ile Arg His Gln Tyr Lys Leu Leu Asn Ala Ile Ala
195 200 205

Arg Val His Ser Ser Glu Ala Leu Leu Ile Thr Lys Ser Gly Ile Cys
210 215 220

Thr Leu Phe Gly Glu Gln Asp Asp Val Ala His Ile Ile Asp Leu Phe
225 230 235 240

Asn Ser Leu Asn Arg Gln Arg Ala His Phe Met Lys Thr Ser Ala Gly
245 250 255

Ala Arg Ile Ala Gln Leu Asn Gly Glu Thr Ser Ser Tyr Arg Arg Ser

260		265		270
Phe Met Ile Ser Tyr Ala Ser	Gln Ile Ser Arg Leu Leu Ile Ser Ala			
275	280	285		
Lys Glu Asp Ala Phe Asn Glu Leu Ala Gly Gln Ala Pro Leu Ala His				
290	295	300		
Ser Ala Ile Val Pro Val Leu Glu Asn Arg Ser Val Arg Ser Lys Glu				
305	310	315	320	
Ala Leu Lys Glu Thr Phe Pro Asn Met Arg Thr Met Thr Phe Lys Ser				
325	330	335		
Thr Asn Arg Arg Gly Ile Ile Asp Gly Phe Asn Ala Ala Asn Glu Ser				
340	345	350		
His Leu Gly Gly Glu Ser Ala Ser Leu Glu Asp Ser Thr Phe Met Phe				
355	360	365		

<210> 1709

<211> 768

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(745)

<223> RXA00325

<400> 1709

aggattttctc tgaggaatct agaagcagat taacttcgcg ttggcagcga ccgggataac 60

accgcggttg	cgggcaacgca	ggctcacaaa	ggacaccact	atg aca agc att att	115
				Met Thr Ser Ile Ile	
				1 5	

gca agc aac agc gac cta tcg gag gcg ctg cgc acc cac act gcg cag	163
Ala Ser Asn Ser Asp Leu Ser Glu Ala Leu Arg Thr His Thr Ala Gln	
10 15 20	

gcc cat gaa gag gcc gag cac tca acg ttt atg aat gat ctg ctc acc	211
Ala His Glu Glu Ala Glu His Ser Thr Phe Met Asn Asp Leu Thr	
25 30 35	

ggg aag ctc gat gcg cag gca ttt atc aag ttg cag gag caa tca tgg	259
Gly Lys Leu Asp Ala Gln Ala Phe Ile Lys Leu Gln Glu Gln Ser Trp	
40 45 50	

ttg ttc tac acc gct ttg gaa gct gca gct cgt gca tgt gca gag gat	307
Leu Phe Tyr Thr Ala Leu Glu Ala Ala Ala Arg Ala Cys Ala Glu Asp	
55 60 65	

tcc cgt gcg gct ggt ctg ctg gac cca cgc ctc gag cgc aag gaa acg	355
Ser Arg Ala Ala Gly Leu Leu Asp Pro Arg Leu Glu Arg Lys Glu Thr	
70 75 80 85	

ttg gaa gct gat ctg gat aag ctg cac gaa aac acc acc tgg cgt gac 403
 Leu Glu Ala Asp Leu Asp Lys Leu His Glu Asn Thr Thr Trp Arg Asp
 90 95 100
 aac gtc acg gcc act gca gcg aca gcg tct tat gtg gaa cgt ctt gaa 451
 Asn Val Thr Ala Thr Ala Ala Thr Ala Ser Tyr Val Glu Arg Leu Glu
 105 110 115
 agc atc gaa gcg gcc aag gat ttc cct cgt ttg gtt gct cat cac tat 499
 Ser Ile Glu Ala Ala Lys Asp Phe Pro Arg Leu Val Ala His His Tyr
 120 125 130
 gtc cgc tac ctg ggt gat ttg tcc ggt ggg cag gtt att gca cgt ctg 547
 Val Arg Tyr Leu Gly Asp Leu Ser Gly Gly Gln Val Ile Ala Arg Leu
 135 140 145
 gtg aac agg gaa tat gga gtt tcg gaa gag gcg ttg agc ttc tac tgc 595
 Val Asn Arg Glu Tyr Gly Val Ser Glu Glu Ala Leu Ser Phe Tyr Cys
 150 155 160 165
 ttt gaa gat ctt gcc aag ctc aaa ccg tac aag gat aat tac cgt gca 643
 Phe Glu Asp Leu Gly Lys Leu Lys Pro Tyr Lys Asp Asn Tyr Arg Ala
 170 175 180
 gag ctt gat gct ttg gaa tta aca gca gag gag cgt gct gcg ttg ctg 691
 Glu Leu Asp Ala Leu Glu Leu Thr Ala Glu Glu Arg Ala Ala Leu Leu
 185 190 195
 gat gaa gca tct gat gcg ttc agg ttt aat cag caa gtt ttt cag gct 739
 Asp Glu Ala Ser Asp Ala Phe Arg Phe Asn Gln Gln Val Phe Gln Ala
 200 205 210
 ctt gct taaccgaagg tgaagtcttg gcg 768
 Leu Ala
 215
 <210> 1710
 <211> 215
 <212> PRT
 <213> *Corynebacterium glutamicum*
 <400> 1710
 Met Thr Ser Ile Ile Ala Ser Asn Ser Asp Leu Ser Glu Ala Leu Arg
 1 5 10 15
 Thr His Thr Ala Gln Ala His Glu Glu Ala Glu His Ser Thr Phe Met
 20 25 30
 Asn Asp Leu Leu Thr Gly Lys Leu Asp Ala Gln Ala Phe Ile Lys Leu
 35 40 45
 Gln Glu Gln Ser Trp Leu Phe Tyr Thr Ala Leu Glu Ala Ala Ala Arg
 50 55 60
 Ala Cys Ala Glu Asp Ser Arg Ala Ala Gly Leu Leu Asp Pro Arg Leu
 65 70 75 80
 Glu Arg Lys Glu Thr Leu Glu Ala Asp Leu Asp Lys Leu His Glu Asn
 85 90 95

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Thr Thr Trp Arg Asp Asn Val Thr Ala Thr Ala Thr Ala Ser Tyr
      100                      105                      110

Val Glu Arg Leu Glu Ser Ile Glu Ala Ala Lys Asp Phe Pro Arg Leu
      115                      120                      125

Val Ala His His Tyr Val Arg Tyr Leu Gly Asp Leu Ser Gly Gly Gln
      130                      135                      140

Val Ile Ala Arg Leu Val Asn Arg Glu Tyr Gly Val Ser Glu Glu Ala
      145                      150                      155                      160

Leu Ser Phe Tyr Cys Phe Glu Asp Leu Gly Lys Leu Lys Pro Tyr Lys
      165                      170                      175

Asp Asn Tyr Arg Ala Glu Leu Asp Ala Leu Glu Leu Thr Ala Glu Glu
      180                      185                      190

Arg Ala Ala Leu Leu Asp Glu Ala Ser Asp Ala Phe Arg Phe Asn Gln
      195                      200                      205

Gln Val Phe Gln Ala Leu Ala
      210                      215

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<210> 1711

<211> 603

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(580)

<223> RXA00326

<400> 1711

cctgatcttt gccctaagt ggtttacggg ctggaaaatg gtacgtagtc tcgggtgtaa 60

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agcacacttc ggtactcgac aggaagttag gaattccacc atg gca atc aag ctg 115
              Met Ala Ile Lys Leu
              1                      5

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tcc att gac cta tca gat gca aca ttc gca gaa ctt tgc gca gtc atc 163
Ser Ile Asp Leu Ser Asp Ala Thr Phe Ala Glu Leu Ser Ala Val Ile
      10                      15                      20

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ggt tac gca cat cag ttg ggt gtt gat gcg gat gag aag ctc acc ttt 211
Gly Tyr Ala His Gln Leu Gly Val Asp Ala Asp Glu Lys Leu Thr Phe
      25                      30                      35

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gaa ggt aca gtc ctt aac att gaa ttc gac ggc gac ctt cag ttt gat 259
Glu Gly Thr Val Leu Asn Ile Glu Phe Asp Gly Asp Leu Gln Phe Asp
      40                      45                      50

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gat gtt ttt gat gcc ttt gat gag gcg gaa att gag ctc gac aac cct 307
Asp Val Phe Asp Ala Phe Asp Glu Ala Glu Ile Glu Leu Asp Asn Pro
      55                      60                      65

```

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cgc gaa gac ggc ccc atc tac gca gat gat ctg atc gat gag gat gag 355
Arg Glu Asp Gly Pro Ile Tyr Ala Asp Asp Leu Ile Asp Glu Asp Glu
      70                      75                      80                      85

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gac tac cgc gca cag acc aag agc cag atc aac gac gag gtt atc aac 403
Asp Tyr Arg Ala Gln Thr Lys Ser Gln Ile Asn Asp Glu Val Ile Asn
          90                      95
gag atc cgc gat ggt att tca agc ttc gtt gat ggc atc gta aat ggc 451
Glu Ile Arg Asp Gly Ile Ser Ser Phe Val Asp Gly Ile Val Asn Gly
          105                      110
ctt ggc cag ggt cgc cgc ggt gga cgt tac ggt gat ttc ggt ggg cca 499
Leu Gly Gln Gly Arg Arg Gly Gly Arg Tyr Gly Asp Phe Gly Gly Pro
          120                      125
cgc ggc cct cgc ggt cca cgc aat gac ggt cca ttc ggc cca ttt gga 547
Arg Gly Pro Arg Gly Pro Arg Asn Asp Gly Pro Phe Gly Pro Phe Gly
          135                      140
cca ttc ggt ccg gga tac cgc ggt ccg cgt ttc tagcgggttac ggtcggttt 600
Pro Phe Gly Pro Gly Tyr Arg Gly Pro Arg Phe
          150                      160
tag
903

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<210> 1712

<211> 160

<212> PRT

<213> Corynebacterium glutamicum

<400> 1712

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Met Ala Ile Lys Leu Ser Ile Asp Leu Ser Asp Ala Thr Phe Ala Glu
  1              5              10              15

```

```

Leu Ser Ala Val Ile Gly Tyr Ala His Gln Leu Gly Val Asp Ala Asp
          20              25              30

```

```

Glu Lys Leu Thr Phe Glu Gly Thr Val Leu Asn Ile Glu Phe Asp Gly
          35              40              45

```

```

Asp Leu Gln Phe Asp Asp Val Phe Asp Ala Phe Asp Glu Ala Glu Ile
          50              55              60

```

```

Glu Leu Asp Asn Pro Arg Glu Asp Gly Pro Ile Tyr Ala Asp Asp Leu
          65              70              75              80

```

```

Ile Asp Glu Asp Glu Asp Tyr Arg Ala Gln Thr Lys Ser Gln Ile Asn
          85              90              95

```

```

Asp Glu Val Ile Asn Glu Ile Arg Asp Gly Ile Ser Ser Phe Val Asp
          100              105              110

```

```

Gly Ile Val Asn Gly Leu Gly Gln Gly Arg Arg Gly Gly Arg Tyr Gly
          115              120              125

```

```

Asp Phe Gly Gly Pro Arg Gly Pro Arg Gly Pro Arg Asn Asp Gly Pro
          130              135              140

```

```

Phe Gly Pro Phe Gly Pro Phe Gly Pro Gly Tyr Arg Gly Pro Arg Phe
          145              150              155              160

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<210> 1713
 <211> 594
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(571)
 <223> RXA00336

<400> 1713
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 gcagtatccg cccctacat gtttggattt gattgtaaca atg gca aag ccg aag 115
 Met Ala Lys Pro Lys
 1 5
 aga agt tgg ctt gac gga ccc gaa att cca gct gat ttt gac gat cct 163
 Arg Ser Trp Leu Asp Gly Pro Glu Ile Pro Ala Asp Phe Asp Asp Pro
 10 15 20
 gat gca ccc gcc agg tgg cct gcc gaa aag ttg ggg ctt cct caa gaa 211
 Asp Ala Pro Gly Arg Trp Pro Gly Glu Lys Leu Gly Leu Pro Gln Glu
 25 30 35
 ggg gcc gcc tct ctg tcc tca gtg gct cgt cgt atc gcc ggg gtc tgc 259
 Gly Ala Gly Ser Leu Ser Ser Val Ala Arg Arg Ile Gly Gly Val Cys
 40 45 50
 gtg gac tgg ggt gtt tcc tgg gtt att gct att gtg ctg tcc aat ttc 307
 Val Asp Trp Gly Val Ser Trp Val Ile Ala Ile Val Leu Ser Asn Phe
 55 60 65
 acg gat gtg ctg gcc gat gta gcg aca tcc acg ctc att att ttc gtg 355
 Thr Asp Val Leu Gly Asp Val Ala Thr Ser Thr Leu Ile Ile Phe Val
 70 75 80 85
 atc ctg ggt tgg ctt acc ggt tgg atc ttt gct cgc acc cca ggt cat 403
 Ile Leu Gly Trp Leu Thr Gly Trp Ile Phe Ala Arg Thr Pro Gly His
 90 95 100
 gcc gtg ttt gcc atg gcc ctt gcg cgt gtg gat gca gag gaa cgt gtg 451
 Ala Val Phe Gly Met Gly Leu Ala Arg Val Asp Ala Glu Glu Arg Val
 105 110 115
 gcc tgg tgg cgt gcg ctg gtt cgc cca ctg ctg acg atc ttg att ctg 499
 Gly Trp Trp Arg Ala Leu Val Arg Pro Leu Leu Thr Ile Leu Ile Leu
 120 125 130
 cct gcc gtg atg gtg gat gct gac gcc cgt ggg ctc cac gac aag gca 547
 Pro Ala Val Met Val Asp Ala Asp Gly Arg Gly Leu His Asp Lys Ala
 135 140 145
 acg gga act gca gtt atc cgc ggg taatttgctc tgagtgaaat tta 594
 Thr Gly Thr Ala Val Ile Arg Gly
 150 155

<210> 1714

<211> 157

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1714

Met Ala Lys Pro Lys Arg Ser Trp Leu Asp Gly Pro Glu Ile Pro Ala
1 5 10 15Asp Phe Asp Asp Pro Asp Ala Pro Gly Arg Trp Pro Gly Glu Lys Leu
20 25 30Gly Leu Pro Gln Glu Gly Ala Gly Ser Leu Ser Ser Val Ala Arg Arg
35 40 45Ile Gly Gly Val Cys Val Asp Trp Gly Val Ser Trp Val Ile Ala Ile
50 55 60Val Leu Ser Asn Phe Thr Asp Val Leu Gly Asp Val Ala Thr Ser Thr
65 70 75 80Leu Ile Ile Phe Val Ile Leu Gly Trp Leu Thr Gly Trp Ile Phe Ala
85 90 95Arg Thr Pro Gly His Ala Val Phe Gly Met Gly Leu Ala Arg Val Asp
100 105 110Ala Glu Glu Arg Val Gly Trp Trp Arg Ala Leu Val Arg Pro Leu Leu
115 120 125Thr Ile Leu Ile Leu Pro Ala Val Met Val Asp Ala Asp Gly Arg Gly
130 135 140Leu His Asp Lys Ala Thr Gly Thr Ala Val Ile Arg Gly
145 150 155

<210> 1715

<211> 525

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(525)

<223> RXA00337

<400> 1715

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Asp Val Glu Gly Gly Val Glu Lys His Ser Leu Ser Thr Ala Asp Ile
1 5 10 15gca gct cgc gca cac gcc cat atg aaa tcc cat gat gtt ttg ggg cgg 96
Ala Ala Arg Ala His Ala His Met Lys Ser His Asp Val Leu Gly Arg
20 25 30cag act acg ccg cct cag ccg gag ggc ggc gtt gct gcc cgg ttg ggc 144
Gln Thr Thr Pro Pro Gln Pro Glu Gly Gly Val Ala Ala Arg Leu Gly
35 40 45

ggg att gcg tgg aca atg atc cat aag caa atg ctt tcg cgt gac aca 192

Gly	Ile	Ala	Trp	Thr	Met	Ile	His	Lys	Gln	Met	Leu	Ser	Arg	Asp	Thr		
50						55					60						
aaa	ggc	ctg	gat	atc	acc	gtg	ttg	agc	acc	att	cct	gag	ggg	gtg	ggg	240	
Lys	Gly	Leu	Asp	Ile	Thr	Val	Leu	Ser	Thr	Ile	Pro	Glu	Gly	Val	Gly		
65					70					75				80			
ctg	ggg	gaa	aat	tcc	gcc	atg	gat	gtg	gcg	ctc	gca	ttg	gcg	ctg	tat	288	
Leu	Gly	Glu	Asn	Ser	Ala	Met	Asp	Val	Ala	Leu	Ala	Leu	Ala	Leu	Tyr		
				85					90					95			
cgg	gaa	aat	att	gag	gaa	gcc	ccc	acg	aag	gcg	cgc	att	gcg	gac	att	336	
Arg	Glu	Asn	Ile	Glu	Glu	Ala	Pro	Thr	Lys	Ala	Arg	Ile	Ala	Asp	Ile		
			100					105					110				
tgt	tcg	cag	tcc	gca	ttc	atg	ttc	agt	gag	act	tca	gtg	ttg	cgt	gcg	384	
Cys	Ser	Gln	Ser	Ala	Phe	Met	Phe	Ser	Glu	Thr	Ser	Val	Leu	Arg	Ala		
			115				120					125					
cgg	cac	acc	gag	gcg	ttg	cgg	ggg	gaa	act	gga	cac	att	tcg	gtg	gtt	432	
Arg	His	Thr	Glu	Ala	Leu	Arg	Gly	Glu	Thr	Gly	His	Ile	Ser	Val	Val		
			130			135					140						
gat	tac	gcc	gat	ggg	tcg	gtc	act	cag	gcg	cca	cat	ccg	gtg	agt	cgt	480	
Asp	Tyr	Ala	Asp	Gly	Ser	Val	Thr	Gln	Ala	Pro	His	Pro	Val	Ser	Arg		
			145			150				155					160		
tcc	gct	ggg	ttg	tcg	gca	ttt	gtt	gct	gct	gcg	caa	act	gaa	act		525	
Ser	Ala	Gly	Leu	Ser	Ala	Phe	Val	Ala	Ala	Ala	Gln	Thr	Glu	Thr			
				165				170						175			

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 <211> 175
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 1716
 Asp Val Glu Gly Gly Val Glu Lys His Ser Leu Ser Thr Ala Asp Ile
 1 5 10 15
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 20 25 30
 Gln Thr Thr Pro Pro Gln Pro Glu Gly Gly Val Ala Ala Arg Leu Gly
 35 40 45
 Gly Ile Ala Trp Thr Met Ile His Lys Gln Met Leu Ser Arg Asp Thr
 50 55 60
 Lys Gly Leu Asp Ile Thr Val Leu Ser Thr Ile Pro Glu Gly Val Gly
 65 70 75 80
 Leu Gly Glu Asn Ser Ala Met Asp Val Ala Leu Ala Leu Ala Leu Tyr
 85 90 95
 Arg Glu Asn Ile Glu Glu Ala Pro Thr Lys Ala Arg Ile Ala Asp Ile
 100 105 110
 Cys Ser Gln Ser Ala Phe Met Phe Ser Glu Thr Ser Val Leu Arg Ala
 115 120 125

Arg His Thr Glu Ala Leu Arg Gly Glu Thr Gly His Ile Ser Val Val
130 135 140

Asp Tyr Ala Asp Gly Ser Val Thr Gln Ala Pro His Pro Val Ser Arg
145 150 155 160

Ser Ala Gly Leu Ser Ala Phe Val Ala Ala Gln Thr Glu Thr
165 170 175

<210> 1717

<211> 840

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(817)

<223> RXA00339

<400> 1717

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agtgaactaa attcttgaga actaaaaaag gagaacttca atg aag ctg gac cca 115
Met Lys Leu Asp Pro
1 5

tct ctg cac aaa acc ctg ctg cag ctc gcc acc acc ctg cgc acc caa 163
Ser Leu His Lys Thr Leu Leu Gln Leu Ala Thr Thr Leu Arg Thr Gln
10 15 20

aac gcc aac tcc gca cgc aag acc acc cgc gag cag gaa gct gta gac 211
Asn Ala Asn Ser Ala Pro Lys Thr Thr Pro Glu Gln Glu Ala Val Asp
25 30 35

aag gct gtc gct gaa ctt tcc cgc aac cgc gac gct gca tcc gct gga 259
Lys Ala Val Ala Glu Leu Ser Arg Asn Arg Asp Ala Ala Ser Ala Gly
40 45 50

caa atg gct gtc gat gac atg gaa aac gaa atc ctg cgc att cag tcc 307
Gln Met Ala Val Asp Asp Met Glu Asn Glu Ile Leu Arg Ile Gln Ser
55 60 65

gac gaa cgc aaa ctg cgc cgc cgc aag aaa gac ggc cag gac gca ctc 355
Asp Glu Arg Lys Leu Arg Arg Arg Lys Lys Asp Gly Gln Asp Ala Leu
70 75 80 85

ggt gca gaa act gac gaa gag cgt cgc cgc gac ctc aac cac gac gtc 403
Gly Ala Glu Thr Asp Glu Glu Arg Arg Arg Asp Leu Asn His Asp Val
90 95 100

tac act gcg aag tcc cgc atc gct gac ctc atg agc gaa ctg caa gaa 451
Tyr Thr Ala Lys Ser Arg Ile Ala Asp Leu Met Ser Glu Leu Gln Glu
105 110 115

gct cac aat gaa atc cat gcg ctg cgc aac aac cgc gac ctc gca cag 499
Ala His Asn Glu Ile His Ala Leu Arg Asn Asn Arg Asp Leu Ala Gln
120 125 130

tct cgc gtc aaa gac acc gaa cgc aaa gtt gcc gac gcc cgc gca gcc 547

Ser Arg Val Lys Asp Thr Glu Arg Lys Val Ala Asp Ala Arg Ala Ala
135 140 145

gca gaa gcc gcc gca gca gca acc cca gaa ggt gaa gac cca gca gta 595
Ala Glu Ala Ala Ala Ala Ala Thr Pro Glu Gly Glu Asp Pro Ala Val
150 155 160 165

gtc atc gca cac ctg gaa gag aaa ctt ccc tcc gaa gca ctg gca gaa 643
Val Ile Ala His Leu Glu Glu Lys Leu Pro Ser Glu Ala Leu Ala Glu
170 175 180

ttc cat gca caa cgc ctc gaa aac ggc gta ggc gca gca ctc ttc aac 691
Phe His Ala Gln Arg Leu Glu Asn Gly Val Gly Ala Ala Leu Phe Asn
185 190 195

ggc cgc tcc tgc agc gga tgc gcc atg gtt ctc cct gca acc ggt atc 739
Gly Arg Ser Cys Ser Gly Cys Ala Met Val Leu Pro Ala Thr Gly Ile
200 205 210

tcc gac atc cgc aac acc ccc aaa gat gag gtt cca cag tgc cca gaa 787
Ser Asp Ile Arg Asn Thr Pro Lys Asp Glu Val Pro Gln Cys Pro Glu
215 220 225

tgt ggc tct tac ctc atc act gac atc tct tagaaagacc acccagttaa 837
Cys Gly Ser Tyr Leu Ile Thr Asp Ile Ser
230 235

att 840

<210> 1718
<211> 239
<212> PRT
<213> Corynebacterium glutamicum

<400> 1718
Met Lys Leu Asp Pro Ser Leu His Lys Thr Leu Leu Gln Leu Ala Thr
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Thr Leu Arg Thr Gln Asn Ala Asn Ser Ala Pro Lys Thr Thr Pro Glu
20 25 30
Gln Glu Ala Val Asp Lys Ala Val Ala Glu Leu Ser Arg Asn Arg Asp
35 40 45
Ala Ala Ser Ala Gly Gln Met Ala Val Asp Asp Met Glu Asn Glu Ile
50 55 60
Leu Arg Ile Gln Ser Asp Glu Arg Lys Leu Arg Arg Arg Lys Lys Asp
65 70 75 80
Gly Gln Asp Ala Leu Gly Ala Glu Thr Asp Glu Glu Arg Arg Arg Asp
85 90 95
Leu Asn His Asp Val Tyr Thr Ala Lys Ser Arg Ile Ala Asp Leu Met
100 105 110
Ser Glu Leu Gln Glu Ala His Asn Glu Ile His Ala Leu Arg Asn Asn
115 120 125
Arg Asp Leu Ala Gln Ser Arg Val Lys Asp Thr Glu Arg Lys Val Ala

130	135	140	
Asp Ala Arg Ala Ala	Ala Glu Ala Ala	Ala Ala Thr Pro Glu Gly	
145	150	155	160
Glu Asp Pro Ala Val	Val Ile Ala His Leu Glu	Glu Lys Leu Pro Ser	
165	170	175	
Glu Ala Leu Ala Glu	Phe His Ala Gln Arg Leu	Glu Asn Gly Val Gly	
180	185	190	
Ala Ala Leu Phe Asn	Gly Arg Ser Cys Ser Gly	Cys Ala Met Val Leu	
195	200	205	
Pro Ala Thr Gly Ile	Ser Asp Ile Arg Asn Thr	Pro Lys Asp Glu Val	
210	215	220	
Pro Gln Cys Pro Glu	Cys Gly Ser Tyr Leu Ile	Thr Asp Ile Ser	
225	230	235	
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<211> 1082			
<212> DNA			
<213> Corynebacterium glutamicum			
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<222> (1)..(1059)			
<223> RXA00349			
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Glu Lys Ile Leu Asp	Glu Leu Glu Gln Ser Pro	Ala Ser Tyr Gly Phe	
1	5	10	15
cct gtt gcg ttg ctt	ggc tgg cca atg atg	ggt ggt gct gtt gct	96
Pro Val Ala Leu Leu	Gly Trp Pro Met Met	Gly Gly Ala Val Ala	
20	25	30	
ctg ttg ggt ggt gga	tgc cag gtt tcc cta att	gct ttt att acc gcg	144
Leu Leu Gly Gly Cys	Gln Val Ser Leu Ile	Ala Phe Ile Thr Ala	
35	40	45	
ttc acg atc att gcc	acg acg tca ttt ttg	gga aag aag ggt ttg	192
Phe Thr Ile Ile Ala	Thr Thr Ser Phe Leu	Gly Lys Lys Gly Leu	
50	55	60	
act ttc ttc caa aat	gtt gtt ggt ggt ttt	att gcc acg ctg cct	240
Thr Phe Phe Gln Asn	Val Val Gly Gly Phe	Ile Ala Thr Leu Pro	
65	70	75	80
tcg att gct tat tct	ttg gcg ttg caa ttt	ggt ctt gag atc aaa	288
Ser Ile Ala Tyr Ser	Leu Ala Leu Gln Phe	Gly Leu Glu Ile Lys	
85	90	95	
agc cag atc atc gca	tct gga att gtt gtg	ctg ttg gca ggt ttg	336
Ser Gln Ile Ile Ala	Ser Gly Ile Val Val	Leu Leu Ala Gly Leu	
100	105	110	
ctc gtg caa tct ctg	cag gac ggc atc acg	ggc gct ccg gtg aca	384

Leu	Val	Gln	Ser	Leu	Gln	Asp	Gly	Ile	Thr	Gly	Ala	Pro	Val	Thr	Ala	
		115					120					125				
agt	gca	cga	ttt	ttc	gaa	aca	ctc	ctg	ttt	acc	ggc	ggc	att	ggt	gct	432
Ser	Ala	Arg	Phe	Phe	Glu	Ile	Leu	Leu	Phe	Thr	Gly	Gly	Ile	Val	Ala	
	130					135					140					
ggc	gtg	ggt	ttg	ggc	att	cag	ctt	tct	gaa	atc	ttg	cat	gtc	atg	ttg	480
Gly	Val	Gly	Leu	Gly	Ile	Gln	Leu	Ser	Glu	Ile	Leu	His	Val	Met	Leu	
	145				150					155					160	
cct	gcc	atg	gag	tcc	gct	gca	gca	cct	aat	tat	tgc	tct	aca	ttc	gcc	528
Pro	Ala	Met	Glu	Ser	Ala	Ala	Ala	Pro	Asn	Tyr	Ser	Ser	Thr	Phe	Ala	
				165					170					175		
cgc	att	atc	gct	ggt	ggc	gtc	acc	gca	gcg	gcc	ttc	gca	gtg	ggt	tgt	576
Arg	Ile	Ile	Ala	Gly	Gly	Val	Thr	Ala	Ala	Ala	Phe	Ala	Val	Gly	Cys	
			180					185					190			
tac	gcg	gag	tggt	tcc	tcg	gtg	att	att	gcg	ggg	ctt	act	gcg	ctg	atg	624
Tyr	Ala	Glu	Trp	Ser	Ser	Val	Ile	Ile	Ala	Gly	Leu	Thr	Ala	Leu	Met	
		195					200					205				
ggt	tct	gcg	ttt	tat	tac	ctc	ttc	gtt	gtt	tat	tta	ggc	ccc	gtc	tct	672
Gly	Ser	Ala	Phe	Tyr	Tyr	Leu	Phe	Val	Val	Tyr	Leu	Gly	Pro	Val	Ser	
		210				215					220					
gcc	gct	gcg	att	gct	gca	aca	gca	gtt	ggt	ttc	act	ggt	ggt	ttg	ctt	720
Ala	Ala	Ala	Ile	Ala	Ala	Thr	Ala	Val	Gly	Phe	Thr	Gly	Gly	Leu	Leu	
	225				230					235				240		
gcc	cgt	cga	ttc	ttg	att	cca	cgg	ttg	att	gtg	gcg	att	gcc	ggc	atc	768
Ala	Arg	Arg	Phe	Leu	Ile	Pro	Pro	Leu	Ile	Val	Ala	Ile	Ala	Gly	Ile	
			245					250					255			
aca	cca	atg	ctt	cca	ggt	cta	gca	att	tac	cgc	gga	atg	tac	gcc	acc	816
Thr	Pro	Met	Leu	Pro	Gly	Leu	Ala	Ile	Tyr	Arg	Gly	Met	Tyr	Ala	Thr	
			260					265					270			
ctg	aat	gat	caa	aca	ctc	atg	ggt	ttc	acc	aac	att	gcg	gtt	gct	tta	864
Leu	Asn	Asp	Gln	Thr	Leu	Met	Gly	Phe	Thr	Asn	Ile	Ala	Val	Ala	Leu	
		275					280					285				
gcc	act	gct	tca	tca	ctt	gcc	gct	ggc	gtg	gtt	ttg	ggt	gag	tggt	att	912
Ala	Thr	Ala	Ser	Ser	Leu	Ala	Ala	Gly	Val	Val	Leu	Gly	Glu	Trp	Ile	
		290				295					300					
gcc	cgc	agg	cta	cgt	cgt	cca	cca	cgc	ttc	aac	cca	tac	cgt	gca	ttt	960
Ala	Arg	Arg	Leu	Arg	Arg	Pro	Pro	Arg	Phe	Asn	Pro	Tyr	Arg	Ala	Phe	
	305				310					315				320		
acc	aag	gcg	aat	gag	ttc	tcc	ttc	cag	gag	gaa	gct	gag	cag	aat	cag	1008
Thr	Lys	Ala	Asn	Glu	Phe	Ser	Phe	Gln	Glu	Glu	Ala	Glu	Gln	Asn	Gln	
			325					330						335		
cgc	cgg	cag	aga	aaa	cgt	cca	aag	act	aat	cag	aga	ttc	ggt	aat	aaa	1056
Arg	Arg	Gln	Arg	Lys	Arg	Pro	Lys	Thr	Asn	Gln	Arg	Phe	Gly	Asn	Lys	
			340					345					350			
agg	taaaaatcaa	cctgcttagg	cgt													1082
Arg																

<210> 1720

<211> 353

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1720

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Glu Lys Ile Leu Asp Glu Leu Glu Gln Ser Pro Ala Ser Tyr Gly Phe
 1           5           10           15

Pro Val Ala Leu Leu Gly Trp Pro Met Met Gly Gly Ala Val Ala Val
           20           25           30

Leu Leu Gly Gly Gly Cys Gln Val Ser Leu Ile Ala Phe Ile Thr Ala
          35           40           45

Phe Thr Ile Ile Ala Thr Thr Ser Phe Leu Gly Lys Lys Gly Leu Pro
 50           55           60

Thr Phe Phe Gln Asn Val Val Gly Gly Phe Ile Ala Thr Leu Pro Ala
 65           70           75           80

Ser Ile Ala Tyr Ser Leu Ala Leu Gln Phe Gly Leu Glu Ile Lys Pro
           85           90           95

Ser Gln Ile Ile Ala Ser Gly Ile Val Leu Leu Ala Gly Leu Thr
          100          105          110

Leu Val Gln Ser Leu Gln Asp Gly Ile Thr Gly Ala Pro Val Thr Ala
          115          120          125

Ser Ala Arg Phe Phe Glu Thr Leu Leu Phe Thr Gly Gly Ile Val Ala
          130          135          140

Gly Val Gly Leu Gly Ile Gln Leu Ser Glu Ile Leu His Val Met Leu
          145          150          155          160

Pro Ala Met Glu Ser Ala Ala Ala Pro Asn Tyr Ser Ser Thr Phe Ala
          165          170          175

Arg Ile Ile Ala Gly Gly Val Thr Ala Ala Ala Phe Ala Val Gly Cys
          180          185          190

Tyr Ala Glu Trp Ser Ser Val Ile Ile Ala Gly Leu Thr Ala Leu Met
          195          200          205

Gly Ser Ala Phe Tyr Tyr Leu Phe Val Val Tyr Leu Gly Pro Val Ser
          210          215          220

Ala Ala Ala Ile Ala Ala Thr Ala Val Gly Phe Thr Gly Gly Leu Leu
          225          230          235          240

Ala Arg Arg Phe Leu Ile Pro Pro Leu Ile Val Ala Ile Ala Gly Ile
          245          250          255

Thr Pro Met Leu Pro Gly Leu Ala Ile Tyr Arg Gly Met Tyr Ala Thr
          260          265          270

Leu Asn Asp Gln Thr Leu Met Gly Phe Thr Asn Ile Ala Val Ala Leu

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275	280	285
Ala Thr Ala Ser Ser Leu Ala Ala Gly Val Val Leu Gly Glu Trp Ile		
290	295	300
Ala Arg Arg Leu Arg Arg Pro Pro Arg Phe Asn Pro Tyr Arg Ala Phe		
305	310	315
Thr Lys Ala Asn Glu Phe Ser Phe Gln Glu Glu Ala Glu Gln Asn Gln		
	325	330
		335
Arg Arg Gln Arg Lys Arg Pro Lys Thr Asn Gln Arg Phe Gly Asn Lys		
	340	345
		350
Arg		

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<211> 149

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(126)

<223> RXA00355

<400> 1721

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Ile Ala Phe Gly Arg Ala Ala His Arg Met Lys Gln Gln Gly Gln Ser

1

5

10

15

gga gct ttc acc gtc ctc gaa gtt gct cca tac ctg ctc tcc cca gag 96

Gly Ala Phe Thr Val Leu Glu Val Ala Pro Tyr Leu Leu Ser Pro Glu

20

25

30

aac ttg gac gat ctg atc gca cgc gac gtc taatttagct cgaggggcaa 146

Asn Leu Asp Asp Leu Ile Ala Arg Asp Val

35

40

gga

149

<210> 1722

<211> 42

<212> PRT

<213> Corynebacterium glutamicum

<400> 1722

Ile Ala Phe Gly Arg Ala Ala His Arg Met Lys Gln Gln Gly Gln Ser

1

5

10

15

Gly Ala Phe Thr Val Leu Glu Val Ala Pro Tyr Leu Leu Ser Pro Glu

20

25

30

Asn Leu Asp Asp Leu Ile Ala Arg Asp Val

35

40

<210> 1723

<213> *Corynebacterium glutamicum*

<223> RXA00375

cagcctgtca aaatgctcac cgactacgca ccagaagacg ctaaacggta agtactgaag 60

gag aag tagaacggtt cgaccgtact ttt 62
Glu Lys

<210> 1724

<211> 167

<212> PRT

<213> Corynebacterium glutamicum

<400> 1724

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20 25 30Val Val Phe Trp Met Leu Phe Ala Thr Ala Ala Phe Met Ile Phe Thr
35 40 45Gly Leu Val Met Tyr Thr Ala Gly Tyr Thr Gly Pro Asp Asp Val Asp
50 55 60Glu Ser Tyr Lys Ala Val Val Asn Asn Gln Glu Phe Ile Gly Gly
65 70 75 80Ile Asn Ala Phe Ala Gly Val Val Ile Ala Ala Leu Thr Ser Gln Leu
85 90 95Pro Lys Gly Gly Lys Asn Pro Arg Arg Leu Leu Leu Ala Ile Met Leu
100 105 110Leu Val Leu Leu Thr Asp Leu Leu Ser Phe Ala Thr Arg Ala Gly Gly
115 120 125Phe Ala Leu Ala Ile Ile Ala Val Leu Leu Ala Leu Glu Ala Leu Leu
130 135 140Met Phe Arg Pro Ala Val Asn Asp His Ile Asp Arg Asn His Met Ala
145 150 155 160Arg Val Met Asn Arg Glu Lys
165

<210> 1725

<211> 744

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(721)

<223> RXA00380

<400> 1725

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cgtgcattac aacgaaccag ctcaggagat ttgatcactc gtg cgt ttg acc aaa 115
Val Arg Leu Thr Lys
1 5cta gca gca aca atc ggc tgc gtg aca ctc agc gga ctt gcg cta gta 163
Leu Ala Ala Thr Ile Gly Cys Val Thr Leu Ser Gly Leu Ala Leu Val
10 15 20

gcc tgc agc agt gac agt acc gct ggt act gac gct gtt gct gtc ggc 211
Ala Cys Ser Ser Asp Ser Thr Ala Gly Thr Asp Ala Val Ala Val Gly
25 30 35

gga acc ttc caa ttc cac tcc ccg gat gga aag atg gaa att ttc tac 259
Gly Thr Phe Gln Phe His Ser Pro Asp Gly Lys Met Glu Ile Phe Tyr
40 45 50

gac gag gct gac cgt caa caa ctc ccc gac att ggt gga gat tcc ctc 307
Asp Glu Ala Asp Arg Gln Gln Leu Pro Asp Ile Gly Gly Asp Ser Leu
55 60 65

atg gaa gag ggc aca cag atc aac ctg tct gat ttc gaa aac caa gtt 355
Met Glu Glu Gly Thr Gln Ile Asn Leu Ser Asp Phe Glu Asn Gln Val
70 75 80 85

gtc atc ctc aat gcg tgg ggg cag tgg tgt gca ccg tgc cgc tcc gaa 403
Val Ile Leu Asn Ala Trp Gly Gln Trp Cys Ala Pro Cys Arg Ser Glu
90 95 100

tcc gat gat ctc cag att atc cat gag gaa ctc caa gct gcc gga aac 451
Ser Asp Asp Leu Gln Ile Ile His Glu Glu Gln Ala Ala Gly Asn
105 110 115

ggc gac acc cct ggt ggc acc gtg ttg ggt atc aat gtg cgt gat tac 499
Gly Asp Thr Pro Gly Gly Thr Val Leu Gly Ile Asn Val Arg Asp Tyr
120 125 130

tcc cgc gac atc gcc caa gac ttt gtc acc gac aac ggc ctt gat tac 547
Ser Arg Asp Ile Ala Gln Asp Phe Val Thr Asp Asn Gly Leu Asp Tyr
135 140 145

cca agc att tac gat cca cca ttt atg aca gca gca tcc ctc ggt ggt 595
Pro Ser Ile Tyr Asp Pro Pro Phe Met Thr Ala Ala Ser Leu Gly Gly
150 155 160 165

gtt ccc gca tcg gtg atc cca acc acc atc gtg ctg gat aaa cag cac 643
Val Pro Ala Ser Val Ile Pro Thr Thr Ile Val Leu Asp Lys Gln His
170 175 180

cgc ccc gca gca gtg ttc ttg cgc gaa gtc acc tcc aaa gat gtg ttg 691
Arg Pro Ala Ala Val Phe Leu Arg Glu Val Thr Ser Lys Asp Val Leu
185 190 195

gat gtt gcg ttg cca ttg gta gat gag gcc taaatgtctg agattgtggt 741
Asp Val Ala Leu Pro Leu Val Asp Glu Ala
200 205

agc 744

<210> 1726

<211> 207

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1726

Val Arg Leu Thr Lys Leu Ala Ala Thr Ile Gly Cys Val Thr Leu Ser
1 5 10 15

Gly Leu Ala Leu Val Ala Cys Ser Ser Asp Ser Thr Ala Gly Thr Asp

20 25 30
 Ala Val Ala Val Gly Gly Thr Phe Gln Phe His Ser Pro Asp Gly Lys
 35 40 45
 Met Glu Ile Phe Tyr Asp Glu Ala Asp Arg Gln Gln Leu Pro Asp Ile
 50 55 60
 Gly Gly Asp Ser Leu Met Glu Glu Gly Thr Gln Ile Asn Leu Ser Asp
 65 70 75 80
 Phe Glu Asn Gln Val Val Ile Leu Asn Ala Trp Gly Gln Trp Cys Ala
 85 90 95
 Pro Cys Arg Ser Glu Ser Asp Asp Leu Gln Ile Ile His Glu Glu Leu
 100 105 110
 Gln Ala Ala Gly Asn Gly Asp Thr Pro Gly Gly Thr Val Leu Gly Ile
 115 120 125
 Asn Val Arg Asp Tyr Ser Arg Asp Ile Ala Gln Asp Phe Val Thr Asp
 130 135 140
 Asn Gly Leu Asp Tyr Pro Ser Ile Tyr Asp Pro Pro Phe Met Thr Ala
 145 150 155 160
 Ala Ser Leu Gly Gly Val Pro Ala Ser Val Ile Pro Thr Thr Ile Val
 165 170 175
 Leu Asp Lys Gln His Arg Pro Ala Ala Val Phe Leu Arg Glu Val Thr
 180 185 190
 Ser Lys Asp Val Leu Asp Val Ala Leu Pro Leu Val Asp Glu Ala
 195 200 205

 <210> 1727
 <211> 836
 <212> DNA
 <213> *Corynebacterium glutamicum*

 <220>
 <221> CDS
 <222> (1)..(813)
 <223> RXA00387

 <400> 1727
 caa aac gac cca gaa acc tgg gaa gac tac gaa ctt cgc gtc aac cac 48
 Gln Asn Asp Pro Glu Thr Trp Glu Asp Tyr Glu Leu Arg Val Asn His
 1 5 10 15
 cca ctg cgc atc gaa ggc gac cgc gtc tac ctt cag ggc cac ggc ttc 96
 Pro Leu Arg Ile Glu Gly Asp Arg Val Tyr Leu Gln Gly His Gly Phe
 20 25 30
 gcc cca aca ttc acc gtg acc tgg cca aat ggc gag acc cgc acc cag 144
 Ala Pro Thr Phe Thr Val Thr Trp Pro Asn Gly Glu Thr Arg Thr Gln
 35 40 45
 acc gtg cag tgg cgc cca gac gac cgc acc ttc ttc ctg tcc tca ggc 192
 Thr Val Gln Trp Arg Pro Asp Asp Pro Thr Phe Phe Leu Ser Ser Gly

50	55	60	
gtg gtc cgt ttc gat cca ccc gcc ggc atg tac cca gac ctt tac gag			240
Val Val Arg Phe Asp Pro Pro Ala Gly Met Tyr Pro Asp Leu Tyr Glu			
65	70	75	80
cgc cgc caa aac cag ttg gcc atc cag gga ctt ttc gca ccg acc gcg			288
Arg Arg Gln Asn Gln Leu Ala Ile Gln Gly Leu Phe Ala Pro Thr Ala			
	85	90	95
gaa tgg gaa ggc gac aac aac gaa ctg ctg acc tcc tcc tac ccg gcg			336
Glu Trp Glu Gly Asp Asn Asn Glu Leu Leu Thr Ser Ser Tyr Pro Ala			
	100	105	110
atg cgt gac cca gcc gtg cgc atc gat att tac cgc ggc gac aat ggc			384
Met Arg Asp Pro Ala Val Ala Ile Asp Ile Tyr Arg Gly Asp Asn Gly			
	115	120	125
ctc gat acc ggc atc gga cag tca ttg ttc agc ctg gac tct agt ctc			432
Leu Asp Thr Gly Ile Gly Gln Ser Leu Phe Ser Ser Asp Ser Ser Leu			
	130	135	140
atg cac agc ggc gtg ctg caa aaa att gag cgc gtc aac ctc caa atc			480
Met His Ser Gly Val Leu Gln Lys Ile Glu Arg Val Asn Leu Gln Ile			
	145	150	155
ggc gac acc gtc acc ctg gat gat ggc acc acc gtc tcc ttc gac ggc			528
Gly Asp Thr Val Thr Leu Asp Asp Gly Thr Thr Val Ser Phe Asp Gly			
	165	170	175
gcg tca gaa ttt gcc aac tac cag atc agc cgc gac ccc aca caa aac			576
Ala Ser Glu Phe Ala Asn Tyr Gln Ile Ser Arg Asp Pro Thr Gln Asn			
	180	185	190
tgg gtg ctg gtc acc acc gtg att tcg ctg gtc tcc ctg gtt gga tcc			624
Trp Val Leu Val Thr Thr Val Ile Ser Leu Val Ser Leu Val Gly Ser			
	195	200	205
ctg atg atc cga cgc cgc cgc att tgg gtg cgt ttc tat cca caa gaa			672
Leu Met Ile Arg Arg Arg Arg Ile Trp Val Arg Phe Tyr Pro Gln Glu			
	210	215	220
aac gga acc acc cgc gtg gaa acc ggc gga ctt gcc cgc acc gac cgc			720
Asn Gly Thr Thr Arg Val Glu Thr Gly Gly Leu Ala Arg Thr Asp Arg			
	225	230	235
gca ggc tgg ggt ggc gaa tac gag aaa ttc cac cgc gaa ctg ctg ggt			768
Ala Gly Trp Gly Gly Glu Tyr Glu Lys Phe His Arg Glu Leu Leu Gly			
	245	250	255
ctg aag gag gaa gat gaa gac gaa gag tac ttc gac cac gac gac			813
Leu Lys Glu Glu Asp Glu Asp Glu Glu Tyr Phe Asp His Asp Asp			
	260	265	270
taacaccgca atttaaaggc ttt			836

<210> 1728

<211> 271

<212> PRT

<213> Corynebacterium glutamicum

<400> 1728

Gln Asn Asp Pro Glu Thr Trp Glu Asp Tyr Glu Leu Arg Val Asn His
 1 5 10 15

Pro Leu Arg Ile Glu Gly Asp Arg Val Tyr Leu Gln Gly His Gly Phe
 20 25 30

Ala Pro Thr Phe Thr Val Thr Trp Pro Asn Gly Glu Thr Arg Thr Gln
 35 40 45

Thr Val Gln Trp Arg Pro Asp Asp Pro Thr Phe Phe Leu Ser Ser Gly
 50 55 60

Val Val Arg Phe Asp Pro Pro Ala Gly Met Tyr Pro Asp Leu Tyr Glu
 65 70 75 80

Arg Arg Gln Asn Gln Leu Ala Ile Gln Gly Leu Phe Ala Pro Thr Ala
 85 90 95

Glu Trp Glu Gly Asp Asn Asn Glu Leu Leu Thr Ser Ser Tyr Pro Ala
 100 105 110

Met Arg Asp Pro Ala Val Ala Ile Asp Ile Tyr Arg Gly Asp Asn Gly
 115 120 125

Leu Asp Thr Gly Ile Gly Gln Ser Leu Phe Ser Leu Asp Ser Ser Leu
 130 135 140

Met His Ser Gly Val Leu Gln Lys Ile Glu Arg Val Asn Leu Gln Ile
 145 150 155 160

Gly Asp Thr Val Thr Leu Asp Asp Gly Thr Thr Val Ser Phe Asp Gly
 165 170 175

Ala Ser Glu Phe Ala Asn Tyr Gln Ile Ser Arg Asp Pro Thr Gln Asn
 180 185 190

Trp Val Leu Val Thr Thr Val Ile Ser Leu Val Ser Leu Val Gly Ser
 195 200 205

Leu Met Ile Arg Arg Arg Arg Ile Trp Val Arg Phe Tyr Pro Gln Glu
 210 215 220

Asn Gly Thr Thr Arg Val Glu Thr Gly Gly Leu Ala Arg Thr Asp Arg
 225 230 235 240

Ala Gly Trp Gly Gly Glu Tyr Glu Lys Phe His Arg Glu Leu Leu Gly
 245 250 255

Leu Lys Glu Glu Asp Glu Asp Glu Glu Tyr Phe Asp His Asp Asp
 260 265 270

<210> 1729

<211> 987

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(964)

<223> RXA00392

<400> 1729

tgcttgaat acgttcggca ggctatgggg gagtgtgaaa cgctattgtg aaatgaatag 60

ataggtttcca tagtcgatcg aggaggagtc gcagaagttt atg tgg gtt ggt tat 115
Met Trp Val Gly Tyr
1 5

gcg gtt cga cag atc gcc agt gtt ttt ctt act ctt ttg cgc atg ctg 163
Ala Val Arg Gln Ile Ala Ser Val Phe Leu Thr Leu Leu Arg Met Leu
10 15 20

cca cta gca gcg cga aat cga gtt gcc agg gga cgc atc ccg gaa acc 211
Pro Leu Ala Ala Arg Asn Arg Val Ala Arg Gly Arg Ile Pro Glu Thr
25 30 35

ggc gat gtg gtg atc tca ttg acc acc cat ggg aag cga att aac tac 259
Gly Asp Val Val Ile Ser Leu Thr Thr His Gly Lys Arg Ile Asn Tyr
40 45 50

gtt cac ttc acc atc gaa tcg atc gca cgc ggc cat gtg aaa gca cca 307
Val His Phe Thr Ile Glu Ser Ile Ala Arg Gly His Val Lys Ala Pro
55 60 65

att gtg ctg tgg ttg gac aaa cca gac ttt gat gcg ccg tgg cct gcc 355
Ile Val Leu Trp Leu Asp Lys Pro Asp Phe Asp Ala Pro Trp Pro Ala
70 75 80 85

acc att aag cga ctt gtc gcc cgc ggt ctg caa gta cgg tgc agc gac 403
Thr Ile Lys Arg Leu Val Ala Arg Gly Leu Gln Val Arg Cys Ser Asp
90 95 100

ggc ttc tac ggc ccc cac acc aaa tac tgg aac caa ttc cga gaa atc 451
Gly Phe Tyr Gly Pro His Thr Lys Tyr Trp Asn Gln Phe Arg Glu Ile
105 110 115

cac ggc acc ggc gtg cgt gtc gcc acc gtc gac gat gac atg atc tac 499
His Gly Thr Gly Val Arg Val Ala Thr Val Asp Asp Met Ile Tyr
120 125 130

ccc gag tgg ttc ctg cag cgc ttg ctt ttt att ggc gac ctg cgc atg 547
Pro Glu Trp Phe Leu Gln Arg Leu Leu Phe Ile Gly Asp Leu Arg Met
135 140 145

gat gcg gtt gtc gcc tac cgg gcg cac aga att gag ctt cgc gac gac 595
Asp Ala Val Val Ala Tyr Arg Ala His Arg Ile Glu Leu Arg Asp Asp
150 155 160 165

cga atg ctc ccg tac gtt aaa tgg agt gcc gca gac acc tca aaa gcg 643
Arg Met Leu Pro Tyr Val Lys Trp Ser Ala Ala Asp Thr Ser Lys Ala
170 175 180

tca ttc ctg cac ttt gcc aag gga gtg tca ggc gtt ttg tac ccc gtg 691
Ser Phe Leu His Phe Ala Thr Gly Val Ser Gly Val Leu Tyr Pro Val
185 190 195

acc ttc att gat tat gtg gtc tcc cag ggc gat gta ttc ctt gag aac 739
Thr Phe Ile Asp Tyr Val Val Ser Gln Gly Asp Val Phe Leu Glu Asn
200 205 210

tgc aag cgc gcc gat gac gta tgg ctg cat gcc tgc gca ctg cgc tct 787
 Cys Lys Arg Ala Asp Asp Val Trp Leu His Ala Cys Ala Leu Arg Ser
 215 220 225

gat cac cct att cgc cag gtc tac gct cag ccc cga cac ttc gct gtc 835
 Asp His Pro Ile Arg Gln Val Tyr Ala Gln Pro Arg His Phe Ala Val
 230 235 240 245

gtg ccc acc acc caa gtg gga gca cta gtt gtt ggc aac acc ctc atg 883
 Val Pro Thr Thr Gln Val Gly Ala Leu Val Val Gly Asn Thr Leu Met
 250 255 260

ggc gga aat gat gag cag atc gcc aaa gtg tac acc gat gaa gat gtg 931
 Gly Gly Asn Asp Glu Gln Ile Ala Lys Val Tyr Thr Asp Glu Asp Val
 265 270 275

gca aaa cta gtt gca gcc agc aag aat gaa gac taaaacagct tcgcgatagc 984
 Ala Lys Leu Val Ala Ala Ser Lys Asn Glu Asp
 280 285

acg 987

<210> 1730

<211> 288

<212> PRT

<213> Corynebacterium glutamicum

<400> 1730

Met Trp Val Gly Tyr Ala Val Arg Gln Ile Ala Ser Val Phe Leu Thr
 1 5 10 15

Leu Leu Arg Met Leu Pro Leu Ala Ala Arg Asn Arg Val Ala Arg Gly
 20 25 30

Arg Ile Pro Glu Thr Gly Asp Val Val Ile Ser Leu Thr Thr His Gly
 35 40 45

Lys Arg Ile Asn Tyr Val His Phe Thr Ile Glu Ser Ile Ala Arg Gly
 50 55 60

His Val Lys Ala Pro Ile Val Leu Trp Leu Asp Lys Pro Asp Phe Asp
 65 70 75 80

Ala Pro Trp Pro Ala Thr Ile Lys Arg Leu Val Ala Arg Gly Leu Gln
 85 90 95

Val Arg Cys Ser Asp Gly Phe Tyr Gly Pro His Thr Lys Tyr Trp Asn
 100 105 110

Gln Phe Arg Glu Ile His Gly Thr Gly Val Arg Val Ala Thr Val Asp
 115 120 125

Asp Asp Met Ile Tyr Pro Glu Trp Phe Leu Gln Arg Leu Leu Phe Ile
 130 135 140

Gly Asp Leu Arg Met Asp Ala Val Val Ala Tyr Arg Ala His Arg Ile
 145 150 155 160

Glu Leu Arg Asp Asp Arg Met Leu Pro Tyr Val Lys Trp Ser Ala Ala

	165		170		175
Asp Thr Ser	Lys Ala Ser Phe Leu His Phe Ala Thr Gly Val Ser Gly				
	180		185		190
Val Leu Tyr	Pro Val Thr Phe Ile Asp Tyr Val Val Ser Gln Gly Asp				
	195		200		205
Val Phe Leu Glu Asn Cys Lys Arg Ala Asp Asp Val Trp Leu His Ala					
	210		215		220
Cys Ala Leu Arg Ser Asp His Pro Ile Arg Gln Val Tyr Ala Gln Pro					
	225		230		235
Arg His Phe Ala Val Val Pro Thr Thr Gln Val Gly Ala Leu Val Val					
	245		250		255
Gly Asn Thr Leu Met Gly Gly Asn Asp Glu Gln Ile Ala Lys Val Tyr					
	260		265		270
Thr Asp Glu Asp Val Ala Lys Leu Val Ala Ala Ser Lys Asn Glu Asp					
	275		280		285

<210> 1731

<211> 456

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(433)

<223> RXA00394

<400> 1731

accacattga acctctcctt aaatatttgc ttcaacctcc cacaatacgg aactttgagg 60

cattcttggg tatcggtatg tattgagtag ggttgaatat	gtg agt gag tcc aat	115
	Val Ser Glu Ser Asn	
	1 5	

acc ccc aat ctc cag aca cac caa gcg cgg gaa tta aac cgg gaa cta	163
Thr Pro Asn Leu Gln Thr His Gln Ala Pro Glu Leu Asn Pro Glu Leu	
10 15 20	

caa aaa gct gcc cgg aaa aac gtg ctg att tac ggt ctg gca cgt ttg	211
Gln Lys Ala Ala Arg Lys Asn Val Leu Ile Tyr Gly Leu Ala Arg Leu	
25 30 35	

ctt ctg ttc gtc gtg ctg acc ttg att att cat agc ctg gct ctg ctg	259
Leu Leu Phe Val Val Leu Thr Leu Ile Ile His Ser Leu Ala Leu Leu	
40 45 50	

att agt gcg cct gtg cca ctc gtt atg tct gcg atg ctg gct ctg att	307
Ile Ser Ala Pro Val Pro Leu Val Met Ser Ala Met Leu Ala Leu Ile	
55 60 65	

gtg gcg ttc cca ttg tcc atg ctg gtg ttc agc aaa ctg cgc atg aat	355
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Val Ala Phe Pro Leu Ser Met Leu Val Phe Ser Lys Leu Arg Met Asn
 70                      75                      80                      85

gcc acc cag gct gtt tcc cag tgg gat gca cag cgc aag gcc cac aag    403
Ala Thr Gln Ala Val Ser Gln Trp Asp Ala Gln Arg Lys Ala His Lys
                      90                      95                      100

gaa tgg gtt cga agc gag ctg gcg gac cgc taaaaaatc ccctcggtct    453
Glu Trp Val Arg Ser Glu Leu Ala Asp Arg
                      105                      110

ttg                                                                456

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<210> 1732
 <211> 111
 <212> PRT
 <213> *Corynebacterium glutamicum*

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<400> 1732
Val Ser Glu Ser Asn Thr Pro Asn Leu Gln Thr His Gln Ala Pro Glu
 1                      5                      10                      15

Leu Asn Pro Glu Leu Gln Lys Ala Ala Arg Lys Asn Val Leu Ile Tyr
                      20                      25                      30

Gly Leu Ala Arg Leu Leu Leu Phe Val Val Leu Thr Leu Ile Ile His
                      35                      40                      45

Ser Leu Ala Leu Leu Ile Ser Ala Pro Val Pro Leu Val Met Ser Ala
 50                      55                      60

Met Leu Ala Leu Ile Val Ala Phe Pro Leu Ser Met Leu Val Phe Ser
 65                      70                      75                      80

Lys Leu Arg Met Asn Ala Thr Gln Ala Val Ser Gln Trp Asp Ala Gln
                      85                      90                      95

Arg Lys Ala His Lys Glu Trp Val Arg Ser Glu Leu Ala Asp Arg
 100                      105                      110

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<210> 1733
 <211> 423
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(400)
 <223> RXA00395

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<400> 1733
actcacatat tcaaccctac tcaatacata ccgataccca agaatgcctc aaagtccgt 60

attgtgggag gttgaagcaa atatttaagg agaggttcaa gtg ggt agg ctt ttg    115
Val Gly Arg Leu Leu
                      1                      5

ctg att att ttg gtt atc gtc gca atc gtc ttg ctg tgg aag gcc ttc    163
Leu Ile Ile Leu Val Ile Val Ala Ile Val Leu Leu Trp Lys Ala Phe

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                10                15                20
aag cca tct  aca tgg aag cgt aac gcg gag atc aat cag ggc cag gca  211
Lys Pro Ser  Thr Trp Lys Arg Asn Ala Glu Ile Asn Gln Gly Gln Ala
                25                30                35

cct cgt gca gtg aaa ggc ccc gac gat gat gaa gaa ttc ttg tgg aat  259
Pro Arg Ala  Val Lys Gly Pro Asp Asp Asp Glu Glu Phe Leu Trp Asn
                40                45                50

att gaa aag aat cgc ttc aaa cag cgt cgc gcc gac gag gct gcc caa  307
Ile Glu Lys  Asn Arg Phe Lys Gln Arg Arg Ala Asp Glu Ala Ala Gln
                55                60                65

tta gaa gag gaa gaa cgt ctc aaa cgg gcc agg gaa cgc tac gca aag  355
Leu Glu Glu  Glu Glu Arg Leu Lys Arg Ala Arg Glu Arg Tyr Ala Lys
                70                75                80                85

cct gaa agc tca gaa gaa ggt cca gag aag ccc act gag gat tct  400
Pro Glu Ser  Ser Glu Glu Gly Pro Glu Lys Pro Thr Glu Asp Ser
                90                95                100

taaaagggct tctttaaaaa gat  423

<210> 1734
<211> 100
<212> PRS
<213> Corynebacterium glutamicum

<400> 1734
Val Gly Arg Leu Leu Leu Ile Ile Leu Val Ile Val Ala Ile Val Leu
  1             5             10             15

Leu Trp Lys Ala Phe Lys Pro Ser Thr Trp Lys Arg Asn Ala Glu Ile
  20             25             30

Asn Gln Gly Gln Ala Pro Arg Ala Val Lys Gly Pro Asp Asp Asp Glu
  35             40             45

Glu Phe Leu Trp Asn Ile Glu Lys Asn Arg Phe Lys Gln Arg Arg Ala
  50             55             60

Asp Glu Ala Ala Gln Leu Glu Glu Glu Arg Leu Lys Arg Ala Arg
  65             70             75             80

Glu Arg Tyr Ala Lys Pro Glu Ser Ser Glu Glu Gly Pro Glu Lys Pro
  85             90             95

Thr Glu Asp Ser
  100

<210> 1735
<211> 594
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(571)

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Asp Leu Pro Ala Pro Gln Tyr Ser Tyr Val Pro Phe Asn Arg Gln Gly
20 25 30

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Asn Thr Leu Tyr Val Ser Gly Gln Ile Ser Arg Thr Ala Ala Gly Asp
    35                      40                      45

Ile Leu Ala Gly Arg Val Gly Glu Asp Ala Thr Leu Glu Glu Gly Ile
    50                      55                      60

His Ala Ala Glu Val Ala Thr Ile Asn Leu Leu Ala Arg Ile His Gln
    65                      70                      75                      80

Ser Ile Gly Leu Asp Asn Val Ala Gln Ile Leu Lys Leu Asn Val Trp
                      85                      90                      95

Val Asn Ser Ser Asp Asp Phe Ile Gln Gln Pro Gln Val Ala Asp Gly
    100                      105                      110

Ala Ser Gln Leu Leu Glu Ala Val Leu Gly Glu Ala Gly Lys His Ala
    115                      120                      125

Arg Thr Ala Leu Pro Thr Asn Thr Leu Pro Gln Gly Ala Leu Val Glu
    130                      135                      140

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Leu Asp Ala Val Val Ala Val Thr Glu Ala Ala Glu Val
145                      150                      155

```

<210> 1737

<211> 563

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(540)

<223> RKA00397

<400> 1737

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aac ctg cac tcc tcc aac aga atg ctc ttc cct gga cct cct gtg gat      48
Asn Leu His Ser Ser Asn Arg Met Leu Phe Pro Gly Pro Pro Val Asp
    1                      5                      10                      15

```

```

ttc ccg atc aac gca gaa acc cga tgc att cag ctc gac gcc ggt gtt      96
Phe Pro Ile Asn Ala Glu Thr Arg Cys Ile Gln Leu Asp Ala Gly Val
    20                      25                      30

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gca gta aag aag gac ggc gtg gtg ctg ggt acc tca gat atg gcg agg      144
Ala Val Lys Lys Asp Gly Val Val Leu Gly Thr Ser Asp Met Ala Arg
    35                      40                      45

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tcc ctg cct cga acc gcc gct ggc caa gaa gcc tat gag tac ttc ttc      192
Ser Leu Pro Arg Thr Ala Ala Gly Gln Glu Ala Tyr Glu Tyr Phe Phe
    50                      55                      60

```

```

aag gtg gtt cgt gaa ggc atc atc ggg cag ctg cgc ccg gcc gtg atc      240
Lys Val Val Arg Glu Gly Ile Ile Gly Gln Leu Arg Pro Gly Val Ile
    65                      70                      75                      80

```

```

tgc gct gac gtg cac gaa gca acc ctt gat tac cta agc ccg cag cta      288
Cys Ala Asp Val His Glu Ala Thr Leu Asp Tyr Leu Ser Pro Gln Leu
    85                      90                      95

```

```

cct cgc atg att gac atc gga atg ctg ggt gcc gac acc gat ttc aac 336
Pro Arg Met Ile Asp Ile Gly Met Leu Gly Ala Asp Thr Asp Phe Asn
      100                      105                      110

acc atc tac cgc aag cgc aat gtt ggc cac ctc atg ggc aag cag gaa 384
Thr Ile Tyr Arg Lys Arg Asn Val Gly His Leu Met Gly Lys Gln Glu
      115                      120                      125

tcc ttt gcc aat gag ctt cgc cct gga tac aag cac att ctt cac cac 432
Ser Phe Ala Asn Glu Leu Arg Pro Gly Tyr Lys His Ile Leu His His
      130                      135                      140

ggc tcc tat ggt gcc gcg gag atc cct tgg cgc tac aac ggt gta gcc 480
Gly Ser Tyr Gly Ala Ala Glu Ile Pro Trp Arg Tyr Asn Gly Val Ala
      145                      150                      155                      160

att ggt acc gag gat ctg tgg tac atc ggc gca gac aag acc tac att 528
Ile Gly Thr Glu Asp Leu Trp Tyr Ile Gly Ala Asp Lys Thr Tyr Ile
      165                      170                      175

ttg agc cag cgc taaggagaac ccagtgacag aaa 563
Leu Ser Gln Arg
      180

<210> 1738
<211> 180
<212> PRT
<213> Corynebacterium glutamicum

<400> 1738
Asn Leu His Ser Ser Asn Arg Met Leu Phe Pro Gly Pro Pro Val Asp
  1          5          10
Phe Pro Ile Asn Ala Glu Thr Arg Cys Ile Gln Leu Asp Ala Gly Val
      20          25          30
Ala Val Lys Lys Asp Gly Val Val Leu Gly Thr Ser Asp Met Ala Arg
      35          40          45
Ser Leu Pro Arg Thr Ala Ala Gly Gln Glu Ala Tyr Glu Tyr Phe Phe
      50          55          60
Lys Val Val Arg Glu Gly Ile Ile Gly Gln Leu Arg Pro Gly Val Ile
      65          70          75          80
Cys Ala Asp Val His Glu Ala Thr Leu Asp Tyr Leu Ser Pro Gln Leu
      85          90          95
Pro Arg Met Ile Asp Ile Gly Met Leu Gly Ala Asp Thr Asp Phe Asn
      100          105          110
Thr Ile Tyr Arg Lys Arg Asn Val Gly His Leu Met Gly Lys Gln Glu
      115          120          125
Ser Phe Ala Asn Glu Leu Arg Pro Gly Tyr Lys His Ile Leu His His
      130          135          140
Gly Ser Tyr Gly Ala Ala Glu Ile Pro Trp Arg Tyr Asn Gly Val Ala
      145          150          155          160

```

Ile Gly Thr Glu Asp Leu Trp Tyr Ile Gly Ala Asp Lys Thr Tyr Ile
 165 170 175

Leu Ser Gln Arg
 180

<210> 1739

<211> 704

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(681)

<223> RXA00398

<400> 1739

tac ctc ccc gag cct ttc acc gtg gag gat tac act gcg cgt gtt gaa 48
 Tyr Leu Pro Glu Pro Phe Thr Val Glu Asp Tyr Thr Ala Arg Val Glu
 1 5 10 15

ggc ctc gaa gtt gct ggc gga gcg att gtt tcc ggt tct ttc cag gct 96
 Gly Leu Glu Val Ala Gly Gly Ala Ile Val Ser Gly Ser Phe Gln Ala
 20 25 30

ttc gac cag ggc tac ctc aaa gat gct ctc gca gtg ctt ggc cca ggc 144
 Phe Asp Gln Gly Tyr Leu Lys Asp Ala Leu Ala Val Leu Gly Pro Gly
 35 40 45

tat gtc ggt gtc act cag atc ccc gca gat acc tct gat cag gag att 192
 Tyr Val Gly Val Thr Gln Ile Pro Ala Asp Thr Ser Asp Gln Glu Ile
 50 55 60

ctt gat ctg gac aaa gct ggc gtg aag gct gtg cgt tta aac ttg aag 240
 Leu Asp Leu Asp Lys Ala Gly Val Lys Ala Val Arg Leu Asn Leu Lys
 65 70 75 80

cgc ggt ggt tcg gca ggt ctt gac gat ctc gag acc ttg gca cgc cga 288
 Arg Gly Gly Ser Ala Gly Leu Asp Asp Leu Glu Thr Leu Ala Arg Arg
 85 90 95

gtc cac gac cta gcc ggt tgg cac acc gaa ctc tat gtg gat gct cgc 336
 Val His Asp Leu Ala Gly Trp His Thr Glu Leu Tyr Val Asp Ala Arg
 100 105 110

gaa cta gac gag ttg gaa tca acc ttg gcc tcc ctc cct gct gtc agc 384
 Glu Leu Asp Glu Leu Glu Ser Thr Leu Ala Ser Leu Pro Ala Val Ser
 115 120 125

att gat cac tta ggg ctc cac cgc gat gga ctt ccc gca ctt ctt cgc 432
 Ile Asp His Leu Gly Leu His Arg Asp Gly Leu Pro Ala Leu Leu Arg
 130 135 140

ttg gta gaa aat ggc att aaa gtc aaa gca acc gga ttc gga cgg gta 480
 Leu Val Glu Asn Gly Ile Lys Val Lys Ala Thr Gly Phe Gly Arg Val
 145 150 155 160

gaa cta gat cca act gaa gtc atc cag gca atc atg gct gtc gat ccc 528
 Glu Leu Asp Pro Thr Glu Val Ile Gln Ala Ile Met Ala Val Asp Pro
 165 170 175

act gct ttg atg atc gga act gat ctt cca tcc acc cgc act aag cga 576
 Thr Ala Leu Met Ile Gly Thr Asp Leu Pro Ser Thr Arg Thr Lys Arg
 180 185 190

cct ttc gaa gac gct gac cta gat ttg atc gct gaa acg gtt ggc gaa 624
 Pro Phe Glu Asp Ala Asp Leu Asp Leu Ile Ala Glu Thr Val Gly Glu
 195 200 205

gat cat gtc gac aac gtc ttc tgg aac aac gct gca gcg ttc tac ctc 672
 Asp His Val Asp Asn Val Phe Trp Asn Asn Ala Ala Phe Tyr Leu
 210 215 220

gga gac cag tagttttaag acccgaaatg tct 704
 Gly Asp Gln
 225

<210> 1740

<211> 227

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1740

Tyr Leu Pro Glu Pro Phe Thr Val Glu Asp Tyr Thr Ala Arg Val Glu
 1 5 10 15

Gly Leu Glu Val Ala Gly Gly Ala Ile Val Ser Gly Ser Phe Gln Ala
 20 25 30

Phe Asp Gln Gly Tyr Leu Lys Asp Ala Leu Ala Val Leu Gly Pro Gly
 35 40 45

Tyr Val Gly Val Thr Gln Ile Pro Ala Asp Thr Ser Asp Gln Glu Ile
 50 55 60

Leu Asp Leu Asp Lys Ala Gly Val Lys Ala Val Arg Leu Asn Leu Lys
 65 70 75 80

Arg Gly Gly Ser Ala Gly Leu Asp Asp Leu Glu Thr Leu Ala Arg Arg
 85 90 95

Val His Asp Leu Ala Gly Trp His Thr Glu Leu Tyr Val Asp Ala Arg
 100 105 110

Glu Leu Asp Glu Leu Glu Ser Thr Leu Ala Ser Leu Pro Ala Val Ser
 115 120 125

Ile Asp His Leu Gly Leu His Arg Asp Gly Leu Pro Ala Leu Leu Arg
 130 135 140

Leu Val Glu Asn Gly Ile Lys Val Lys Ala Thr Gly Phe Gly Arg Val
 145 150 155 160

Glu Leu Asp Pro Thr Glu Val Ile Gln Ala Ile Met Ala Val Asp Pro
 165 170 175

Thr Ala Leu Met Ile Gly Thr Asp Leu Pro Ser Thr Arg Thr Lys Arg
 180 185 190

Pro Phe Glu Asp Ala Asp Leu Asp Leu Ile Ala Glu Thr Val Gly Glu

195	200	205	
Asp His Val Asp Asn Val Phe Trp Asn Asn Ala Ala Ala Phe Tyr Leu			
210	215	220	
Gly Asp Gln			
225			
<210> 1741			
<211> 570			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(547)			
<223> RXA00408			
<400> 1741			
gggggagttt ctcagccgtg gctcagcaga ttttcgataa ttggcacaag tggacattat 60			
gacaaatacg cacaggcgaa cccagagaacc acatgagggc atg aat cca gtg tca 115			
Met Asn Pro Val Ser 5			
cca aaa ctg acc acg gcc agg tac ctc acc cgc att cca tgg ctg ctg 163			
Pro Lys Leu Thr Thr Ala Arg Tyr Leu Thr Arg Ile Pro Trp Leu Leu			
10 15 20			
atc agc gcg att gtg ttt ggg gtg ctt gga gtt ttt gtg tct tgc tgg 211			
Ile Ser Ala Ile Val Phe Gly Val Leu Gly Val Phe Val Ser Ser Trp			
25 30 35			
ttt tac gcc ggt gtg atc gta gtt gcc gtc att ctt atc tgg cag ctg 259			
Phe Tyr Ala Gly Val Ile Val Val Ala Val Ile Leu Ile Trp Gln Leu			
40 45 50			
tgg ctg atc ccg cag cag gtc aag cga ctg gga tgg ctg gaa acc tcc 307			
Trp Leu Ile Pro Gln Gln Val Lys Arg Leu Gly Trp Leu Glu Thr Ser			
55 60 65			
gat gag ctg ctg atc acc aag gga aaa ctg tgg cac acc ttc acg gtt 355			
Asp Glu Leu Leu Ile Thr Lys Gly Lys Leu Trp His Thr Phe Thr Val			
70 75 80 85			
gtt ccc tat ggc cgc atc cag ttt gtt gat gtc acc gca ggt ccc ctc 403			
Val Pro Tyr Gly Arg Ile Gln Phe Val Asp Val Thr Ala Gly Pro Leu			
90 95 100			
gag cgc gcg ttt ggc atg aaa caa gtg caa ttg cat acc gcg tgc gcg 451			
Glu Arg Ala Phe Gly Met Lys Gln Val Gln Leu His Thr Ala Ser Ala			
105 110 115			
tcc tct gac tcc acc att caa ggc ctg cct gtc gcg gaa gcc gat gcc 499			
Ser Ser Asp Ser Thr Ile Gln Gly Leu Pro Val Ala Glu Ala Asp Ala			
120 125 130			
tta cgt gag cga ctg gct att aag gcc cgg gag agg atg agc gga cta 547			
Leu Arg Glu Arg Leu Ala Ile Lys Ala Arg Glu Arg Met Ser Gly Leu			
135 140 145			

tgagcagcct tgaagggttt cga

570

<210> 1742

<211> 149

<212> PRT

<213> Corynebacterium glutamicum

<400> 1742

Met Asn Pro Val Ser Pro Lys Leu Thr Thr Ala Arg Tyr Leu Thr Arg
1 5 10 15

Ile Pro Trp Leu Leu Ile Ser Ala Ile Val Phe Gly Val Leu Gly Val
20 25 30

Phe Val Ser Ser Trp Phe Tyr Ala Gly Val Ile Val Val Ala Val Ile
35 40 45

Leu Ile Trp Gln Leu Trp Leu Ile Pro Gln Gln Val Lys Arg Leu Gly
50 55 60

Trp Leu Glu Thr Ser Asp Glu Leu Leu Ile Thr Lys Gly Lys Leu Trp
65 70 75 80

His Thr Phe Thr Val Val Pro Tyr Gly Arg Ile Gln Phe Val Asp Val
85 90 95

Thr Ala Gly Pro Leu Glu Arg Ala Phe Gly Met Lys Gln Val Gln Leu
100 105 110

His Thr Ala Ser Ala Ser Ser Asp Ser Thr Ile Gln Gly Leu Pro Val
115 120 125

Ala Glu Ala Asp Ala Leu Arg Glu Arg Leu Ala Ile Lys Ala Arg Glu
130 135 140

Arg Met Ser Gly Leu
145

<210> 1743

<211> 1536

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1513)

<223> RXA00409

<400> 1743

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agcgactggc tattaaggcc cgaggagagga tgagcggact atg agc agc ctt gaa 115
Met Ser Ser Leu Glu
1 5

ggg ttt cga aaa gtc cac cgc gcc acc cca ttc ctt cgc atc tgg acc 163
Gly Phe Arg Lys Val His Arg Ala Thr Pro Phe Leu Arg Ile Trp Thr
10 15 20

atc atc gtc gca gtt ctc gcg gca ttc gca ttc aat tcc ggc gca tcc	211
Ile Ile Val Ala Val Leu Ala Ala Phe Asn Ser Gly Ala Ser	
25 30 35	
gtt tta agt ttc atc tgg ggt gtc gtc acc ggc gaa tac gga ttc gca	259
Val Leu Ser Phe Ile Trp Gly Val Val Thr Gly Glu Tyr Gly Phe Ala	
40 45 50	
gtg ctg ccg att cta ttg acc gtc ggt ggc gcc gtc att gtg gtg gca	307
Val Leu Pro Ile Leu Leu Thr Val Gly Gly Ala Val Ile Val Val Ala	
55 60 65	
ctg gcc tgg att atc acc gga att tgg tgg aaa gcc gtc gga ttc cgc	355
Leu Ala Trp Ile Ile Thr Gly Ile Trp Trp Lys Ala Val Gly Phe Arg	
70 75 80 85	
atc acc aat gaa gag gtg cag ctg caa cgc gga gtg atc agc aaa gac	403
Ile Thr Asn Glu Val Gln Leu Gln Arg Gly Val Ile Ser Lys Asp	
90 95 100	
ctc cgc acc gcc cga ttt gac cgt atc caa gcc gtt gac ctg gtg gaa	451
Leu Arg Thr Ala Arg Phe Asp Arg Ile Gln Ala Val Asp Leu Val Glu	
105 110 115	
tca ttc atc gcc cgt atc ttc cga ctg gca gaa gtc cgc atc gaa acc	499
Ser Phe Ile Ala Arg Ile Phe Arg Leu Ala Glu Val Arg Ile Glu Thr	
120 125 130	
gcc ggc ggc agc gac tcc gcc atc agc att ggc ttt tta aga aaa agc	547
Ala Gly Gly Ser Asp Ser Ala Ile Ser Ile Gly Phe Leu Arg Lys Ser	
135 140 145	
gag gcc gag gcc cta aaa agg gag ctt ctc gac gcc tcc cag cac tca	595
Glu Ala Glu Ala Leu Lys Arg Glu Leu Leu Asp Ala Ser Gln His Ser	
150 155 160 165	
gtc gcc acc acc cca gcc gga gtt ccg gct gag cct ggg gta ggg gag	643
Val Ala Thr Thr Pro Ala Gly Val Pro Ala Glu Pro Gly Val Gly Glu	
170 175 180	
acc gtt gta gtt gag agc gcg ggc gat gtt ctg gtt cca caa atc ccc	691
Thr Val Val Val Glu Ser Ala Gly Asp Val Leu Val Pro Gln Ile Pro	
185 190 195	
gtg caa cgc acc ctc gcc agc acc gcc tta tca cta gca acc atc atc	739
Val Gln Arg Thr Leu Ala Ser Thr Ala Leu Ser Leu Ala Thr Ile Ile	
200 205 210	
acc gcg atc ggt att gtg att ttg ctc ttc gtt cct ttc gga gtg agc	787
Thr Ala Ile Gly Ile Val Ile Leu Leu Phe Val Phe Gly Val Ser	
215 220 225	
att gcc gtg ccg ttc ttt gta ggc atg gtg cca gcg gtc tgg aac ttg	835
Ile Ala Val Pro Phe Val Gly Met Val Pro Ala Val Trp Asn Leu	
230 235 240 245	
atc gat aag tcg tgg caa ttc acc gca aca cag cgc aac gat gtc ctg	883
Ile Asp Lys Ser Trp Gln Phe Thr Ala Thr Gln Arg Asn Asp Val Leu	
250 255 260	

cat gtc agc tat gga ctt gcc aac cgc cgc aaa caa tca atc cca ctg 931
 His Val Ser Tyr Gly Leu Ala Asn Arg Arg Lys Gln Ser Ile Pro Leu
 265 270 275

gga cgc atc cac gca gtg aaa cta aaa cag cca ttg ctg tgg cga ctg 979
 Gly Arg Ile His Ala Val Lys Leu Lys Gln Pro Leu Leu Trp Arg Leu
 280 285 290

gtt ggc tgg tgg acc gtg acc gtg cct gta gtt ggc tac ggc gac acc 1027
 Val Gly Trp Trp Thr Val Thr Val Pro Val Val Gly Tyr Gly Asp Thr
 295 300 305

acc caa ggc gga acc tcc aaa atc ttg ccc gtg ggt tcc aaa gaa ctc 1075
 Thr Gln Gly Gly Thr Ser Lys Ile Leu Pro Val Gly Ser Lys Glu Leu
 310 315 320 325

gca cta aaa gtc ctt gaa gcg gtg ggg cca cta aac agc gcc gac atc 1123
 Ala Leu Lys Val Leu Glu Ala Val Gly Pro Leu Asn Ser Ala Asp Ile
 330 335 340

gcc gaa tct gca gac cca tca cat atg agc aga ccc cag tac aca cca 1171
 Ala Glu Ser Ala Asp Pro Ser His Met Ser Arg Pro Gln Tyr Thr Pro
 345 350 355

cca gtt gct gca cgc ctg ctc aca cca gtc gat cgg acc cgc caa ggc 1219
 Pro Val Ala Ala Arg Leu Leu Thr Pro Val Asp Arg Thr Arg Gln Gly
 360 365 370

gtc acg ttg att ggt gtg gct ggt gcc cct ggt gcg gtg gtc gtg cat 1267
 Val Thr Leu Ile Gly Val Ala Gly Ala Pro Gly Ala Val Val Val His
 375 380 385

gaa ggc aga ttc atg cca cgt atg tct gtg att gat acc tcc cac atc 1315
 Glu Gly Arg Phe Met Pro Arg Met Ser Val Ile Asp Thr Ser His Ile
 390 395 400 405

caa gaa ctc acc ctt aaa cac ggg ccg atc caa aga ata ctg gga ctc 1363
 Gln Glu Leu Thr Leu Lys His Gly Pro Ile Gln Arg Ile Leu Gly Leu
 410 415 420

tcc acc gtt gtg ttt aac ctg gtc caa ggg cca gtg gga atg gcc gca 1411
 Ser Thr Val Val Phe Asn Leu Val Gln Gly Pro Val Gly Met Ala Ala
 425 430 435

tgc gat ctc agt gca gct gat gga aaa gaa ctt ctc aac att ctc cgc 1459
 Ser Asp Leu Ser Ala Ala Asp Gly Lys Glu Leu Leu Asn Ile Leu Arg
 440 445 450

aac aga aaa cta ccc gca ctg gaa tca gct ccg ctg gga caa aac agc 1507
 Asn Arg Lys Leu Pro Ala Leu Glu Ser Ala Pro Leu Gly Gln Asn Ser
 455 460 465

ctg gac taaggtgtaa tcatgcacat ctc 1536
 Leu Asp
 470

<210> 1744

<211> 471

<212> PRT

<213> Corynebacterium glutamicum

<400> 1744

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Met Ser Ser Leu Glu Gly Phe Arg Lys Val His Arg Ala Thr Pro Phe
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Leu Arg Ile Trp Thr Ile Ile Val Ala Val Leu Ala Ala Phe Ala Phe
 20          25          30

Asn Ser Gly Ala Ser Val Leu Ser Phe Ile Trp Gly Val Val Thr Gly
 35          40          45

Glu Tyr Gly Phe Ala Val Leu Pro Ile Leu Leu Thr Val Gly Gly Ala
 50          55          60

Val Ile Val Val Ala Leu Ala Trp Ile Ile Thr Gly Ile Trp Trp Lys
 65          70          75

Ala Val Gly Phe Arg Ile Thr Asn Glu Glu Val Gln Leu Gln Arg Gly
 85          90          95

Val Ile Ser Lys Asp Leu Arg Thr Ala Arg Phe Asp Arg Ile Gln Ala
100          105          110

Val Asp Leu Val Glu Ser Phe Ile Ala Arg Ile Phe Arg Leu Ala Glu
115          120          125

Val Arg Ile Glu Thr Ala Gly Gly Ser Asp Ser Ala Ile Ser Ile Gly
130          135          140

Phe Leu Arg Lys Ser Glu Ala Glu Ala Leu Lys Arg Glu Leu Leu Asp
145          150          155          160

Ala Ser Gln His Ser Val Ala Thr Thr Pro Ala Gly Val Pro Ala Glu
165          170          175

Pro Gly Val Gly Glu Thr Val Val Val Glu Ser Ala Gly Asp Val Leu
180          185          190

Val Pro Gln Ile Pro Val Gln Arg Thr Leu Ala Ser Thr Ala Leu Ser
195          200          205

Leu Ala Thr Ile Ile Thr Ala Ile Gly Ile Val Ile Leu Leu Phe Val
210          215          220

Pro Phe Gly Val Ser Ile Ala Val Pro Phe Phe Val Gly Met Val Pro
225          230          235          240

Ala Val Trp Asn Leu Ile Asp Lys Ser Trp Gln Phe Thr Ala Thr Gln
245          250          255

Arg Asn Asp Val Leu His Val Ser Tyr Gly Leu Ala Asn Arg Arg Lys
260          265          270

Gln Ser Ile Pro Leu Gly Arg Ile His Ala Val Lys Leu Lys Gln Pro
275          280          285

Leu Leu Trp Arg Leu Val Gly Trp Trp Thr Val Thr Val Pro Val Val
290          295          300

Gly Tyr Gly Asp Thr Thr Gln Gly Gly Thr Ser Lys Ile Leu Pro Val
305          310          315          320

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Gly Ser Lys Glu Leu Ala Leu Lys Val Leu Glu Ala Val Gly Pro Leu
325 330 335

Asn Ser Ala Asp Ile Ala Glu Ser Ala Asp Pro Ser His Met Ser Arg
340 345 350

Pro Gln Tyr Thr Pro Pro Val Ala Ala Arg Leu Leu Thr Pro Val Asp
355 360 365

Arg Thr Arg Gln Gly Val Thr Leu Ile Gly Val Ala Gly Ala Pro Gly
370 375 380

Ala Val Val Val His Glu Gly Arg Phe Met Pro Arg Met Ser Val Ile
385 390 395 400

Asp Thr Ser His Ile Gln Glu Leu Thr Leu Lys His Gly Pro Ile Gln
405 410 415

Arg Ile Leu Gly Leu Ser Thr Val Val Phe Asn Leu Val Gln Gly Pro
420 425 430

Val Gly Met Ala Ala Ser Asp Leu Ser Ala Ala Asp Gly Lys Glu Leu
435 440 445

Leu Asn Ile Leu Arg Asn Arg Lys Leu Pro Ala Leu Glu Ser Ala Pro
450 455 460

Leu Gly Gln Asn Ser Leu Asp
465 470

<210> 1745

<211> 798

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(775)

<223> RXA00411

<400> 1745

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aaaccttgac caagaccacg accatcaagg agatcaccgc atg aac gag atg atc 115
Met Asn Glu Met Ile
1 5

ctc gca gct gac tgg aac cgg cta gga ccc acc ttc caa aca gcc atc 163
Leu Ala Ala Asp Trp Asn Arg Leu Gly Pro Thr Phe Gln Thr Ala Ile
10 15 20

att gac acc ctg ttg atg gtc atc atc acc atg gtg gtg gct gcc tta 211
Ile Asp Thr Leu Leu Met Val Ile Ile Thr Met Val Val Ala Ala Gly Leu
25 30 35

ctg ggt ctt gtc gtc ggc ctg ctg ctt tac acc acc cgc gct ggt gga 259
Leu Gly Leu Val Val Gly Leu Leu Leu Tyr Thr Thr Arg Ala Gly Gly
40 45 50

atc ttg aag aac aag gtc atc tac acc att ttg aat gtg ctg gtg aac 307
 Ile Leu Lys Asn Lys Val Ile Tyr Thr Ile Leu Asn Val Leu Val Asn
 55 60 65

 ttt gtt cga ccc atc cca ttc att att ttg atc gcc gcc atc aag cca 355
 Phe Val Arg Pro Ile Pro Phe Ile Ile Leu Ile Ala Ala Ile Lys Pro
 70 75 80 85

 cta acg gtc gcc gtc atg ggc acc tcc atc ggc cga gat gcc ggc atc 403
 Leu Thr Val Ala Val Met Gly Thr Ser Ile Gly Arg Asp Ala Gly Ile
 90 95 100

 ttc gtc atg gtt gtc gca gcg att ttc tct gtg gct cga atc gtg gag 451
 Phe Val Met Val Val Ala Ala Ile Phe Ser Val Ala Arg Ile Val Glu
 105 110 115

 caa aac ttg gtc tcc att gat cct ggt gtc atc gag gca gct cgc tcc 499
 Gln Asn Leu Val Ser Ile Asp Pro Gly Val Ile Glu Ala Ala Arg Ser
 120 125 130

 atg ggt gcg tcc ccg atg cgc atc atc gcc acc gtg atc att cca gaa 547
 Met Gly Ala Ser Pro Met Arg Ile Ile Ala Thr Val Ile Ile Pro Glu
 135 140 145

 gca ctt gga cca ttg gtt ctg ggt tac acc ttc ctg ttc atc gcg atc 595
 Ala Leu Gly Pro Leu Val Leu Gly Tyr Thr Phe Leu Phe Ile Ala Ile
 150 155 160 165

 gtc gat atg tcc gca atg gtc ggc tac atc ggt ggc ggt ggt ctt ggt 643
 Val Asp Met Ser Ala Met Val Gly Tyr Ile Gly Gly Gly Leu Gly
 170 175 180

 gac ttc gcc att gtt tac ggc tac cgc gcc ttc gac aac gaa gtt atg 691
 Asp Phe Ala Ile Val Tyr Gly Tyr Arg Ala Phe Asp Asn Glu Val Met
 185 190 195

 tac gtt gcc gtc ctg gtt atc gtc atc atc gtg cag gca gcc cag ctt 739
 Tyr Val Ala Val Leu Val Ile Val Ile Ile Val Gln Ala Ala Gln Leu
 200 205 210

 ctg ggc aat tgg ctg tcc aag aag atc atg cgc cgc taaacctctt 785
 Leu Gly Asn Trp Leu Ser Lys Lys Ile Met Arg Arg
 215 220 225

 gcatagaaaa acc 798

<210> 1746

<211> 225

<212> PRT

<213> Corynebacterium glutamicum

<400> 1746

 Met Asn Glu Met Ile Leu Ala Ala Asp Trp Asn Arg Leu Gly Pro Thr
 1 5 10 15

 Phe Gln Thr Ala Ile Ile Asp Thr Leu Leu Met Val Ile Ile Thr Met
 20 25 30

 Val Val Ala Gly Leu Leu Gly Leu Val Val Gly Leu Leu Leu Tyr Thr
 35 40 45

```

Thr Arg Ala Gly Gly Ile Leu Lys Asn Lys Val Ile Tyr Thr Ile Leu
  50          55          60
Asn Val Leu Val Asn Phe Val Arg Pro Ile Pro Phe Ile Ile Leu Ile
  65          70          75          80
Ala Ala Ile Lys Pro Leu Thr Val Ala Val Met Gly Thr Ser Ile Gly
          85          90          95
Arg Asp Ala Gly Ile Phe Val Met Val Val Ala Ala Ile Phe Ser Val
 100          105          110
Ala Arg Ile Val Glu Gln Asn Leu Val Ser Ile Asp Pro Gly Val Ile
 115          120          125
Glu Ala Ala Arg Ser Met Gly Ala Ser Pro Met Arg Ile Ile Ala Thr
 130          135          140
Val Ile Ile Pro Glu Ala Leu Gly Pro Leu Val Leu Gly Tyr Thr Phe
 145          150          155          160
Leu Phe Ile Ala Ile Val Asp Met Ser Ala Met Val Gly Tyr Ile Gly
          165          170          175
Gly Gly Gly Leu Gly Asp Phe Ala Ile Val Tyr Gly Tyr Arg Ala Phe
          180          185          190
Asp Asn Glu Val Met Tyr Val Ala Val Leu Val Ile Val Ile Val
          195          200          205
Gln Ala Ala Gln Leu Leu Gly Asn Trp Leu Ser Lys Lys Ile Met Arg
 210          215          220
Arg
225

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<210> 1747

<211> 576

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(553)

<223> RXA00423

<400> 1747

agttctttga aaaacgtggc gcttccaggc cattcacctg cactggcatg gtgtacgccg 60

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cttttattta cgcaatctgt gagctggagg cccgcacaaa atg acc tat ccc gtg 115
Met Thr Tyr Pro Val
          1          5

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```

ttg agt gtt ttg gat aat tct ggc gat cac aac atc atc tgg cat gtg 163
Leu Ser Val Leu Asp Asn Ser Gly Asp His Asn Ile Ile Trp His Val
          10          15          20

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```

caa act tat ccc gcg gcg ctg ccc acc ggg gcg tgg att gcc gat gag 211
Gln Thr Tyr Pro Ala Ala Leu Pro Thr Gly Ala Trp Ile Ala Asp Glu

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	25	30	35	
caa caa ctg act gac ctg ctg aaa gac aca gta gtg ttc ctt acc cct				259
Gln Gln Leu Thr Asp Leu Leu Lys Asp Thr Val Val Phe Leu Thr Pro				
	40	45	50	
ggg agc acc gct ccg gaa aat gcc ccc gtg gcg acg ata gaa ggg gtg				307
Gly Ser Thr Ala Pro Glu Asn Ala Pro Val Ala Thr Ile Glu Gly Val				
	55	60	65	
cgg gtt gac gtc gat aag cag gtg gca gag tac aac aaa cat ggg atc				355
Arg Val Asp Val Asp Lys Gln Val Ala Glu Tyr Asn Lys His Gly Ile				
	70	75	80	85
cgc ctg ccc agc ttg ggc gcg cgc act gtg gag gcg cag tac cgc ggc				403
Arg Leu Pro Ser Leu Gly Ala Arg Thr Val Glu Ala Gln Tyr Arg Gly				
	90	95	100	
gag ccg gag gca gag gct gcg tgg cgc acg gcg atg gag ctc gta gag				451
Glu Pro Glu Ala Glu Ala Ala Trp Arg Thr Ala Met Glu Leu Val Glu				
	105	110	115	
atc gca ggc ggc tgg cta gaa att gaa gcc aag cgc cgg gcg cgg aag				499
Ile Ala Gly Gly Trp Leu Glu Ile Glu Ala Lys Arg Arg Ala Arg Lys				
	120	125	130	
gcg ctg gct gag gcc ttc ggc gcg gag gtc cag cca ctg ccg ctt gac				547
Ala Leu Ala Glu Ala Phe Gly Ala Glu Val Gln Pro Leu Pro Leu Asp				
	135	140	145	
acc gaa taggacaaat gggtctatcc tgg				576
Thr Glu				
150				
<210> 1748				
<211> 151				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 1748				
Met Thr Tyr Pro Val Leu Ser Val Leu Asp Asn Ser Gly Asp His Asn				
1 5 10 15				
Ile Ile Trp His Val Gln Thr Tyr Pro Ala Ala Leu Pro Thr Gly Ala				
20 25 30				
Trp Ile Ala Asp Glu Gln Gln Leu Thr Asp Leu Leu Lys Asp Thr Val				
35 40 45				
Val Phe Leu Thr Pro Gly Ser Thr Ala Pro Glu Asn Ala Pro Val Ala				
50 55 60				
Thr Ile Glu Gly Val Arg Val Asp Val Asp Lys Gln Val Ala Glu Tyr				
65 70 75 80				
Asn Lys His Gly Ile Arg Leu Pro Ser Leu Gly Ala Arg Thr Val Glu				
85 90 95				
Ala Gln Tyr Arg Gly Glu Pro Glu Ala Glu Ala Ala Trp Arg Thr Ala				
100 105 110				

Met Glu Leu Val Glu Ile Ala Gly Gly Trp Leu Glu Ile Glu Ala Lys
 115 120
 Arg Arg Ala Arg Lys Ala Leu Ala Glu Ala Phe Gly Ala Glu Val Gln
 130 135 140
 Pro Leu Pro Leu Asp Thr Glu
 145 150

<210> 1749
 <211> 594
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(571)
 <223> RXA00424

<400> 1749
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 atcagtgtgag agtcttggca acatggatgac caggatgaga ttg cag gta gca gca 115
 Leu Gln Val Ala Ala
 1 5
 ggt tcc gcg ctg att ggt gct ggg gtt gcg gtt aat gat tac gta caa 163
 Gly Ser Ala Leu Ile Gly Ala Gly Val Ala Val Asn Asp Tyr Val Gln
 10 15 20
 agc cca gtc cgc cgg gcc atc agt tat ggt gcg ttg gcg ctt tct ggg 211
 Ser Pro Val Arg Arg Ala Ile Ser Tyr Gly Ala Leu Ala Leu Ser Gly
 25 30 35
 gcg acg gtg att gcg atg ggt cag gac ccg act ggg gag cgg tcc atc 259
 Ala Thr Val Ile Ala Met Gly Gln Asp Pro Thr Gly Glu Arg Ser Ile
 40 45 50
 att gcg aaa gat tcc gcg acg atg gtt gat caa atc cgc cag gag atc 307
 Ile Ala Lys Asp Ser Ala Thr Met Val Asp Gln Ile Arg Gln Glu Ile
 55 60 65
 ggc gat ttg ggt gtc acg cct ggt cca gaa tct gat gtg gat gcc atc 355
 Gly Asp Leu Gly Val Thr Pro Gly Pro Glu Ser Asp Val Asp Ala Ile
 70 75 80 85
 acg gag cga ggt ccg ctg gtg acg tgg ctg ttg ctt gct gtt ttt gtc 403
 Thr Glu Arg Gly Pro Leu Val Thr Trp Leu Leu Ala Val Phe Val
 90 95 100
 gtg gca ttt ttc acc ttg gcg tat ttc tcc atg cgc atg gat gtg gcg 451
 Val Ala Phe Phe Thr Leu Ala Tyr Phe Ser Met Arg Met Asp Val Ala
 105 110 115
 gtg atg aga agg atc gct aag ttc ttt gaa aaa cgt ggc gct tcc agg 499
 Val Met Arg Arg Ile Ala Lys Phe Phe Glu Lys Arg Gly Ala Ser Arg
 120 125 130
 cca ttc acc tgc act ggc atg gtg tac gcc gct ttt att tac gca atc 547

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Pro Phe Thr Cys Thr Gly Met Val Tyr Ala Ala Phe Ile Tyr Ala Ile
   135                               140                               145

tgt gag ctg gag gcc cgc aca aaa tgacctatcc cgtgttgagt gtt      594
Cys Glu Leu Glu Ala Arg Thr Lys
   150                               155

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<210> 1750

<211> 157

<212> PRT

<213> Corynebacterium glutamicum

<400> 1750

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Leu Gln Val Ala Ala Gly Ser Ala Leu Ile Gly Ala Gly Val Ala Val
   1                               5                               10                               15

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Asn Asp Tyr Val Gln Ser Pro Val Arg Arg Ala Ile Ser Tyr Gly Ala
   20                               25                               30

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```

Leu Ala Leu Ser Gly Ala Thr Val Ile Ala Met Gly Gln Asp Pro Thr
   35                               40                               45

```

```

Gly Glu Arg Ser Ile Ile Ala Lys Asp Ser Ala Thr Met Val Asp Gln
   50                               55                               60

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```

Ile Arg Gln Glu Ile Gly Asp Leu Gly Val Thr Pro Gly Pro Glu Ser
   65                               70                               75                               80

```

```

Asp Val Asp Ala Ile Thr Glu Arg Gly Pro Leu Val Thr Trp Leu Leu
   85                               90                               95

```

```

Leu Ala Val Phe Val Val Ala Phe Phe Thr Leu Ala Tyr Phe Ser Met
  100                               105                               110

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```

Arg Met Asp Val Ala Val Met Arg Arg Ile Ala Lys Phe Phe Glu Lys
  115                               120                               125

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```

Arg Gly Ala Ser Arg Pro Phe Thr Cys Thr Gly Met Val Tyr Ala Ala
  130                               135                               140

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Phe Ile Tyr Ala Ile Cys Glu Leu Glu Ala Arg Thr Lys
  145                               150                               155

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<210> 1751

<211> 348

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(325)

<223> RXA00425

<400> 1751

accgcaaccc cagcaccaat cagcgcgga cctgctgcta cctgcaatct catcctggta 60

```

tccatgttgc caagactact cactgattaa ggtgggtgggc atg ttt gaa aga ttc      115
Met Phe Glu Arg Phe
   1                               5

```



```

aaa aaa gcc aag gct ccc gag gtc cac atc gcg gcg gaa cgc acc aac 163
Lys Lys Ala Lys Ala Pro Glu Val His Ile Ala Ala Glu Arg Thr Asn
          10                      15                      20

ctt ccg ctt aac gat ttc atg acc cgc ctc ttc gcc cag gaa ctc ccc 211
Leu Pro Leu Asn Asp Phe Met Thr Arg Leu Phe Ala Gln Glu Leu Pro
          25                      30                      35

ctg ctc gat agc acc tca cgt tca gag gtc tac cgc ctg ctt cgg gaa 259
Leu Leu Asp Ser Thr Ser Arg Ser Glu Val Tyr Arg Leu Leu Arg Glu
          40                      45                      50

tac gac ggc cca aca att agc tcc cag gaa gaa atc ccc gca gag att 307
Tyr Asp Gly Pro Thr Ile Ser Ser Gln Glu Glu Ile Pro Ala Glu Ile
          55                      60                      65

cgt gaa ctc atg gat ctt taggcaataa atgtgagatt gga 348
Arg Glu Leu Met Asp Leu
          70                      75

```

```

<210> 1752
<211> 75
<212> PRT
<213> Corynebacterium glutamicum

<400> 1752
Met Phe Glu Arg Phe Lys Lys Ala Lys Ala Pro Glu Val His Ile Ala
 1          5          10          15

Ala Glu Arg Thr Asn Leu Pro Leu Asn Asp Phe Met Thr Arg Leu Phe
          20          25          30

Ala Gln Glu Leu Pro Leu Leu Asp Ser Thr Ser Arg Ser Glu Val Tyr
          35          40          45

Arg Leu Leu Arg Glu Tyr Asp Gly Pro Thr Ile Ser Ser Gln Glu Glu
          50          55          60

Ile Pro Ala Glu Ile Arg Glu Leu Met Asp Leu
          65          70          75

```

```

<210> 1753
<211> 756
<212> DNA
<213> Corynebacterium glutamicum

```

```

<220>
<221> CDS
<222> (101)..(733)
<223> RXA00428

```

```

<400> 1753
agcgtcgag ggatcggcgc gatcttcttc cttecgatcg gcatcatcat gtgcctcatc 60

gccggattca accgctacta cgcagccctt aaggtctaaa atg ccc ggt cta gtt 115
          Met Pro Gly Leu Val
          1                      5

```

```

ctc tcc aca aac gtc gcc cat atc caa caa gac cca ggt ggc gat gac 163
Leu Ser Thr Asn Val Ala His Ile Gln Gln Asp Pro Gly Gly Asp Asp
10 15 20

cgc atc agc ggc atc aac aaa ctc ccc gtc gcc acc ggc atc gat gta 211
Arg Ile Ser Gly Ile Asn Lys Leu Pro Val Ala Thr Gly Ile Asp Val
25 30 35

ttc atc ccc gga ccc aac tac ggc gac ggc tcc ggc gta gtc ggc gac 259
Phe Ile Pro Gly Pro Asn Tyr Gly Asp Gly Ser Gly Val Val Gly Asp
40 45 50

gcc atc ggc gat tcc ctc cac cac ggc ggc gcc cac aaa gcc atc tac 307
Ala Ile Gly Asp Ser Leu His His Gly Gly Ala His Lys Ala Ile Tyr
55 60 65

gcc tac agc cgc gaa gaa ctc gac ttc ttt gac ccc acc tac cgc aac 355
Ala Tyr Ser Arg Glu Leu Leu Asp Phe Phe Asp Pro Thr Tyr Arg Asn
70 75 80 85

gga tac ttc ggc gaa aac ctc acc acc agc gga atc gtg ttg gaa gac 403
Gly Tyr Phe Gly Glu Asn Leu Thr Thr Ser Gly Ile Val Leu Glu Asp
90 95 100

ctc ctg atc aac caa caa gtg cgc atc ggc acc acg ctg ctc gaa gtc 451
Leu Leu Ile Asn Gln Gln Val Arg Ile Gly Thr Thr Leu Leu Glu Val
105 110 115

tcc att ccc cgc cga ccc tgc cgc acg ttc gcc cac tgg ctc gac atc 499
Ser Ile Pro Arg Arg Pro Cys Arg Thr Phe Ala His Trp Leu Asp Ile
120 125 130

aaa ggc tgg cta aaa acc ttc acc caa cgc ggc ctc ccc ggc agc tac 547
Lys Gly Trp Leu Lys Thr Phe Thr Gln Arg Gly Leu Pro Gly Ser Tyr
135 140 145

ttc cga gtc atc gaa gaa ggc cac atc aac ccc ggc gac ccc att gaa 595
Phe Arg Val Ile Glu Glu Gly His Ile Asn Pro Gly Asp Pro Ile Glu
150 155 160 165

gtt ctg cag gcc ccc gac cac gac atc acc atg tcc atg gcc ttc cgt 643
Val Leu Gln Ala Pro Asp His Asp Ile Thr Met Ser Met Ala Phe Arg
170 175 180

gca aaa atg gga aac aaa gac ctc gcg cgc cgg gtt gtt gca gcc aac 691
Ala Lys Met Gly Asn Lys Asp Leu Ala Arg Arg Val Val Ala Ala Asn
185 190 195

tgt ctc cca gcg cgc tac cac gag gaa cta cta aaa ctg atc 733
Cys Leu Pro Ala Arg Tyr His Glu Glu Leu Leu Lys Leu Ile
200 205 210

tagggcctat tgaattctc gtc 756

```

<210> 1754

<211> 211

<212> PRT

<213> Corynebacterium glutamicum

<400> 1754

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Met Pro Gly Leu Val Leu Ser Thr Asn Val Ala His Ile Gln Gln Asp
 1           5           10           15

Pro Gly Gly Asp Asp Arg Ile Ser Gly Ile Asn Lys Leu Pro Val Ala
      20           25           30

Thr Gly Ile Asp Val Phe Ile Pro Gly Pro Asn Tyr Gly Asp Gly Ser
      35           40           45

Gly Val Val Gly Asp Ala Ile Gly Asp Ser Leu His His Gly Gly Ala
      50           55           60

His Lys Ala Ile Tyr Ala Tyr Ser Arg Glu Glu Leu Asp Phe Phe Asp
      65           70           75           80

Pro Thr Tyr Arg Asn Gly Tyr Phe Gly Glu Asn Leu Thr Thr Ser Gly
      85           90           95

Ile Val Leu Glu Asp Leu Leu Ile Asn Gln Gln Val Arg Ile Gly Thr
      100          105          110

Thr Leu Leu Glu Val Ser Ile Pro Arg Arg Pro Cys Arg Thr Phe Ala
      115          120          125

His Trp Leu Asp Ile Lys Gly Trp Leu Lys Thr Phe Thr Gln Arg Gly
      130          135          140

Leu Pro Gly Ser Tyr Phe Arg Val Ile Glu Glu Gly His Ile Asn Pro
      145          150          155          160

Gly Asp Pro Ile Glu Val Leu Gln Ala Pro Asp His Asp Ile Thr Met
      165          170          175

Ser Met Ala Phe Arg Ala Lys Met Gly Asn Lys Asp Leu Ala Arg Arg
      180          185          190

Val Val Ala Ala Asn Cys Leu Pro Ala Arg Tyr His Glu Glu Leu Leu
      195          200          205

Lys Leu Ile
      210

```

<210> 1755

<211> 525

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(502)

<223> RXA00429

<400> 1755

cgatgggtgt cgccttcgtg atcgcccaag gcacccggaa cgggtcatcaa cttcatcgtc 60

caaagaacca tcattttccg agtgaagtaa ggtacccttc atg aag acc ttc aat 115

Met Lys Thr Phe Asn

1

5

ccc acc atg att gcc gga etc atc ggc gta etc tac ttc gtg ctg etc 163

```

Pro Thr Met Ile Ala Gly Leu Ile Gly Val Leu Tyr Phe Val Leu Leu
              10                      15                      20

acc ctg att ttc tcc atc caa gac atg gaa cta gca gca gaa atc gcc 211
Thr Leu Ile Phe Ser Ile Gln Asp Met Glu Leu Ala Ala Glu Ile Ala
              25                      30                      35

ttc gga atc gtc acc atc gtc ggc ctg atc gcg gtg tgg gac aac ttc 259
Phe Gly Ile Val Thr Ile Val Gly Leu Ile Ala Val Trp Asp Asn Phe
              40                      45                      50

cgc gac cgc aac aac tcc acc tgg aaa acc tgg acc ggc ctc gtc ggc 307
Arg Asp Arg Asn Asn Ser Thr Trp Lys Thr Trp Thr Gly Leu Val Gly
              55                      60                      65

gga ctg cta atc gcc gtc ccc gga atc tgc ctt ctt gtg gga aac ctc 355
Gly Leu Leu Ile Ala Val Pro Gly Ile Cys Leu Val Gly Asn Leu
              70                      75                      80                      85

gtg ctc ctc gca gtc gac ggc aac ccc tca acc atg gtg aac acc ctg 403
Val Leu Leu Ala Val Asp Gly Asn Pro Ser Thr Met Val Asn Thr Leu
              90                      95                      100

ctc agc gtc gca ggg atc ggc gcg atc ttc ctc ctt ccg atc ggc atc 451
Leu Ser Val Ala Gly Ile Gly Ala Ile Phe Leu Leu Pro Ile Gly Ile
              105                      110                      115

atc atg tgc ctc atc gcc gga ttc aac cgc tac tac gca gcc ctt aag 499
Ile Met Cys Leu Ile Ala Gly Phe Asn Arg Tyr Tyr Ala Ala Leu Lys
              120                      125                      130

gtc taaaatgccc ggtctagttc tct 525
Val

<210> 1756
<211> 134
<212> PRT
<213> Corynebacterium glutamicum

<400> 1756
Met Lys Thr Phe Asn Pro Thr Met Ile Ala Gly Leu Ile Gly Val Leu
  1                      5                      10                      15

Tyr Phe Val Leu Leu Thr Leu Ile Phe Ser Ile Gln Asp Met Glu Leu
  20                      25                      30

Ala Ala Glu Ile Ala Phe Gly Ile Val Thr Ile Val Gly Leu Ile Ala
  35                      40                      45

Val Trp Asp Asn Phe Arg Asp Arg Asn Asn Ser Thr Trp Lys Thr Trp
  50                      55                      60

Thr Gly Leu Val Gly Gly Leu Leu Ile Ala Val Pro Gly Ile Cys Leu
  65                      70                      75                      80

Leu Val Gly Asn Leu Val Leu Leu Ala Val Asp Gly Asn Pro Ser Thr
  85                      90                      95

Met Val Asn Thr Leu Leu Ser Val Ala Gly Ile Gly Ala Ile Phe Leu

```

```

100              105              110
Leu Pro Ile Gly Ile Ile Met Cys Leu Ile Ala Gly Phe Asn Arg Tyr
115              120              125

Tyr Ala Ala Leu Lys Val
130

<210> 1757
<211> 534
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(511)
<223> RXA00430

<400> 1757
tgcccccggtg gatcgcttgg acatttatag ggagctgctg tgtttctagg tattgtgtaa 60
cctcgtgtgcc gaaaatcttg atgttacgat cgtccgacca atg agc ctg aaa acc 115
Met Ser Leu Lys Thr
1 5
caa gct ttc cgg ttc atc ctc acc ggt ggc ctc tca gcc atc gtg gac 163
Gln Ala Phe Arg Phe Ile Leu Thr Gly Gly Leu Ser Ala Ile Val Asp
10 15 20
ctc ggc ctg ctg tca ctt ttg cag cta gtg ttc ggc ctt ccc gta cct 211
Leu Gly Leu Leu Ser Leu Leu Gln Leu Val Phe Gly Leu Pro Val Pro
25 30 35
gtt gcc cgc acg atc tcc ttc atc gcc ggc acc acc acc gcc tac atg 259
Val Ala Arg Thr Ile Ser Phe Ile Ala Gly Thr Thr Thr Ala Tyr Met
40 45 50
atc aac cgc cgg tgg acc ttc caa gca gaa agc tcc acc tcc agg ttc 307
Ile Asn Arg Arg Trp Thr Phe Gln Ala Glu Ser Ser Thr Ser Arg Phe
55 60 65
ctt gct gtg gtg gcc ctc tac ggc gtg acc ttc ctg atc aac att gga 355
Leu Ala Val Val Ala Leu Tyr Gly Val Thr Phe Leu Ile Asn Ile Gly
70 75 80 85
ctg caa acc ctc tgc tcc gca ttg ttt gag aat tgg ggc tgg aac gaa 403
Leu Gln Thr Leu Cys Ser Ala Leu Phe Glu Asn Trp Gly Trp Asn Glu
90 95 100
gcc gtc gcg atg gtg gtc gcc ttc gtg atc gcc caa ggc acc cgg aac 451
Ala Val Ala Met Val Val Ala Phe Val Ile Ala Gln Gly Thr Arg Asn
105 110 115
ggg cat caa ctt cat cgt cca aag aac cat cat ttt ccg agt gaa gta 499
Gly His Gln Leu His Arg Pro Lys Asn His His Phe Pro Ser Glu Val
120 125 130
agg tac ccc tca tgaagacctt caatcccacc atg 534
Arg Tyr Pro Ser
135

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<210> 1758
 <211> 137
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 1758
 Met Ser Leu Lys Thr Gln Ala Phe Arg Phe Ile Leu Thr Gly Gly Leu
 1 5 10 15
 Ser Ala Ile Val Asp Leu Gly Leu Leu Ser Leu Leu Gln Leu Val Phe
 20 25 30
 Gly Leu Pro Val Pro Val Ala Arg Thr Ile Ser Phe Ile Ala Gly Thr
 35 40 45
 Thr Thr Ala Tyr Met Ile Asn Arg Arg Trp Thr Phe Gln Ala Glu Ser
 50 55 60
 Ser Thr Ser Arg Phe Leu Ala Val Val Ala Leu Tyr Gly Val Thr Phe
 65 70 75 80
 Leu Ile Asn Ile Gly Leu Gln Thr Leu Cys Ser Ala Leu Phe Glu Asn
 85 90 95
 Trp Gly Trp Asn Glu Ala Val Ala Met Val Val Ala Phe Val Ile Ala
 100 105 110
 Gln Gly Thr Arg Asn Gly His Gln Leu His Arg Pro Lys Asn His His
 115 120 125
 Phe Pro Ser Glu Val Arg Tyr Pro Ser
 130 135

<210> 1759
 <211> 648
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(625)
 <223> RXA00433

<400> 1759
 gtctccagcg actcaaacat caaaaattga tatttgcgac aagttgaaat catacccgat 60
 agtctcgaac atactaaatc acctaatacag ggggaattac atg gat gtg tta aag 115
 Met Asp Val Leu Lys
 1 5
 atc gcc atc atc gct gca gcc atg att ggt gtg ccg gtt ctg gtg gtt 163
 Ile Ala Ile Ile Ala Ala Ala Met Ile Gly Val Pro Val Leu Val Val
 10 15 20
 ttc ctc att gtg ttt gcg gtg cac aag ttg gct aag gaa gtg ccg cgg 211
 Phe Leu Ile Val Phe Ala Val His Lys Leu Ala Lys Glu Val Pro Arg
 25 30 35

tct ggt cgt cgt ccg ggt att ggg ttg ggg ttg ttg ctt ggt ttt gtt 259
 Ser Gly Arg Arg Pro Gly Ile Gly Leu Gly Leu Leu Leu Gly Phe Val
 40 45 50
 gcg ggg ctc atc gtg tgg ttt gtg tgg ttg agt tgg ggt ggt tat tac 307
 Ala Gly Leu Ile Val Trp Phe Val Trp Leu Ser Trp Gly Gly Tyr Tyr
 55 60 65
 gag aat gag ttt ggg cag atg caa ggt ccg tat cgt ccg tgg cag gtt 355
 Glu Asn Glu Phe Gly Gln Met Gln Gly Pro Tyr Arg Pro Trp Gln Val
 70 75 80 85
 gtt gct tgt ggt gtc acg atg gtc gcg gtc act gtg att ctt ggt ctg 403
 Val Ala Cys Gly Val Thr Met Val Ala Val Thr Val Ile Leu Gly Leu
 90 95 100
 tgg act agg tgg act gcg tct ggt ccg ttt tat tcg gcg ttg ggt ggt 451
 Trp Thr Arg Trp Thr Ala Ser Gly Pro Phe Tyr Ser Ala Leu Gly Gly
 105 110 115
 gcg tcg ggg ttt agt ttc gcg tgg gcc atg gat gcc att cct cag gat 499
 Ala Ser Gly Phe Ser Phe Ala Trp Ala Met Asp Ala Ile Pro Gln Asp
 120 125 130
 gaa acc gga ttg tcg gcg ttt ggc tta gtg atg gtc att gtt ggt gtt 547
 Glu Thr Gly Leu Ser Ala Phe Gly Leu Val Met Val Ile Val Gly Val
 135 140 145
 ggt gcg ggg cta aat gtg gtg gca act ctg acg tca atc ggc gca acg 595
 Gly Ala Gly Leu Asn Val Val Ala Thr Leu Thr Ser Ile Gly Ala Thr
 150 155 160 165
 atc tgg aat aac cgg cta ccc tcg aat gca tgactaaaac cacgcgccaa 645
 Ile Trp Asn Asn Arg Leu Pro Ser Asn Ala
 170 175
 acc 648

<210> 1760

<211> 175

<212> PRT

<213> Corynebacterium glutamicum

<400> 1760

Met Asp Val Leu Lys Ile Ala Ile Ile Ala Ala Ala Met Ile Gly Val
 1 5 10 15
 Pro Val Leu Val Val Phe Leu Ile Val Phe Ala Val His Lys Leu Ala
 20 25 30
 Lys Glu Val Pro Arg Ser Gly Arg Arg Pro Gly Ile Gly Leu Gly Leu
 35 40 45
 Leu Leu Gly Phe Val Ala Gly Leu Ile Val Trp Phe Val Trp Leu Ser
 50 55 60
 Trp Gly Gly Tyr Tyr Glu Asn Glu Phe Gly Gln Met Gln Gly Pro Tyr
 65 70 75 80
 Arg Pro Trp Gln Val Val Ala Cys Gly Val Thr Met Val Ala Val Thr

85 90 95

Val Ile Leu Gly Leu Trp Thr Arg Trp Thr Ala Ser Gly Pro Phe Tyr
100 105 110

Ser Ala Leu Gly Gly Ala Ser Gly Phe Ser Phe Ala Trp Ala Met Asp
115 120 125

Ala Ile Pro Gln Asp Glu Thr Gly Leu Ser Ala Phe Gly Leu Val Met
130 135 140

Val Ile Val Gly Val Gly Ala Gly Leu Asn Val Val Ala Thr Leu Thr
145 150 155 160

Ser Ile Gly Ala Thr Ile Trp Asn Asn Arg Leu Pro Ser Asn Ala
165 170 175

<210> 1761
<211> 615
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(592)
<223> RXA00451

<400> 1761
ggatccgcgc atgagccga ggcccaggat gcatactggg cgggaaatgt ctttggtagt 60

cacctgacaa gtgtggcaca tacctactac gggtatctct atg aac act gaa gag 115
Met Asn Thr Glu Glu
1 5

gat ggc ctg agc ttt gca gtt acg gct acc tta gtt gaa ggt aaa tgg 163
Asp Gly Leu Ser Phe Ala Val Thr Ala Thr Leu Val Glu Gly Lys Trp
10 15 20

cag gta cgc gag ttt gag gat cac ttc tcc aag ctc tct acc tct att 211
Gln Val Arg Glu Phe Glu Asp His Phe Ser Lys Leu Ser Thr Ser Ile
25 30 35

aat gcg gtt cgc tcg ctg cgt agc gag ggg ccg gcg ttt gcg ctg ttg 259
Asn Ala Val Arg Ser Leu Arg Ser Glu Gly Pro Ala Phe Ala Leu Leu
40 45 50

tgc gtt gat gat gaa tat ttt gtg atg gtg cgt ccc acc cca agt agg 307
Cys Val Asp Asp Glu Tyr Phe Val Met Val Arg Pro Thr Pro Ser Arg
55 60 65

gta ttc ctt ttc ctt tcg gat gcg ccg atg gct gtc gac gat gat ttc 355
Val Phe Leu Phe Leu Ser Asp Ala Pro Met Ala Val Asp Asp Asp Phe
70 75 80 85

gcc gcc gcg gtg atg gat gaa ctc gat gcg gat ctt cca gat atc aac 403
Ala Ala Ala Val Met Asp Glu Leu Asp Ala Asp Leu Pro Asp Ile Asn
90 95 100

cct gat gat ttg gac gac atc gat cca tgg cca gaa ggt gat ttc gat 451
Pro Asp Asp Leu Asp Asp Ile Asp Pro Trp Glu Gly Asp Phe Asp

	105	110	115	
att ttg gcg gat ttg ggg ctg tct gag gag gtt ctt tcc gtg att tgc				499
Ile Leu Ala Asp Leu Gly Leu Ser Glu Glu Val Leu Ser Val Ile Cys				
	120	125	130	
gat gac atg gat ttg gat cct tcc gaa caa ttg ctg cgc atc gcg gaa				547
Asp Asp Met Asp Leu Asp Pro Ser Glu Gln Leu Leu Arg Ile Ala Glu				
	135	140	145	
gaa ctc ggt ttt gat aat gat ctg gct cgg gtg gtg gga ttc gac				592
Glu Leu Gly Phe Asp Asn Asp Leu Ala Arg Val Val Gly Phe Asp				
	150	155	160	
tagtgggcgt ttacctgtg cag				615
<210> 1762				
<211> 164				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 1762				
Met Asn Thr Glu Glu Asp Gly Leu Ser Phe Ala Val Thr Ala Thr Leu				
	1	5	10	15
Val Glu Gly Lys Trp Gln Val Arg Glu Phe Glu Asp His Phe Ser Lys				
	20	25	30	
Leu Ser Thr Ser Ile Asn Ala Val Arg Ser Leu Arg Ser Glu Gly Pro				
	35	40	45	
Ala Phe Ala Leu Leu Cys Val Asp Asp Glu Tyr Phe Val Met Val Arg				
	50	55	60	
Pro Thr Pro Ser Arg Val Phe Leu Phe Leu Ser Asp Ala Pro Met Ala				
	65	70	75	80
Val Asp Asp Asp Phe Ala Ala Ala Val Met Asp Glu Leu Asp Ala Asp				
	85	90	95	
Leu Pro Asp Ile Asn Pro Asp Asp Leu Asp Asp Ile Asp Pro Trp Pro				
	100	105	110	
Glu Gly Asp Phe Asp Ile Leu Ala Asp Leu Gly Leu Ser Glu Glu Val				
	115	120	125	
Leu Ser Val Ile Cys Asp Asp Met Asp Leu Asp Pro Ser Glu Gln Leu				
	130	135	140	
Leu Arg Ile Ala Glu Glu Leu Gly Phe Asp Asn Asp Leu Ala Arg Val				
	145	150	155	160
Val Gly Phe Asp				

<210> 1763

<211> 1203

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1180)

<223> RXA00457

<400> 1763

aaactctcat gttggtttca tcgtggtttc atgaggcggg atttaactag agattgttag 60

ccaatcggcc agacacttcc tcctagaaag gtccctcctc atg acc att gct ctt 115
Met Thr Ile Ala Leu
1 5

gaa cac cca gta ctg cac tcc acg gcg atc gcg ttg cct gct cgt ttt 163
Glu His Pro Val Leu His Ser Thr Ala Ile Ala Leu Pro Ala Arg Phe
10 15 20

cag gcg agc tat acg acg cgt ttg gtg gcg gtg ggc gtc gat aag cgt 211
Gln Ala Ser Tyr Thr Thr Arg Leu Val Ala Val Gly Val Asp Lys Arg
25 30 35

cct tct gat ttt tgg ttg gaa aca gcc gcc acg ccg cag gcg gcc gat 259
Pro Ser Asp Phe Trp Leu Glu Thr Ala Gly Thr Pro Gln Ala Gly Asp
40 45 50

gtg gtg att gcg cgg gtg acg gcg att aat aat cac aag cgg gtg gag 307
Val Val Ile Ala Arg Val Thr Ala Ile Asn Asn His Lys Arg Val Glu
55 60 65

acg ccg gag tcg cgc aag gcc att ttg ttt gag ggg gtg ttg gtg atg 355
Thr Pro Glu Ser Arg Lys Ala Ile Leu Phe Glu Gly Val Leu Val Met
70 75 80 85

ttg gcg tat ggg cac cgg tat gcg gcg gat cag ttt tta gcg cat gta 403
Leu Ala Tyr Gly His Arg Tyr Ala Ala Asp Gln Phe Leu Ala His Val
90 95 100

ccg gag gat ttg ggg cca tgc cat ttg gtg gcg gct ggt gcc atc gcg 451
Pro Glu Asp Leu Gly Pro Cys His Leu Val Ala Ala Gly Ile Ala
105 110 115

gga acg gtg acg gcg ctg cac gat cgg gtg gat gaa ccc aca gag att 499
Gly Thr Val Thr Ala Leu His Asp Arg Val Asp Glu Pro Thr Glu Ile
120 125 130

gaa ccg ttg gga ttg ctg acc aat gcg cgc gga act gtg aat gta cgg 547
Glu Pro Leu Gly Leu Leu Thr Asn Ala Arg Gly Thr Val Asn Val Arg
135 140 145

gac ttt gcg gct ttt gat aat cct ttg aaa gtg gag gct ccc aac aag 595
Asp Phe Ala Ala Phe Asp Asn Pro Leu Lys Val Glu Ala Pro Asn Lys
150 155 160 165

cgt gcg cag gtg atc gcg gtg ctg gga acg tcg atg aac tct gga aaa 643
Arg Ala Gln Val Ile Ala Val Leu Gly Thr Ser Met Asn Ser Gly Lys
170 175 180

tcc acc acg ctt gcc tgc ttg gtc aat ggt ttg gct gcg gcg ggg cag 691
Ser Thr Thr Leu Ala Cys Leu Val Asn Gly Leu Ala Ala Gly Gln
185 190 195

aag gtg gcg gct gga aag atc acg ggc act ggt gct gga aat gac cgc 739
 Lys Val Ala Ala Gly Lys Ile Thr Gly Thr Gly Ala Gly Asn Asp Arg
 200 205 210

atg att tat cac gat gct ggt gct cac agc gtt att gat ttc acc gac 787
 Met Ile Tyr His Asp Ala Gly Ala His Ser Val Ile Asp Phe Thr Asp
 215 220 225

ttt ggc tac cca act acg ttc aag ctg aat ttc gcg gag att cgt gcg 835
 Phe Gly Tyr Pro Thr Phe Lys Leu Asn Phe Ala Glu Ile Arg Ala
 230 235 240 245

ctg agc gtc aac atg att aat gtg ctg gct gat tct ggt gcg gat acc 883
 Leu Ser Val Asn Met Ile Asn Val Leu Ala Asp Ser Gly Ala Asp Thr
 250 255 260

gtg atc gtg gaa atc gcg gac gga att tat cag ggc gaa acc tcg cgg 931
 Val Ile Val Glu Ile Ala Asp Gly Ile Tyr Gln Gly Glu Thr Ser Arg
 265 270 275

ctg ttg gcg gat caa gtg ttc cag gaa gcc gtg gat cat gtg gtg ttc 979
 Leu Leu Arg Asp Gln Val Phe Gln Glu Ala Val Asp His Val Val Phe
 280 285 290

tcc gct gtt gat gcc ttg ggc gcg aag gcc ggt gtg cag gaa ctg cag 1027
 Ser Ala Val Asp Ala Leu Gly Ala Lys Ala Gly Val Gln Glu Leu Gln
 295 300 305

gcg gcg ggg ctt cat gtg gct gcg gcc tcc gga gtg atg acg gct tcg 1075
 Ala Ala Gly Leu His Val Ala Ala Ala Ser Gly Val Met Thr Ala Ser
 310 315 320 325

ccg ctg gcc acc gcg gaa gct gcc gct gtg ctt gaa gtt cca gtg gtg 1123
 Pro Leu Ala Thr Ala Glu Ala Ala Val Leu Glu Val Pro Val Val
 330 335 340

ccc act ttt gat ctc acc aac ccg gag atc gtc aca gcg gtg cta acg 1171
 Pro Thr Phe Asp Leu Thr Asn Pro Glu Ile Val Thr Ala Val Leu Thr
 345 350 355

gat cat gcc tagcttatgg cgtgctcgtc gca 1203
 Asp His Ala
 360

<210> 1764
 <211> 360
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1764
 Met Thr Ile Ala Leu Glu His Pro Val Leu His Ser Thr Ala Ile Ala
 1 5 10 15

Leu Pro Ala Arg Phe Gln Ala Ser Tyr Thr Thr Arg Leu Val Ala Val
 20 25 30

Gly Val Asp Lys Arg Pro Ser Asp Phe Trp Leu Glu Thr Ala Gly Thr
 35 40 45

Pro Gln Ala Gly Asp Val Val Ile Ala Arg Val Thr Ala Ile Asn Asn

50 55 60
 His Lys Arg Val Glu Thr Pro Glu Ser Arg Lys Ala Ile Leu Phe Glu
 65 70 75 80
 Gly Val Leu Val Met Leu Ala Tyr Gly His Arg Tyr Ala Ala Asp Gln
 85 90 95
 Phe Leu Ala His Val Pro Glu Asp Leu Gly Pro Cys His Leu Val Ala
 100 105 110
 Ala Gly Gly Ile Ala Gly Thr Val Thr Ala Leu His Asp Arg Val Asp
 115 120 125
 Glu Pro Thr Glu Ile Glu Pro Leu Gly Leu Leu Thr Asn Ala Arg Gly
 130 135 140
 Thr Val Asn Val Arg Asp Phe Ala Ala Phe Asp Asn Pro Leu Lys Val
 145 150 155 160
 Glu Ala Pro Asn Lys Arg Ala Gln Val Ile Ala Val Leu Gly Thr Ser
 165 170 175
 Met Asn Ser Gly Lys Ser Thr Thr Leu Ala Cys Leu Val Asn Gly Leu
 180 185 190
 Ala Ala Ala Gly Gln Lys Val Ala Ala Gly Lys Ile Thr Gly Thr Gly
 195 200 205
 Ala Gly Asn Asp Arg Met Ile Tyr His Asp Ala Gly Ala His Ser Val
 210 215 220
 Ile Asp Phe Thr Asp Phe Gly Tyr Pro Thr Thr Phe Lys Leu Asn Phe
 225 230 235 240
 Ala Glu Ile Arg Ala Leu Ser Val Asn Met Ile Asn Val Leu Ala Asp
 245 250 255
 Ser Gly Ala Asp Thr Val Ile Val Glu Ile Ala Asp Gly Ile Tyr Gln
 260 265 270
 Gly Glu Thr Ser Arg Leu Leu Arg Asp Gln Val Phe Gln Glu Ala Val
 275 280 285
 Asp His Val Val Phe Ser Ala Val Asp Ala Leu Gly Ala Lys Ala Gly
 290 295 300
 Val Gln Glu Leu Gln Ala Ala Gly Leu His Val Ala Ala Ala Ser Gly
 305 310 315 320
 Val Met Thr Ala Ser Pro Leu Ala Thr Ala Glu Ala Ala Ala Val Leu
 325 330 335
 Glu Val Pro Val Val Pro Thr Phe Asp Leu Thr Asn Pro Glu Ile Val
 340 345 350
 Thr Ala Val Leu Thr Asp His Ala
 355 360

<210> 1765

<211> 1503

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1480)

<223> RXA00462

<400> 1765

tgaagccttg tcattttcta catgtgcac gcctttgact accgcccttt tccgccagc 60

ccttttagaa accagcaaca cagaaagcaa gtgatcattt atg gaa gct att gcc 115
 Met Glu Ala Ile Ala
 1 5

ata cta ttt gtc att ggg gcg att ctt gtc gtc gcg gtc att gtc ctc 163
 Ile Leu Phe Val Ile Gly Ala Ile Leu Val Val Ala Val Ile Val Leu
 10 15 20

ggg att ttc ttc tta act tca cgc acc tgg atc aag gtg gct gca gct 211
 Gly Ile Phe Phe Leu Thr Ser Arg Thr Trp Ile Lys Val Ala Ala Ala
 25 30 35

gat gaa gcg ctc att gtc tct gcg aag aag aag ggg gaa tcg cag gtc 259
 Asp Glu Ala Leu Ile Val Ser Ala Lys Lys Lys Gly Glu Ser Gln Val
 40 45 50

att gtc cac ggc aaa gct gtg gta atg cct att acc cag act cac cag 307
 Ile Val His Gly Lys Ala Val Val Met Pro Ile Thr Gln Thr His Gln
 55 60 65

aag atc tct ctg cgt tcc cgt cag gta aat atg cag gtg acg gca caa 355
 Lys Ile Ser Leu Arg Ser Arg Gln Val Asn Met Gln Val Thr Ala Gln
 70 75 80 85

agc gat gac aat gtc acg ttg aat gtc gag gct gtt gcg ctg gtg aag 403
 Ser Asp Asp Asn Val Thr Leu Asn Val Glu Ala Val Ala Leu Val Lys
 90 95 100

atc ggt tcc gaa gct gag ttt att cgt cgc gct gcc cag cgc ttc gct 451
 Ile Gly Ser Glu Ala Glu Phe Ile Arg Arg Ala Ala Gln Arg Phe Ala
 105 110 115

tcc agt gac aaa gaa att gtt cgg ttc aca cag gat cag ctg gaa ggt 499
 Ser Ser Asp Lys Glu Ile Val Arg Phe Thr Gln Asp Gln Leu Glu Gly
 120 125 130

gtg ctt cgt ggt gtc gtg gcg cag caa aca gtc acg tcg ctc atg cgt 547
 Val Leu Arg Gly Val Val Ala Gln Gln Thr Val Thr Ser Leu Met Arg
 135 140 145

gag cgt aaa aaa ttc tcc gag cag atc gct gaa aca gtc atc ccc gag 595
 Glu Arg Lys Lys Phe Ser Glu Gln Ile Ala Glu Thr Val Ile Pro Glu
 150 155 160 165

cta gag aag cag ggt ttg att ctt gac tcc ttc cag att cgt ggc atc 643
 Leu Glu Lys Gln Gly Leu Ile Leu Asp Ser Phe Gln Ile Arg Gly Ile
 170 175 180

acc gat gat gtg gga tac atc aaa tcc ctc ggc gca ccg gaa att cag 691

Thr Asp Asp Val Gly Tyr Ile Lys Ser Leu Gly Ala Pro Glu Ile Gln	
185 190 195	
gca aag aag cag gct gcg gaa att gca gaa act gaa gct gct cgt gcg	739
Ala Lys Lys Gln Ala Ala Glu Ile Ala Glu Thr Glu Ala Ala Arg Ala	
200 205 210	
atc gct aaa tca cgc att gct aac caa gag gca gat ctg gtt gaa cag	787
Ile Ala Lys Ser Arg Ile Ala Asn Gln Glu Ala Asp Leu Val Glu Gln	
215 220 225	
acc caa ctt gat gcc aac aag gct gcc gct gat gct cag gtc ggt gaa	835
Thr Gln Leu Asp Ala Asn Lys Ala Ala Ala Asp Ala Gln Val Gly Glu	
230 235 240 245	
gcc cgt gcc cag gct atg cag gct gaa cgc ctt gcc gat gaa aaa gct	883
Ala Arg Ala Gln Ala Met Gln Ala Glu Arg Leu Ala Asp Glu Lys Ala	
250 255 260	
cga cta gag gtt ctt cgc caa cag gct gaa aat aag cag atc gag ctg	931
Arg Leu Glu Val Leu Arg Gln Gln Ala Glu Asn Lys Gln Ile Glu Leu	
265 270 275	
gaa gcc gaa gtg aac aag gtg gcc gac gct gaa cgc tac cgc cgc aag	979
Glu Ala Glu Val Asn Lys Val Ala Asp Ala Glu Arg Tyr Arg Arg Lys	
280 285 290	
cag gaa gtc gaa gcc gat act ttc gag caa acc agg cgc gca cag gct	1027
Gln Glu Val Glu Ala Asp Thr Phe Glu Gln Thr Arg Arg Ala Gln Ala	
295 300 305	
cag gtc gaa atc gca gaa gcc gaa gct acc gct gca aag gtt cgt gca	1075
Gln Val Glu Ile Ala Glu Ala Glu Ala Thr Ala Ala Lys Val Arg Ala	
310 315 320 325	
atg gct gaa gcc gaa gct gtt cga ttg aag gga cag gca gag gca gac	1123
Met Ala Glu Ala Glu Ala Val Arg Leu Lys Gly Gln Ala Glu Ala Asp	
330 335 340	
gct atc aag gca aag gcc gag gcc tac cgc gaa aac caa gaa gca cta	1171
Ala Ile Lys Ala Lys Ala Glu Ala Tyr Arg Glu Asn Gln Gln Ala Leu	
345 350 355	
ctc gcc cag caa gcc atg gaa atc ctg ccg gaa ctc atg agc aac ttc	1219
Leu Ala Gln Gln Ala Met Glu Ile Leu Pro Glu Leu Met Ser Asn Phe	
360 365 370	
gcc tct gga tac gca aac att gga tcc atg aca gtg ctc tcc ggt gga	1267
Ala Ser Gly Tyr Ala Asn Ile Gly Ser Met Thr Val Leu Ser Gly Gly	
375 380 385	
gaa gga tcc gag aat tcc gtg ggt tca cgt ttt gcc ggt gaa caa gca	1315
Glu Gly Ser Glu Asn Ser Val Gly Ser Arg Phe Ala Gly Glu Gln Ala	
390 395 400 405	
ctt gga ctg aaa tcc att att gaa tca gtc aag caa acc acc ggc att	1363
Leu Gly Leu Lys Ser Ile Ile Glu Ser Val Lys Gln Thr Thr Gly Ile	
410 415 420	
gat cta gct gag atc atc caa gcc cgt gct gct gga cat gca cag gcc	1411
Asp Leu Ala Glu Ile Ile Gln Gly Arg Ala Ala Gly His Ala Gln Gly	

425 430 435
 tcc gct cag ggt gca gcg att gct gaa gcg ctt tca cgc gat gaa act 1459
 Ser Ala Gln Gly Ala Ala Ile Ala Glu Ala Leu Ser Arg Asp Glu Thr
 440 445 450
 gtg gaa gat cgc tct gaa aaa taatctagct gccccagcgca tcg 1503
 Val Glu Asp Arg Ser Glu Lys
 455 460

 <210> 1766
 <211> 460
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 1766
 Met Glu Ala Ile Ala Ile Leu Phe Val Ile Gly Ala Ile Leu Val Val
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 Ala Val Ile Val Leu Gly Ile Phe Phe Leu Thr Ser Arg Thr Trp Ile
 20 25 30
 Lys Val Ala Ala Ala Asp Glu Ala Leu Ile Val Ser Ala Lys Lys Lys
 35 40 45
 Gly Glu Ser Gln Val Ile Val His Gly Lys Ala Val Val Met Pro Ile
 50 55 60
 Thr Gln Thr His Gln Lys Ile Ser Leu Arg Ser Arg Gln Val Asn Met
 65 70 75 80
 Gln Val Thr Ala Gln Ser Asp Asp Asn Val Thr Leu Asn Val Glu Ala
 85 90 95
 Val Ala Leu Val Lys Ile Gly Ser Glu Ala Glu Phe Ile Arg Arg Ala
 100 105 110
 Ala Gln Arg Phe Ala Ser Ser Asp Lys Glu Ile Val Arg Phe Thr Gln
 115 120 125
 Asp Gln Leu Glu Gly Val Leu Arg Gly Val Val Ala Gln Gln Thr Val
 130 135 140
 Thr Ser Leu Met Arg Glu Arg Lys Lys Phe Ser Glu Gln Ile Ala Glu
 145 150 155 160
 Thr Val Ile Pro Glu Leu Glu Lys Gln Gly Leu Ile Leu Asp Ser Phe
 165 170 175
 Gln Ile Arg Gly Ile Thr Asp Asp Val Gly Tyr Ile Lys Ser Leu Gly
 180 185 190
 Ala Pro Glu Ile Gln Ala Lys Lys Gln Ala Ala Glu Ile Ala Glu Thr
 195 200 205
 Glu Ala Ala Arg Ala Ile Ala Lys Ser Arg Ile Ala Asn Gln Glu Ala
 210 215 220
 Asp Leu Val Glu Gln Thr Gln Leu Asp Ala Asn Lys Ala Ala Ala Asp
 225 230 235 240

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Ala Gln Val Gly Glu Ala Arg Ala Gln Ala Met Gln Ala Glu Arg Leu
      245                      250                      255

Ala Asp Glu Lys Ala Arg Leu Glu Val Leu Arg Gln Gln Ala Glu Asn
      260                      265                      270

Lys Gln Ile Glu Leu Glu Ala Glu Val Asn Lys Val Ala Asp Ala Glu
      275                      280                      285

Arg Tyr Arg Arg Lys Gln Glu Val Glu Ala Asp Thr Phe Glu Gln Thr
      290                      295                      300

Arg Arg Ala Gln Ala Gln Val Glu Ile Ala Glu Ala Glu Ala Thr Ala
      305                      310                      315                      320

Ala Lys Val Arg Ala Met Ala Glu Ala Glu Ala Val Arg Leu Lys Gly
      325                      330                      335

Gln Ala Glu Ala Asp Ala Ile Lys Ala Lys Ala Glu Ala Tyr Arg Glu
      340                      345                      350

Asn Gln Glu Ala Leu Leu Ala Gln Gln Ala Met Glu Ile Leu Pro Glu
      355                      360                      365

Leu Met Ser Asn Phe Ala Ser Gly Tyr Ala Asn Ile Gly Ser Met Thr
      370                      375                      380

Val Leu Ser Gly Gly Glu Gly Ser Glu Asn Ser Val Gly Ser Arg Phe
      385                      390                      395                      400

Ala Gly Glu Gln Ala Leu Gly Leu Lys Ser Ile Ile Glu Ser Val Lys
      405                      410                      415

Gln Thr Thr Gly Ile Asp Leu Ala Glu Ile Ile Gln Gly Arg Ala Ala
      420                      425                      430

Gly His Ala Gln Gly Ser Ala Gln Gly Ala Ala Ile Ala Glu Ala Leu
      435                      440                      445

Ser Arg Asp Glu Thr Val Glu Asp Arg Ser Glu Lys
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<210> 1767

<211> 945

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(922)

<223> RXA00463

<400> 1767

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tacgagctcc cctgaaccgc cgactaaagt tgcggcggca atg cag aca acg act 115

Met Gln Thr Thr Thr

1

5

ggg gag acg tcg ata agc aat gaa acc tcg ttt aac gcc tca cgc gaa 163
 Gly Glu Thr Ser Ile Ser Asn Glu Thr Ser Phe Asn Ala Ser Arg Glu
 10 15 20

acc tcg ctg acg gcg ctg ggt ttc ttg gac tat ctt gac gag gag caa 211
 Thr Ser Leu Thr Ala Leu Gly Phe Leu Asp Tyr Leu Asp Glu Glu Gln
 25 30 35

cgc gcc gcc ttg ctc ggt gaa ggc ctg gac atc agc acg ctg acc tgg 259
 Arg Ala Ala Leu Leu Gly Glu Gly Leu Asp Ile Ser Thr Leu Thr Trp
 40 45 50

gcc aac cag gtt acc gcg ctg cgt gtg ctg gaa tcc ctc ttc aat gag 307
 Ala Asn Gln Val Thr Ala Leu Arg Val Leu Glu Ser Leu Phe Asn Glu
 55 60 65

cat gca tac gag ctg gtt tct gca gtg att cag cat gta gct caa gaa 355
 His Ala Tyr Glu Leu Val Ser Ala Val Ile Gln His Val Ala Gln Glu
 70 75 80 85

cct ggc gat aat cca cac cac ttt ctg aag ttc tcg cct gaa cca tcc 403
 Pro Gly Asp Asn Pro His His Phe Leu Lys Phe Ser Pro Glu Pro Ser
 90 95 100

acc gag aat tct tgg gaa ttg acc ctg gat gga cca act gtc gga ttg 451
 Thr Glu Asn Ser Trp Glu Leu Thr Leu Asp Gly Pro Thr Val Gly Leu
 105 110 115

aaa gtc act ttc gat ccg gac ggt cag atc act ttc aag gat gct cat 499
 Lys Val Thr Phe Asp Pro Asp Gly Gln Ile Thr Phe Lys Asp Ala His
 120 125 130

ttg ggc ctg agc cca gct gag gtc gtt agt gtc act gag gcg tta gat 547
 Leu Gly Leu Ser Pro Ala Glu Val Val Ser Val Thr Glu Ala Leu Asp
 135 140 145

acc tcc tat tcg gaa tcg caa atc aaa aaa gct gcg gaa caa ctg gtg 595
 Thr Ser Tyr Ser Glu Ser Gln Ile Lys Lys Ala Ala Glu Gln Leu Val
 150 155 160 165

gga agc ctc aat cca acc cag cag gca gcg ctc caa gga tcc ggt ttg 643
 Gly Ser Leu Asn Pro Thr Gln Gln Ala Ala Leu Gln Gly Ser Gly Leu
 170 175 180

cga gga gca cag ctc act gaa gag caa aag acc ctg ttc tta aag atg 691
 Arg Gly Ala Gln Leu Thr Glu Glu Gln Lys Thr Leu Phe Leu Lys Met
 185 190 195

acc tcc aac tgg atc gac ctt gcc aat ggc gat tcc ggc tct gaa cag 739
 Thr Ser Asn Trp Ile Asp Leu Ala Asn Gly Asp Ser Gly Ser Glu Gln
 200 205 210

caa gaa gaa atc gct gat acg ttc agt gat acc tac atc att tgg aat 787
 Gln Glu Glu Ile Ala Asp Thr Phe Ser Asp Thr Tyr Ile Ile Trp Asn
 215 220 225

gag cag aaa gat ggc tca gca ttc ttc cag atg aaa ggc cct gag ctc 835
 Glu Gln Lys Asp Gly Ser Ala Phe Phe Gln Met Lys Gly Pro Glu Leu
 230 235 240 245

gac ttc agc tat aaa gag agc gtg cct gaa aac gct gaa ctc tct gca 883

Asp Phe Ser Tyr Lys Glu Ser Val Pro Glu Asn Ala Glu Leu Ser Ala
 250 255 260

egg gga gtc ccc aat att cag acc tct ttt cag tca cct taactggcat 932
 Arg Gly Val Pro Asn Ile Gln Thr Ser Phe Gln Ser Pro
 265 270

tggttttagtt tgg 945

<210> 1768

<211> 274

<212> PRT

<213> Corynebacterium glutamicum

<400> 1768

Met Gln Thr Thr Gly Glu Thr Ser Ile Ser Asn Glu Thr Ser Phe
 1 5 10 15

Asn Ala Ser Arg Glu Thr Ser Leu Thr Ala Leu Gly Phe Leu Asp Tyr
 20 25 30

Leu Asp Glu Glu Gln Arg Ala Ala Leu Leu Gly Glu Gly Leu Asp Ile
 35 40 45

Ser Thr Leu Thr Trp Ala Asn Gln Val Thr Ala Leu Arg Val Leu Glu
 50 55 60

Ser Leu Phe Asn Glu His Ala Tyr Glu Leu Val Ser Ala Val Ile Gln
 65 70 75 80

His Val Ala Gln Glu Pro Gly Asp Asn Pro His His Phe Leu Lys Phe
 85 90 95

Ser Pro Glu Pro Ser Thr Glu Asn Ser Trp Glu Leu Thr Leu Asp Gly
 100 105 110

Pro Thr Val Gly Leu Lys Val Thr Phe Asp Pro Asp Gly Gln Ile Thr
 115 120 125

Phe Lys Asp Ala His Leu Gly Leu Ser Pro Ala Glu Val Val Ser Val
 130 135 140

Thr Glu Ala Leu Asp Thr Ser Tyr Ser Glu Ser Gln Ile Lys Lys Ala
 145 150 155 160

Ala Glu Gln Leu Val Gly Ser Leu Asn Pro Thr Gln Gln Ala Ala Leu
 165 170 175

Gln Gly Ser Gly Leu Arg Gly Ala Gln Leu Thr Glu Glu Gln Lys Thr
 180 185 190

Leu Phe Leu Lys Met Thr Ser Asn Trp Ile Asp Leu Ala Asn Gly Asp
 195 200 205

Ser Gly Ser Glu Gln Gln Glu Glu Ile Ala Asp Thr Phe Ser Asp Thr
 210 215 220

Tyr Ile Ile Trp Asn Glu Gln Lys Asp Gly Ser Ala Phe Phe Gln Met
 225 230 235 240

Lys Gly Pro Glu Leu Asp Phe Ser Tyr Lys Glu Ser Val Pro Glu Asn
245 250 255

Ala Glu Leu Ser Ala Arg Gly Val Pro Asn Ile Gln Thr Ser Phe Gln
260 265 270

Ser Pro

<210> 1769

<211> 942

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(919)

<223> RXA00468

<400> 1769

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gggtttattct tgaactcact taagttttga attttttagtt gtg aaa gta gtt gat 115
Val Lys Val Val Asp
1 5

gca caa gtg gtt atg ggg cca acc cac gct atg agc ggt gca gcc gtg 163
Ala Gln Val Val Met Gly Pro Thr His Ala Met Ser Gly Ala Ala Val
10 15 20

ggg ctt gct gtt gct caa att ctg cca gca gaa tgg ggt ggg gtt acc 211
Gly Leu Ala Val Ala Gln Ile Leu Pro Ala Glu Trp Gly Gly Val Thr
25 30 35

acc gcc acg gag gct ttt att tat gcg ggt tta gcg gcg ggt gca gcg 259
Thr Ala Thr Glu Ala Phe Ile Tyr Ala Gly Leu Ala Ala Gly Ala Ala
40 45 50

ctg ctg ccg gac ctt gat tca ccg cag gcc acg gtg tcg cgt tct ttt 307
Leu Leu Pro Asp Leu Asp Ser Pro Gln Ala Thr Val Ser Arg Ser Phe
55 60 65

ggg ccg att acc caa gtg att tcg cgt ttt aca gag aat att tgc caa 355
Gly Pro Ile Thr Gln Val Ile Ser Arg Phe Thr Glu Asn Ile Cys Gln
70 75 80 85

act ttc gtc aat gtc acc agg ggc agg aaa gac aaa cac tgc aac aac 403
Thr Phe Val Asn Val Thr Arg Gly Arg Lys Asp Lys His Cys Asn Asn
90 95 100

ggg cac cgc acg ttg aca cat acg gtg tgg agc gct gct gcc aca ggc 451
Gly His Arg Thr Leu Thr His Thr Val Trp Ser Ala Ala Thr Gly
105 110 115

gct ggt gcc aca gcg cta att ggc gcc tat gga aaa cct gcg gtg att 499
Ala Gly Ala Thr Ala Leu Ile Gly Ala Tyr Gly Lys Pro Ala Val Ile
120 125 130

ggg ttg ctg ttt ttc ttc ctg ggc ctg gcc att aga ggt ctg atg cct 547
Gly Leu Leu Phe Phe Phe Leu Gly Leu Ala Ile Arg Gly Leu Met Pro

135 140 145

gaa tgg tca aag aac gca gat tgg ctt tta gtt act gga gct tcc gct 595
 Glu Trp Ser Lys Asn Ala Asp Trp Leu Leu Val Thr Gly Ala Ser Ala
 150 155 160 165

gca tta gca gtg gga gta tgg aat tat gct ccc gaa agt tca ttc ggc 643
 Ala Leu Ala Val Gly Val Trp Asn Tyr Ala Pro Glu Ser Ser Phe Gly
 170 175 180

att gtg tta ggc tcc gcc att aca gtt gga agc ctg acc cac ttg gct 691
 Ile Val Leu Gly Ser Ala Ile Thr Val Gly Ser Leu Thr His Leu Ala
 185 190 195

ggc gat atg gcc act aag gcc ggt atc cca gca ttt gcc cgg gtc att 739
 Gly Asp Met Ala Thr Lys Ala Gly Ile Pro Ala Phe Ala Pro Val Ile
 200 205 210

ccg ctg aag ggc aaa cgc tgg tgg aac ctc aaa ttg cct aag ttt tta 787
 Pro Leu Lys Gly Lys Arg Trp Trp Asn Leu Lys Leu Pro Lys Phe Leu
 215 220 225

agc att cgt gcc aac ggt cct gcc gat aag ttc tta ctg ttc gta ttc 835
 Ser Ile Arg Ala Asn Gly Pro Ala Asp Lys Phe Leu Leu Phe Val Phe
 230 235 240 245

tcg gtg gcg gtc atc att cag att ggt ttg gtc tca tcg gga aat atg 883
 Ser Val Ala Val Ile Ile Gln Ile Gly Leu Val Ser Ser Gly Asn Met
 250 255 260

agc acc att atg atg aat ctg ctt agt cct gca ctg taattaatgg 929
 Ser Thr Ile Met Met Asn Leu Leu Ser Pro Ala Leu
 265 270

cagttgcgtt tcg 942

<210> 1770
 <211> 273
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1770
 Val Lys Val Val Asp Ala Gln Val Val Met Gly Pro Thr His Ala Met
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Ser Gly Ala Ala Val Gly Leu Ala Val Ala Gln Ile Leu Pro Ala Glu
 20 25 30

Trp Gly Gly Val Thr Thr Ala Thr Glu Ala Phe Ile Tyr Ala Gly Leu
 35 40 45

Ala Ala Gly Ala Ala Leu Leu Pro Asp Leu Asp Ser Pro Gln Ala Thr
 50 55 60

Val Ser Arg Ser Phe Gly Pro Ile Thr Gln Val Ile Ser Arg Phe Thr
 65 70 75 80

Glu Asn Ile Cys Gln Thr Phe Val Asn Val Thr Arg Gly Arg Lys Asp
 85 90 95

Lys His Cys Asn Asn Gly His Arg Thr Leu Thr His Thr Val Trp Ser
100 105 110

Ala Ala Ala Thr Gly Ala Gly Ala Thr Ala Leu Ile Gly Ala Tyr Gly
115 120 125

Lys Pro Ala Val Ile Gly Leu Leu Phe Phe Phe Leu Gly Leu Ala Ile
130 135 140

Arg Gly Leu Met Pro Glu Trp Ser Lys Asn Ala Asp Trp Leu Leu Val
145 150 155 160

Thr Gly Ala Ser Ala Ala Leu Ala Val Gly Val Trp Asn Tyr Ala Pro
165 170 175

Glu Ser Ser Phe Gly Ile Val Leu Gly Ser Ala Ile Thr Val Gly Ser
180 185 190

Leu Thr His Leu Ala Gly Asp Met Ala Thr Lys Ala Gly Ile Pro Ala
195 200 205

Phe Ala Pro Val Ile Pro Leu Lys Gly Lys Arg Trp Trp Asn Leu Lys
210 215 220

Leu Pro Lys Phe Leu Ser Ile Arg Ala Asn Gly Pro Ala Asp Lys Phe
225 230 235 240

Leu Leu Phe Val Phe Ser Val Ala Val Ile Ile Gln Ile Gly Leu Val
245 250 255

Ser Ser Gly Asn Met Ser Thr Ile Met Met Asn Leu Leu Ser Pro Ala
260 265 270

Leu

<210> 1771

<211> 1299

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1276)

<223> RXA00469

<400> 1771

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cccattcact tatcagcctc aacactccac aatagagtct atg agt act ttt cag 115
Met Ser Thr Phe Gln
1 5

gag ccc cac cac aac cag gga ttc atc cct ttt gcc caa cct ggt tat 163
Glu Pro His His Asn Gln Gly Phe Ile Pro Phe Ala Gln Pro Gly Tyr
10 15 20

gaa gct cca aca cca cac ctt gca act ggt act ttt cag caa atg tgg 211
Glu Ala Pro Thr Pro His Leu Ala Thr Gly Thr Phe Gln Gln Met Trp
25 30 35

cag acc cgc ccc gca cgc atc cct gcc aag caa ggt ggt cac gcc aaa	259
Gln Thr Arg Pro Ala Arg Ile Pro Ala Lys Gln Gly Tyr His Ala Lys	
40 45 50	
gta gct ggt gtc tgt gaa ggc att ggt gtg cgt tat caa atc gac cgg	307
Val Ala Gly Val Cys Glu Gly Ile Gly Val Arg Tyr Gln Ile Asp Pro	
55 60 65	
gtg ctc att cgt cta ttt ttc gtg gtc act ggt gtc ttc ggc gcc ggt	355
Val Leu Ile Arg Leu Phe Phe Val Val Thr Gly Val Phe Gly Ala Gly	
70 75 80 85	
gtc gca gcc tat ctc att gca tgg ctg tgc atg ccc cgc tac tcc gtt	403
Val Ala Ala Tyr Leu Ile Ala Trp Leu Cys Met Pro Arg Tyr Ser Val	
90 95 100	
ccg gtc tcc ccc atc gaa gct ctc tgg acc ccg ggc cac acc aaa gac	451
Pro Val Ser Pro Ile Glu Ala Leu Trp Thr Pro Gly His Thr Lys Asp	
105 110 115	
cgc aac cac ggc tgg tgg ctg gtc atc gcg ttc ttt atg ttc tca ggt	499
Arg Asn His Gly Trp Trp Leu Val Ile Ala Phe Phe Met Phe Ser Gly	
120 125 130	
gtt tta tcc tcc ggc gct gga gga ata tcc ggc cca gca gca gcc att	547
Val Leu Ser Ser Ser Gly Ala Gly Gly Ile Ser Gly Pro Ala Ala Ala Ile	
135 140 145	
act tac ctt tgc ctt tta gcc atg tgg tgg gcg ttg cat aag aaa caa	595
Thr Tyr Leu Cys Leu Leu Ala Met Trp Trp Ala Leu His Lys Lys Gln	
150 155 160 165	
cca ctt cca ccc cgc gga cta ctc acc act gaa ttc act gtt tct gag	643
Pro Leu Pro Pro Arg Gly Leu Leu Thr Thr Glu Phe Thr Val Ser Glu	
170 175 180	
gat gcc acc atg aaa aac gaa gat ctc tac cca cga ccc caa cca gat	691
Asp Ala Thr Met Lys Asn Glu Asp Leu Tyr Pro Arg Pro Gln Pro Asp	
185 190 195	
cta agc act atc acc ccc gtt gag ggc tac tat gca ccc ttc gcg caa	739
Leu Ser Thr Ile Thr Pro Val Glu Gly Tyr Tyr Ala Pro Phe Ala Gln	
200 205 210	
caa acc ccc gaa gcg cct cat tgg gat cca ctt gcc caa aac caa tac	787
Gln Thr Pro Glu Ala Pro His Trp Asp Pro Leu Ala Gln Asn Gln Tyr	
215 220 225	
aac acc tgg gat gta caa gtc cct cca caa aag cct cag aaa aag cgc	835
Asn Thr Trp Asp Val Gln Val Pro Pro Gln Lys Pro Gln Lys Lys Arg	
230 235 240 245	
cat gtg tgg cca tgg att gtc ggc ggt gta gtt ggt acc gga gtt gtc	883
His Val Trp Pro Trp Ile Val Gly Gly Val Val Gly Thr Gly Val Val	
250 255 260	
atg agc gcc ctc gca ggc ctg ttt att tca aat atc gat ccc atc tac	931
Met Ser Ala Leu Ala Gly Leu Phe Ile Ser Asn Ile Asp Pro Ile Tyr	
265 270 275	

ttt gaa gac gac cct gga atc ggc gat gtc aat ctc atc ccc acc aac 979
 Phe Glu Asp Asp Pro Gly Ile Gly Asp Val Asn Leu Ile Pro Thr Asn
 280 285 290

gat gaa ctc ctc agc agc tac acc tct ggt gtg ggc gaa atg aac cta 1027
 Asp Glu Leu Leu Ser Ser Tyr Thr Ser Gly Val Gly Glu Met Asn Leu
 295 300 305

gat ttc agc aac ctc acc caa ctt gat cag gaa caa aac gtt caa atc 1075
 Asp Phe Ser Asn Leu Thr Gln Leu Asp Gln Glu Asn Val Gln Ile
 310 315 320 325

acc tca ggt atc ggt gaa gtc atg gtg acc ctg cct gat gac gtg cca 1123
 Thr Ser Gly Ile Gly Glu Val Met Val Thr Leu Pro Asp Asp Val Pro
 330 335 340

gta agc ttg agt tgc tcc gcc ggt gtg ggc aca gcg cgc tgt gat gtt 1171
 Val Ser Leu Ser Cys Ser Ala Gly Val Gly Thr Ala Arg Cys Asp Val
 345 350 355

gga gac ctc gcc gcc cac aat gct gat ttg gaa ggt ccg atg ttg aat 1219
 Gly Asp Leu Ala Ala His Asn Ala Asp Leu Glu Gly Pro Met Leu Asn
 360 365 370

ctg gtt gta aat tct gga atc ggc gat gtg aag gtg gag ttc gct gat 1267
 Leu Val Val Asn Ser Gly Ile Gly Asp Val Lys Val Glu Phe Ala Asp
 375 380 385

cag aat gac tagcccgacc ctatgtgagt agt 1299
 Gln Asn Asp
 390

<210> 1772
 <211> 392
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 1772
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 Ala Gln Pro Gly Tyr Glu Ala Pro Thr Pro His Leu Ala Thr Gly Thr
 20 25 30
 Phe Gln Gln Met Trp Gln Thr Arg Pro Ala Arg Ile Pro Ala Lys Gln
 35 40 45
 Gly Gly His Ala Lys Val Ala Gly Val Cys Glu Gly Ile Gly Val Arg
 50 55 60
 Tyr Gln Ile Asp Pro Val Leu Ile Arg Leu Phe Phe Val Val Thr Gly
 65 70 75 80
 Val Phe Gly Ala Gly Val Ala Ala Tyr Leu Ile Ala Trp Leu Cys Met
 85 90 95
 Pro Arg Tyr Ser Val Pro Val Ser Pro Ile Glu Ala Leu Trp Thr Pro
 100 105 110
 Gly His Thr Lys Asp Arg Asn His Gly Trp Trp Leu Val Ile Ala Phe

115					120					125					
Phe	Met	Phe	Ser	Gly	Val	Leu	Ser	Ser	Gly	Ala	Gly	Gly	Ile	Ser	Gly
130						135					140				
Pro	Ala	Ala	Ala	Ile	Thr	Tyr	Leu	Cys	Leu	Leu	Ala	Met	Trp	Trp	Ala
145					150					155					160
Leu	His	Lys	Lys	Gln	Pro	Leu	Pro	Pro	Arg	Gly	Leu	Leu	Thr	Thr	Glu
				165					170					175	
Phe	Thr	Val	Ser	Glu	Asp	Ala	Thr	Met	Lys	Asn	Glu	Asp	Leu	Tyr	Pro
			180					185					190		
Arg	Pro	Gln	Pro	Asp	Leu	Ser	Thr	Ile	Thr	Pro	Val	Glu	Gly	Tyr	Tyr
		195					200					205			
Ala	Pro	Phe	Ala	Gln	Gln	Thr	Pro	Glu	Ala	Pro	His	Trp	Asp	Pro	Leu
	210					215					220				
Ala	Gln	Asn	Gln	Tyr	Asn	Thr	Trp	Asp	Val	Gln	Val	Pro	Pro	Gln	Lys
225					230					235					240
Pro	Gln	Lys	Lys	Arg	His	Val	Trp	Pro	Trp	Ile	Val	Gly	Gly	Val	Val
				245					250					255	
Gly	Thr	Gly	Val	Val	Met	Ser	Ala	Leu	Ala	Gly	Leu	Phe	Ile	Ser	Asn
			260					265					270		
Ile	Asp	Pro	Ile	Tyr	Phe	Glu	Asp	Asp	Pro	Gly	Ile	Gly	Asp	Val	Asn
		275					280					285			
Leu	Ile	Pro	Thr	Asn	Asp	Glu	Leu	Leu	Ser	Ser	Tyr	Thr	Ser	Gly	Val
	290					295					300				
Gly	Glu	Met	Asn	Leu	Asp	Phe	Ser	Asn	Leu	Thr	Gln	Leu	Asp	Gln	Glu
305				310					315					320	
Gln	Asn	Val	Gln	Ile	Thr	Ser	Gly	Ile	Gly	Glu	Val	Met	Val	Thr	Leu
			325					330						335	
Pro	Asp	Asp	Val	Pro	Val	Ser	Leu	Ser	Cys	Ser	Ala	Gly	Val	Gly	Thr
			340					345					350		
Ala	Arg	Cys	Asp	Val	Gly	Asp	Leu	Ala	Ala	His	Asn	Ala	Asp	Leu	Glu
		355					360					365			
Gly	Pro	Met	Leu	Asn	Leu	Val	Val	Asn	Ser	Gly	Ile	Gly	Asp	Val	Lys
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Val	Glu	Phe	Ala	Asp	Gln	Asn	Asp								
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<211> 984

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(961)

<223> RXA00472

<400> 1773

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ctgctctact acggaagata ccgctatatc ggagacgaca gtg tct agt gtt gca 115
 Val Ser Ser Val Ala
 1 5

acg aaa aca acc tcg act ctg cct gaa atg aac tcc gca gta tca gca 163
 Thr Lys Thr Thr Ser Thr Leu Pro Glu Met Asn Ser Ala Val Ser Ala
 10 15 20

gac ggc gtg acg atc act atc gat tct gcc ttc acg aca gac tct gta 211
 Asp Gly Val Thr Ile Thr Ile Asp Ser Ala Phe Thr Thr Asp Ser Val
 25 30 35

gaa atg gaa tcc cta gac aga cct tct ggc gac atc caa ccc gag atg 259
 Glu Met Glu Ser Leu Asp Arg Pro Ser Gly Asp Ile Gln Pro Glu Met
 40 45 50

tct aga gaa gac gga atc ttt gtc gta gtc gaa acc act ata aag aac 307
 Ser Arg Glu Asp Gly Ile Phe Val Val Val Glu Thr Thr Ile Lys Asn
 55 60 65

gag agt gga gca gat atg gac atc acc tgt gca tcc act ggt tca act 355
 Glu Ser Gly Ala Asp Met Asp Ile Thr Cys Ala Ser Thr Gly Ser Thr
 70 75 80 85

gtc tat gca gaa atc tcc act aat caa gag gcc gta tac caa cca ata 403
 Val Tyr Ala Glu Ile Ser Thr Asn Gln Glu Ala Val Tyr Gln Pro Ile
 90 95 100

cgc gat tta ttc ctc atc cca gga aac ccg gaa tgc aac cat aat cta 451
 Arg Asp Leu Phe Leu Ile Pro Gly Asn Pro Glu Cys Asn His Asn Leu
 105 110 115

gga tcc ggt ttc gac gca cca atg act tgg gta ttt caa atc cct aaa 499
 Gly Ser Gly Phe Asp Ala Pro Met Thr Trp Val Phe Gln Ile Pro Lys
 120 125 130

gat gcc act cgc gag cga ttt gga ttc aca cat agt gag ctc ggt gat 547
 Asp Ala Thr Ala Glu Arg Phe Gly Phe Thr His Ser Glu Leu Gly Asp
 135 140 145

ggg aaa cta act tgg att gca ctc aat gat ttg agt aat tcg gag cca 595
 Gly Lys Leu Thr Trp Ile Ala Leu Asn Asp Leu Ser Asn Ser Glu Pro
 150 155 160 165

gct act gaa tca act atg cga gac gaa gca gca atc gat ccg agc acc 643
 Ala Thr Glu Ser Thr Met Arg Asp Glu Ala Ala Ile Asp Pro Ser Thr
 170 175 180

cct cag caa act cca gta cag gaa act gtg atc tca caa aac acc att 691
 Pro Gln Gln Thr Pro Val Gln Glu Thr Val Ile Ser Gln Asn Thr Ile
 185 190 195

gaa act cct gta gcc cct gct cct gcg gta cct gct tat ggc gct tct 739
 Glu Thr Pro Val Ala Pro Ala Pro Ala Val Pro Ala Tyr Gly Ala Ser
 200 205 210

tgc cct gtc tgc atg ctc cag cag cca agt caa gct gca gat ggt tca 787
 Cys Pro Val Ser Met Leu Gln Gln Pro Ser Gln Ala Ala Asp Gly Ser
 215 220 225

gct ttg gtc tgc att tat gca gga acc ccc aac cca atc tgg gtc tac 835
 Ala Leu Val Cys Ile Tyr Ala Gly Thr Pro Asn Pro Ile Trp Val Tyr
 230 235 240 245

ggc cca gaa cct ctc gga gtc ggg act gct aca ccg ggt ggg gca tgc 883
 Gly Pro Glu Pro Leu Gly Val Gly Thr Ala Thr Pro Gly Gly Ala Cys
 250 255 260

gaa gga tac gag gcc ggt ggg caa gat gct tct gga aat ata atg atg 931
 Glu Gly Tyr Glu Ala Gly Gly Gln Asp Ala Ser Gly Asn Ile Met Met
 265 270 275

tgc tca ggc gga caa tgg gtc tat ggg cca taaatctaaa atcaaagagt 981
 Cys Ser Gly Gln Trp Val Tyr Gly Pro
 280 285

gca 984

<210> 1774
 <211> 287
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 1774
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Ser Ala Val Ser Ala Asp Gly Val Thr Ile Thr Ile Asp Ser Ala Phe
 20 25 30

Thr Thr Asp Ser Val Glu Met Glu Ser Leu Asp Arg Pro Ser Gly Asp
 35 40 45

Ile Gln Pro Glu Met Ser Arg Glu Asp Gly Ile Phe Val Val Val Glu
 50 55 60

Thr Thr Ile Lys Asn Glu Ser Gly Ala Asp Met Asp Ile Thr Cys Ala
 65 70 75 80

Ser Thr Gly Ser Thr Val Tyr Ala Glu Ile Ser Thr Asn Gln Glu Ala
 85 90 95

Val Tyr Gln Pro Ile Arg Asp Leu Phe Leu Ile Pro Gly Asn Pro Glu
 100 105 110

Cys Asn His Asn Leu Gly Ser Gly Phe Asp Ala Pro Met Thr Trp Val
 115 120 125

Phe Gln Ile Pro Lys Asp Ala Thr Ala Glu Arg Phe Gly Phe Thr His
 130 135 140

Ser Glu Leu Gly Asp Gly Lys Leu Thr Trp Ile Ala Leu Asn Asp Leu
 145 150 155 160

Ser Asn Ser Glu Pro Ala Thr Glu Ser Thr Met Arg Asp Glu Ala Ala

[illegible]

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Val Ala Ser Ser Val Glu Val Leu Arg Pro Gly Leu Val Ala Val Asp	
90 95 100	
gcg gga gct gcc gcg cgc tat tac ggt tca gag gac atc gct gct cag	451
Ala Gly Ala Ala Arg Tyr Tyr Gly Ser Glu Asp Ile Ala Ala Gln	
105 110 115	
atg ctt atc gac gcc gcc ctg cgc caa ggc atc gac gtt ttc gcc ggg	499
Met Leu Ile Asp Ala Ala Leu Arg Gln Gly Ile Asp Val Phe Ala Gly	
120 125 130	
gtt gcg gat gag atc acg acg gcc gtc atc gcg gcg agg gcg aat ggt	547
Val Ala Asp Glu Ile Thr Thr Ala Val Ile Ala Arg Ala Asn Gly	
135 140 145	
ggg act gtg gtg aag agg gag gcg tcg aga agc ttt tta cag cag caa	595
Gly Thr Val Val Lys Arg Glu Ala Ser Arg Ser Phe Leu Gln Gln Gln	
150 155 160 165	
ccc ctg gcc gtg ctg gcg gcc gag gaa gcg ctg ggt tgt gag gcg gag	643
Pro Leu Gly Val Leu Ala Ala Glu Glu Ala Leu Gly Cys Glu Ala Glu	
170 175 180	
gtg gtg cgc gcg ctg gcg gat ctg gcc atg cgc acg ctt ggt gag ctg	691
Val Val Arg Ala Leu Ala Asp Leu Gly Met Arg Thr Leu Gly Glu Leu	
185 190 195	
gcg gaa ctg ccg gta gaa gcc gtg gcg acg cgt ttc gcc aac gct ggt	739
Ala Glu Leu Pro Val Glu Ala Val Ala Thr Arg Phe Gly Asn Ala Gly	
200 205 210	
ctg ccg tgt cac aac att gcg cgt gcc agg cac gat cgt aag gtc gcg	787
Leu Arg Cys His Asn Ile Ala Arg Ala Arg His Asp Arg Lys Val Ala	
215 220 225	
cca ccg atc acg cat gca gat tgg gag gtt tcg cat gtg ccg gag gag	835
Pro Pro Ile Thr His Ala Asp Trp Glu Val Ser His Val Pro Glu Glu	
230 235 240 245	
cct att ttg cgt gtc gac gcc gcc tcg ttt gtt gcg cgc aac ctt gcc	883
Pro Ile Leu Arg Val Asp Ala Ala Ser Phe Val Ala Arg Asn Leu Ala	
250 255 260	
tcg cgc ctg cat caa ctg ctg agc aaa ggt gcc gtg gtg tgc caa ttg	931
Ser Arg Leu His Gln Leu Leu Ser Lys Gly Gly Val Val Cys Gln Leu	
265 270 275	
ctc aag gtc aca gcc gat ttc agt act ggt gat acg gtg agc aga att	979
Leu Lys Val Thr Ala Asp Phe Ser Thr Gly Asp Thr Val Ser Arg Ile	
280 285 290	
tgg cgt acc ggt gaa cct tta acg gaa cag gca act gcg gat ccg gtg	1027
Trp Arg Thr Gly Glu Pro Leu Thr Glu Gln Ala Thr Ala Asp Arg Val	
295 300 305	
cgt tgg cag ttg gat ggg tgg ttg act gcg cgc ggt gtg cat tcc gat	1075
Arg Trp Gln Leu Asp Gly Trp Leu Thr Ala Arg Gly Val His Ser Asp	
310 315 320 325	
gat ccg aat gag cac gat ggg att acg gcg ttg tgg ctt att cct ttg	1123

Asp	Pro	Asn	Glu	His	Asp	Gly	Ile	Thr	Ala	Leu	Trp	Leu	Ile	Pro	Leu	
				330					335					340		
gaa	tgt	gtg	cca	ccg	gat	atg	gcc	agc	ggc	gga	ttg	tgg	gat	acc	ggg	1171
Glu	Cys	Val	Pro	Pro	Asp	Met	Ala	Ser	Gly	Gly	Leu	Trp	Asp	Thr	Gly	
			345				350						355			
cgc	agc	cag	cag	cat	gtg	gcc	aga	caa	gtc	att	gag	cgt	gtg	caa	tca	1219
Arg	Ser	Gln	Gln	His	Val	Ala	Arg	Gln	Val	Ile	Glu	Arg	Val	Gln	Ser	
			360				365					370				
agc	ttg	ggc	gtg	gat	gcg	gtg	ctg	cag	cct	gtt	ccg	gct	ggg	ggg	cgg	1267
Ser	Leu	Gly	Val	Asp	Ala	Val	Leu	Gln	Pro	Val	Pro	Ala	Gly	Gly	Arg	
			375			380					385					
gga	gta	gaa	gaa	cgc	att	cat	ttt	gtt	ccc	tat	ggg	gaa	aaa	cgt	gat	1315
Gly	Val	Glu	Glu	Arg	Ile	His	Phe	Val	Pro	Tyr	Gly	Glu	Lys	Arg	Asp	
				395					400					405		
gct	atc	cgc	aat	cca	gcg	ggg	tcg	tgg	cca	ggg	aaa	ata	cca	ggg	ccg	1363
Ala	Ile	Arg	Asn	Pro	Ala	Gly	Ser	Trp	Pro	Gly	Lys	Ile	Pro	Gly	Pro	
				410					415					420		
ctg	cct	gct	cgg	ttg	ggc	ggg	ggg	atc	aac	cac	ccg	gcc	tcg	caa	gtg	1411
Leu	Pro	Ala	Arg	Leu	Gly	Gly	Gly	Ile	Asn	His	Pro	Ala	Ser	Gln	Val	
			425				430						435			
acc	atg	att	gat	aca	gaa	ggg	cag	cgt	att	tac	gtc	acc	gca	gag	gca	1459
Thr	Met	Ile	Asp	Thr	Glu	Gly	Gln	Arg	Ile	Tyr	Val	Thr	Ala	Glu	Ala	
			440				445					450				
ttg	ctc	agc	tcg	tcg	ccg	tat	gcc	ttg	tcc	tgg	ggg	ccg	gcc	cgc	tat	1507
Leu	Leu	Ser	Ser	Ser	Pro	Tyr	Ala	Leu	Ser	Trp	Gly	Pro	Ala	Arg	Tyr	
			455			460					465					
ttg	atc	act	ggc	tgg	get	ggg	cca	tgg	ccg	gtg	gat	gat	cga	tgg	tgg	1555
Leu	Ile	Thr	Gly	Trp	Ala	Gly	Pro	Trp	Pro	Val	Asp	Asp	Arg	Trp	Trp	
			470		475					480				485		
gag	aaa	aac	ggc	aca	aaa	tat	gcc	cgc	ctc	caa	gtg	gtg	gga	cgg	gca	1603
Glu	Lys	Asn	Gly	Thr	Lys	Tyr	Ala	Arg	Leu	Gln	Val	Val	Gly	Arg	Ala	
			490					495					500			
gta	tct	gaa	gaa	agg	cag	ctc	aat	gcg	tgg	ctg	ttg	atg	tgg	aaa	gac	1651
Val	Ser	Glu	Glu	Arg	Gln	Leu	Asn	Ala	Trp	Leu	Leu	Met	Trp	Lys	Asp	
			505				510						515			
aac	aag	tgg	cgg	att	gag	gcc	aca	tat	taggaaacta	ctgcgctaaa						1698
Asn	Lys	Trp	Arg	Ile	Glu	Ala	Thr	Tyr								
			520			525										
aca																1701

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 <211> 526
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 1776
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 Glu Asp Ala Pro Ala His Asn Lys Pro Val Ala Ile Ala Ala His Tyr
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 Arg Ile Gln Val Cys Gly Val Ala Ala Arg Lys Arg Gly Val Arg Arg
 35 40 45
 Gly Met Lys Val Arg Gln Ala Gln Ala Val Cys Pro Glu Leu Glu Val
 50 55 60
 Val Asp Ala Asp Ala Asp Arg Asp Ala Arg Met Phe Glu Gly Ile Val
 65 70 75 80
 Ala Ser Leu Gly Glu Val Ala Ser Ser Val Glu Val Leu Arg Pro Gly
 85 90 95
 Leu Val Ala Val Asp Ala Gly Ala Ala Arg Tyr Tyr Gly Ser Glu
 100 105 110
 Asp Ile Ala Ala Gln Met Leu Ile Asp Ala Ala Leu Arg Gln Gly Ile
 115 120 125
 Asp Val Phe Ala Gly Val Ala Asp Glu Ile Thr Thr Ala Val Ile Ala
 130 135 140
 Ala Arg Ala Asn Gly Gly Thr Val Val Lys Arg Glu Ala Ser Arg Ser
 145 150 155 160
 Phe Leu Gln Gln Gln Pro Leu Gly Val Leu Ala Ala Glu Glu Ala Leu
 165 170 175
 Gly Cys Glu Ala Glu Val Val Arg Ala Leu Ala Asp Leu Gly Met Arg
 180 185 190
 Thr Leu Gly Glu Leu Ala Glu Leu Pro Val Glu Ala Val Ala Thr Arg
 195 200 205
 Phe Gly Asn Ala Gly Leu Arg Cys His Asn Ile Ala Arg Ala Arg His
 210 215 220
 Asp Arg Lys Val Ala Pro Pro Ile Thr His Ala Asp Trp Glu Val Ser
 225 230 235 240
 His Val Pro Glu Glu Pro Ile Leu Arg Val Asp Ala Ala Ser Phe Val
 245 250 255
 Ala Arg Asn Leu Ala Ser Arg Leu His Gln Leu Leu Ser Lys Gly Gly
 260 265 270
 Val Val Cys Gln Leu Leu Lys Val Thr Ala Asp Phe Ser Thr Gly Asp
 275 280 285
 Thr Val Ser Arg Ile Trp Arg Thr Gly Glu Pro Leu Thr Glu Gln Ala
 290 295 300
 Thr Ala Asp Arg Val Arg Trp Gln Leu Asp Gly Trp Leu Thr Ala Arg
 305 310 315 320
 Gly Val His Ser Asp Asp Pro Asn Glu His Asp Gly Ile Thr Ala Leu
 325 330 335

Trp Leu Ile Pro Leu Glu Cys Val Pro Pro Asp Met Ala Ser Gly Gly
 340 345 350
 Leu Trp Asp Thr Gly Arg Ser Gln Gln His Val Ala Arg Gln Val Ile
 355 360 365
 Glu Arg Val Gln Ser Ser Leu Gly Val Asp Ala Val Leu Gln Pro Val
 370 375 380
 Pro Ala Gly Gly Arg Gly Val Glu Glu Arg Ile His Phe Val Pro Tyr
 385 390 395 400
 Gly Glu Lys Arg Asp Ala Ile Arg Asn Pro Ala Gly Ser Trp Pro Gly
 405 410 415
 Lys Ile Pro Gly Pro Leu Pro Ala Arg Leu Gly Gly Gly Ile Asn His
 420 425 430
 Pro Ala Ser Gln Val Thr Met Ile Asp Thr Glu Gly Gln Arg Ile Tyr
 435 440 445
 Val Thr Ala Glu Ala Leu Leu Ser Ser Ser Pro Tyr Ala Leu Ser Trp
 450 455 460
 Gly Pro Ala Arg Tyr Leu Ile Thr Gly Trp Ala Gly Pro Trp Pro Val
 465 470 475 480
 Asp Asp Arg Trp Trp Glu Lys Asn Gly Thr Lys Tyr Ala Arg Leu Gln
 485 490 495
 Val Val Gly Arg Ala Val Ser Glu Glu Arg Gln Leu Asn Ala Trp Leu
 500 505 510
 Leu Met Trp Lys Asp Asn Lys Trp Arg Ile Glu Ala Thr Tyr
 515 520 525

<210> 1777

<211> 783

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(760)

<223> RXA00475

<400> 1777

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acgattgagc gaaattgggc gtcttgctta ggtttcgggg gtg acc cag ggt tac 115
 Val Thr Gln Gly Tyr
 1 5

ggt gtg tgc atg att gtg cag cca act tct cat tca aag cat cgt gcc 163
 Gly Val Cys Met Ile Val Gln Pro Thr Ser His Ser Lys His Arg Ala
 10 15 20

cgc ctg aag act cta gcg att gtc ggc gct agc gcg ttg act ctt gcg 211
 Arg Leu Lys Thr Leu Ala Ile Val Gly Ala Ser Ala Leu Thr Leu Ala

	25	30	35	
ggt tgt gga acc tcc aat tcc acc acc aac gat gct tct tct gta acc				259
Gly Cys Gly Thr Ser Asn Ser Thr Thr Asn Asp Ala Ser Ser Val Thr				
	40	45	50	
caa act atg tcc gca act gcg gat ggc gca cag ttg tcc aac gaa gct				307
Gln Thr Met Ser Ala Thr Ala Asp Gly Ala Gln Leu Ser Asn Glu Ala				
	55	60	65	
tcc acc ggc cca acc gca ttg ggc gaa gcc gat gta gca atg aag act				355
Ser Thr Gly Pro Thr Ala Leu Gly Glu Ala Asp Val Ala Met Lys Thr				
	70	75	80	85
ctc cga cct gat gcg cct gca cag ctc atg gtc acc gat gtt cgg att				403
Leu Arg Pro Asp Ala Pro Ala Gln Leu Met Val Thr Asp Val Arg Ile				
	90	95	100	
ggc tct cac agt ggc ttt gac cgc gtg gta ttt gat ctc act ggc acc				451
Gly Ser His Ser Gly Phe Asp Arg Val Val Phe Asp Leu Thr Gly Thr				
	105	110	115	
gga act cct ggt tgg ttc att gat tac acc tcc aat ccc acc cag cag				499
Gly Thr Pro Gly Trp Phe Ile Asp Tyr Thr Ser Asn Pro Thr Gln Gln				
	120	125	130	
ggc agc gga aac acc atc aac ttc acg ggc gat aca gcg ctg aac gta				547
Gly Ser Gly Asn Thr Ile Asn Phe Thr Gly Asp Thr Ala Leu Asn Val				
	135	140	145	
aat att gac ggt act gtt tat cct ttc gat ttg ggc ctt gag gat cca				595
Asn Ile Asp Gly Thr Val Tyr Pro Phe Asp Leu Gly Leu Glu Asp Pro				
	150	155	160	165
gag atc ggc acc gtg gat ggc tcc ggc agc att gtc acc cag gtc gtc				643
Glu Ile Gly Thr Val Asp Gly Ser Gly Ser Ile Val Thr Gln Val Val				
	170	175	180	
agc gca ggt act ttt gag gga cgc tcc cag ttc gtc atc ggc ctc aac				691
Ser Ala Gly Thr Phe Glu Gly Arg Ser Gln Phe Val Ile Gly Leu Asn				
	185	190	195	
ggc aag cac cgc tac tcg gtc act gag ttg cag gat ccg cac cgt ctc				739
Gly Lys His Arg Tyr Ser Val Thr Glu Leu Gln Asp Pro His Arg Leu				
	200	205	210	
gtt gtg gat gtt tta gcg cag tagtttccta atatgtggcc tca				783
Val Val Asp Val Leu Ala Gln				
	215	220		
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<213> Corynebacterium glutamicum				
<400> 1778				
Val Thr Gln Gly Tyr Gly Val Cys Met Ile Val Gln Pro Thr Ser His				
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Ser Lys His Arg Ala Arg Leu Lys Thr Leu Ala Ile Val Gly Ala Ser				

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Ala Leu Thr Leu Ala Gly Cys Gly Thr Ser Asn Ser Thr Thr Asn Asp
35 40 45

Ala Ser Ser Val Thr Gln Thr Met Ser Ala Thr Ala Asp Gly Ala Gln
50 55 60

Leu Ser Asn Glu Ala Ser Thr Gly Pro Thr Ala Leu Gly Glu Ala Asp
65 70 75 80

Val Ala Met Lys Thr Leu Arg Pro Asp Ala Pro Ala Gln Leu Met Val
85 90 95

Thr Asp Val Arg Ile Gly Ser His Ser Gly Phe Asp Arg Val Val Phe
100 105 110

Asp Leu Thr Gly Thr Gly Thr Pro Gly Trp Phe Ile Asp Tyr Thr Ser
115 120 125

Asn Pro Thr Gln Gln Gly Ser Gly Asn Thr Ile Asn Phe Thr Gly Asp
130 135 140

Thr Ala Leu Asn Val Asn Ile Asp Gly Thr Val Tyr Pro Phe Asp Leu
145 150 155 160

Gly Leu Glu Asp Pro Glu Ile Gly Thr Val Asp Gly Ser Gly Ser Ile
165 170 175

Val Thr Gln Val Val Ser Ala Gly Thr Phe Glu Gly Arg Ser Gln Phe
180 185 190

Val Ile Gly Leu Asn Gly Lys His Arg Tyr Ser Val Thr Glu Leu Gln
195 200 205

Asp Pro His Arg Leu Val Val Asp Val Leu Ala Gln
210 215 220

<210> 1779
<211> 984
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (101)..(961)
<223> RXA00476

<400> 1779
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Met Thr Leu Arg Cys
1 5

tct gac gtc aat gtt gaa ccc ctg ccg gga acg gca aaa aca ggt tct 163
Ser Asp Val Asn Val Glu Pro Leu Pro Gly Thr Ala Lys Thr Gly Ser
10 15 20

ggg ttt gtt ctc ctt gaa cat gct ggc tcg tgg agc cgt gat gtt tta 211

Gly	Phe	Val	Leu	Leu	Glu	His	Ala	Gly	Ser	Trp	Ser	Arg	Asp	Val	Leu		
			25					30					35				
gac	ggc	gga	aca	ttt	gat	cct	gag	ttg	act	gat	caa	ttg	aag	agg	cac	259	
Asp	Gly	Gly	Thr	Phe	Asp	Pro	Glu	Leu	Thr	Asp	Gln	Leu	Lys	Arg	His		
		40					45				50						
ctg	aaa	gct	tcc	gga	atg	ggt	ctg	caa	tta	att	agg	aag	ccg	gga	agg	307	
Leu	Lys	Ala	Ser	Gly	Met	Gly	Leu	Gln	Leu	Ile	Arg	Lys	Pro	Gly	Arg		
	55					60				65							
gag	ggt	cga	aac	gtc	gaa	aag	cat	aat	ctt	ttt	ctc	gtt	ttt	gct	gag	355	
Glu	Gly	Arg	Asn	Val	Glu	Lys	His	Asn	Leu	Phe	Leu	Val	Phe	Ala	Glu		
	70				75				80					85			
gcc	tca	att	att	gag	cac	ctg	gtg	gtg	gac	gcg	ccg	gct	gat	gtt	ttg	403	
Ala	Ser	Ile	Ile	Glu	His	Leu	Val	Val	Asp	Ala	Pro	Ala	Asp	Val	Leu		
				90					95					100			
gat	ctt	gat	tta	agc	ggg	ccg	ggc	aaa	aac	aat	gcg	cag	cgc	atg	gat	451	
Asp	Leu	Asp	Leu	Ser	Gly	Pro	Gly	Lys	Asn	Asn	Ala	Gln	Arg	Met	Asp		
			105				110					115					
gat	ccg	atg	ctg	ctg	att	tgt	acg	cat	tcg	aag	cgc	gat	gtg	tgc	tgc	499	
Asp	Pro	Met	Leu	Leu	Ile	Cys	Thr	His	Ser	Lys	Arg	Asp	Val	Cys	Cys		
		120				125					130						
gcg	atc	aag	ggg	cgt	ccg	ctg	gca	gct	gcc	gtg	gag	cca	caa	ttt	ggg	547	
Ala	Ile	Lys	Gly	Arg	Pro	Leu	Ala	Ala	Ala	Val	Glu	Pro	Gln	Phe	Gly		
	135					140					145						
ccg	ctg	cat	gtg	tgg	gag	gct	tcg	cac	acc	aag	ggc	cac	cgt	ttt	gcg	595	
Pro	Leu	His	Val	Trp	Glu	Ala	Ser	His	Thr	Lys	Gly	His	Arg	Phe	Ala		
	150				155					160				165			
cca	tcg	atg	ctg	ctc	atg	ccg	tgg	aat	tac	tct	tat	ggc	cta	ctt	gat	643	
Pro	Ser	Met	Leu	Leu	Met	Pro	Trp	Asn	Tyr	Ser	Tyr	Gly	Leu	Leu	Asp		
			170						175					180			
gag	gcc	gaa	acc	gtg	cag	ctt	ttc	caa	ggc	gcg	ttg	gac	aac	aaa	ctc	691	
Glu	Ala	Glu	Thr	Val	Gln	Leu	Phe	Gln	Gly	Ala	Leu	Asp	Asn	Lys	Leu		
		185						190				195					
ttc	ctg	ccg	ggc	aac	cgt	ggc	cga	gga	acc	tta	gat	gct	cgt	ggc	cag	739	
Phe	Leu	Pro	Gly	Asn	Arg	Gly	Arg	Gly	Thr	Leu	Asp	Ala	Arg	Gly	Gln		
		200				205					210						
gtt	gca	gaa	att	gcc	gtg	gcg	gaa	gct	ttc	ggc	gag	gcg	gtt	gct	cct	787	
Val	Ala	Glu	Ile	Ala	Val	Ala	Glu	Ala	Phe	Gly	Glu	Ala	Val	Ala	Pro		
	215				220						225						
gcg	agt	ttg	cag	gtt	gaa	ttc	gaa	gat	gat	tct	gtt	ttg	gtt	act	cat	835	
Ala	Ser	Leu	Gln	Val	Glu	Phe	Glu	Asp	Asp	Ser	Val	Leu	Val	Thr	His		
	230				235				240					245			
ccc	gat	ggg	cgc	acg	tgg	gtt	gtg	gag	ctt	gaa	cgc	atc	gag	gtc	gac	883	
Pro	Asp	Gly	Arg	Thr	Trp	Val	Val	Glu	Leu	Glu	Arg	Ile	Glu	Val	Asp		
			250					255					260				
ggc	gtg	gtg	tcc	tcg	tgt	ggt	gat	cag	ccg	aaa	act	gga	aaa	gcg	tgg	931	
Gly	Val	Val	Ser	Ser	Cys	Gly	Asp	Gln	Pro	Lys	Thr	Gly	Lys	Ala	Trp		

265 270 275
 gtg gct agg caa gtt aca gaa ctg atc gga taaaagcaga gttatatctg 981
 Val Ala Arg Gln Val Thr Glu Leu Ile Gly
 280 285
 atg 984
 <210> 1780
 <211> 287
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 1780
 Met Thr Leu Arg Cys Ser Asp Val Asn Val Glu Pro Leu Pro Gly Thr
 1 5 10 15
 Ala Lys Thr Gly Ser Gly Phe Val Leu Leu Glu His Ala Gly Ser Trp
 20 25 30
 Ser Arg Asp Val Leu Asp Gly Gly Thr Phe Asp Pro Glu Leu Thr Asp
 35 40 45
 Gln Leu Lys Arg His Leu Lys Ala Ser Gly Met Gly Leu Gln Leu Ile
 50 55 60
 Arg Lys Pro Gly Arg Glu Gly Arg Asn Val Glu Lys His Asn Leu Phe
 65 70 75 80
 Leu Val Phe Ala Glu Ala Ser Ile Ile Glu His Leu Val Val Asp Ala
 85 90 95
 Pro Ala Asp Val Leu Asp Leu Asp Leu Ser Gly Pro Gly Lys Asn Asn
 100 105 110
 Ala Gln Arg Met Asp Asp Pro Met Leu Leu Ile Cys Thr His Ser Lys
 115 120 125
 Arg Asp Val Cys Cys Ala Ile Lys Gly Arg Pro Leu Ala Ala Val
 130 135 140
 Glu Pro Gln Phe Gly Pro Leu His Val Trp Glu Ala Ser His Thr Lys
 145 150 155 160
 Gly His Arg Phe Ala Pro Ser Met Leu Leu Met Pro Trp Asn Tyr Ser
 165 170 175
 Tyr Gly Leu Leu Asp Glu Ala Glu Thr Val Gln Leu Phe Gln Gly Ala
 180 185 190
 Leu Asp Asn Lys Leu Phe Leu Pro Gly Asn Arg Gly Arg Gly Thr Leu
 195 200 205
 Asp Ala Arg Gly Gln Val Ala Glu Ile Ala Val Ala Glu Ala Phe Gly
 210 215 220
 Glu Ala Val Ala Pro Ala Ser Leu Gln Val Glu Phe Glu Asp Asp Ser
 225 230 235 240
 Val Leu Val Thr His Pro Asp Gly Arg Thr Trp Val Val Glu Leu Glu

gct ttc gcc ctc atg gtc act gat gcc act cgt gga gag gcg atg cgg 547
Ala Phe Ala Leu Met Val Thr Asp Ala Thr Arg Gly Glu Ala Met Arg
135 140 145

acg ctt ggt aag cat cag gcg cgt cgt ttt gat gct gct aaa cga tta 595
 Thr Leu Gly Lys His Gln Ala Arg Arg Phe Asp Ala Ala Lys Arg Leu
 150 155 160 165

act cca caa gag cgt gaa gtg gtt atc cga ttc ctt cag gat atg gca 643
 Thr Pro Gln Glu Arg Glu Val Val Ile Arg Phe Leu Gln Asp Met Ala
 170 175 180

cag gag tta tcc ctt aat aat gca cca tgg ctc aac acg gag 685
 Gln Glu Leu Ser Leu Asn Asn Ala Pro Trp Leu Asn Thr Glu
 185 190 195

tagatgacca tctacgttaa tta 708

<210> 1782

<211> 195

<212> PRT

<213> Corynebacterium glutamicum

<400> 1782

Met Leu Asn Met Gln Glu Pro Asp Lys Ile His Pro Ala Glu Pro Thr
 1 5 10 15

Leu Arg Asn Ile Tyr Asp Val Lys Thr Ser Asp Pro Lys Ser Glu Leu
 20 25 30

Val Asp Arg Ser Gly Met Ser Glu Glu Asp Ile Ala Gln Ile Gly Arg
 35 40 45

Leu Met Lys Ser Leu Ala Ser Leu Arg Asp Val Glu Arg Ser Ile Gly
 50 55 60

Glu Ala Ser Ala Arg Tyr Met Glu Leu Ser Ala Pro Asp Met Arg Ala
 65 70 75 80

Leu His Tyr Leu Ile Val Ala Gly Asn Ala Gly Glu Val Val Thr Pro
 85 90 95

Gly Met Leu Gly Ala His Leu Lys Leu Ser Pro Ala Ser Val Thr Lys
 100 105 110

Thr Leu Asn Arg Leu Glu Lys Gly Gly His Ile Val Arg Asn Val His
 115 120 125

Pro Val Asp Arg Arg Ala Phe Ala Leu Met Val Thr Asp Ala Thr Arg
 130 135 140

Gly Glu Ala Met Arg Thr Leu Gly Lys His Gln Ala Arg Arg Phe Asp
 145 150 155 160

Ala Ala Lys Arg Leu Thr Pro Gln Glu Arg Glu Val Val Ile Arg Phe
 165 170 175

Leu Gln Asp Met Ala Gln Glu Leu Ser Leu Asn Asn Ala Pro Trp Leu
 180 185 190

Asn Thr Glu
 195

<210> 1783

<211> 725

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(702)

<223> RXA00486

<400> 1783

cat	gcg	atc	atg	gca	gca	gtc	gac	cat	gcc	cgc	gca	gcc	gtt	cta	gat	48
His	Ala	Ile	Met	Ala	Ala	Val	Asp	His	Ala	Arg	Ala	Ala	Val	Leu	Asp	
1				5					10					15		

tcg	ctg	tct	gaa	gtg	tcc	gga	acg	ttg	aaa	gtc	acc	tcc	ttc	caa	tcc	96
Ser	Leu	Ser	Glu	Val	Ser	Gly	Thr	Leu	Lys	Val	Thr	Ser	Phe	Gln	Ser	
			20				25						30			

ctg	ctg	ttc	acc	ctt	gcc	ccg	aaa	gcc	atc	gcg	cgc	ctg	acc	gag	aaa	144
Leu	Leu	Phe	Thr	Leu	Ala	Pro	Lys	Ala	Ile	Ala	Arg	Leu	Thr	Glu	Lys	
		35				40						45				

tac	cca	cac	ctg	caa	gta	gaa	atc	tcc	caa	cta	gaa	gtc	acc	gca	gcg	192
Tyr	Pro	His	Leu	Gln	Val	Glu	Ile	Ser	Gln	Leu	Glu	Val	Thr	Ala	Ala	
	50					55				60						

ctc	gaa	gaa	ctc	cgc	gcc	cgc	cgc	gtc	gac	gtc	gca	ctc	ggc	gag	gaa	240
Leu	Glu	Glu	Leu	Arg	Ala	Arg	Arg	Val	Asp	Val	Ala	Leu	Gly	Glu	Glu	
	65			70				75						80		

tac	ccc	gtg	gaa	gtc	ccc	ctt	gtt	gag	gcc	agc	att	cac	cgc	gaa	gtc	288
Tyr	Pro	Val	Glu	Val	Pro	Leu	Val	Glu	Ala	Ser	Ile	His	Arg	Glu	Val	
			85					90						95		

ctc	ttc	gaa	gac	ccc	atg	ctg	ctc	gtc	acc	cca	gca	agc	ggc	cca	tac	336
Leu	Phe	Glu	Asp	Pro	Met	Leu	Leu	Val	Thr	Pro	Ala	Ser	Gly	Pro	Tyr	
		100						105					110			

tct	ggc	ctc	acc	ctg	cca	gaa	ctc	cgc	gac	atc	ccc	atc	gcc	atc	gat	384
Ser	Gly	Leu	Thr	Leu	Pro	Glu	Leu	Arg	Asp	Ile	Pro	Ile	Ala	Ile	Asp	
	115					120					125					

cca	ccc	gac	ctt	ccc	gcg	ggc	gaa	tgg	gtc	cat	agg	ctc	tgc	cgg	cgc	432
Pro	Pro	Asp	Leu	Pro	Ala	Gly	Glu	Trp	Val	His	Arg	Leu	Cys	Arg	Arg	
	130				135						140					

gcc	ggg	ttt	gag	ccc	cgc	gtg	acc	ttt	gaa	acc	agc	gat	ccc	atg	ctc	480
Ala	Gly	Phe	Glu	Pro	Arg	Val	Thr	Phe	Glu	Thr	Ser	Asp	Pro	Met	Leu	
	145				150				155					160		

caa	gca	cac	ctc	gtg	cgt	agc	ggc	ttg	gcc	gtg	aca	ttt	tcc	ccc	aca	528
Gln	Ala	His	Leu	Val	Arg	Ser	Gly	Leu	Ala	Val	Thr	Phe	Ser	Pro	Thr	
			165					170						175		

ctg	ctc	acc	ccg	atg	ctg	gaa	agc	gtg	cac	atc	cag	ccg	ctg	ccc	ggc	576
Leu	Leu	Thr	Pro	Met	Leu	Glu	Ser	Val	His	Ile	Gln	Pro	Leu	Pro	Gly	
			180					185					190			

aac	ccc	acg	cgc	acg	ctc	tac	acc	gcg	gtc	agg	gaa	ggg	cgc	cag	ggg	624
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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Asn Pro Thr Arg Thr Leu Tyr Thr Ala Val Arg Glu Gly Arg Gln Gly
    195                      200                      205

cat cca gcc att aaa gct ttt cga cga gcc ctc gcc cat gtg gcc aaa 672
His Pro Ala Ile Lys Ala Phe Arg Arg Ala Leu Ala His Val Ala Lys
    210                      215                      220

gaa tct tat ttg gag gct cgt cta gta gag tgagttcttg tgagccttca 722
Glu Ser Tyr Leu Glu Ala Arg Leu Val Glu
    225                      230

gac 725

<210> 1784
<211> 234
<212> PRT
<213> Corynebacterium glutamicum

<400> 1784
His Ala Ile Met Ala Ala Val Asp His Ala Arg Ala Ala Val Leu Asp
    1           5           10           15

Ser Leu Ser Glu Val Ser Gly Thr Leu Lys Val Thr Ser Phe Gln Ser
    20           25           30

Leu Leu Phe Thr Leu Ala Pro Lys Ala Ile Ala Arg Leu Thr Glu Lys
    35           40           45

Tyr Pro His Leu Gln Val Glu Ile Ser Gln Leu Glu Val Thr Ala Ala
    50           55           60

Leu Glu Glu Leu Arg Ala Arg Arg Val Asp Val Ala Leu Gly Glu Glu
    65           70           75           80

Tyr Pro Val Glu Val Pro Leu Val Glu Ala Ser Ile His Arg Glu Val
    85           90           95

Leu Phe Glu Asp Pro Met Leu Leu Val Thr Pro Ala Ser Gly Pro Tyr
    100          105          110

Ser Gly Leu Thr Leu Pro Glu Leu Arg Asp Ile Pro Ile Ala Ile Asp
    115          120          125

Pro Pro Asp Leu Pro Ala Gly Glu Trp Val His Arg Leu Cys Arg Arg
    130          135          140

Ala Gly Phe Glu Pro Arg Val Thr Phe Glu Thr Ser Asp Pro Met Leu
    145          150          155          160

Gln Ala His Leu Val Arg Ser Gly Leu Ala Val Thr Phe Ser Pro Thr
    165          170          175

Leu Leu Thr Pro Met Leu Glu Ser Val His Ile Gln Pro Leu Pro Gly
    180          185          190

Asn Pro Thr Arg Thr Leu Tyr Thr Ala Val Arg Glu Gly Arg Gln Gly
    195                      200                      205

His Pro Ala Ile Lys Ala Phe Arg Arg Ala Leu Ala His Val Ala Lys
    210                      215                      220

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Glu Ser Tyr Leu Glu Ala Arg Leu Val Glu
225 230

<210> 1785

<211> 1026

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1003)

<223> RXA00490

<400> 1785

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gatctagttcc ttaaagggttt ctttggcaat aatcaagggc atg aat aaa cag tcc 115
Met Asn Lys Gln Ser
1 5

gct gca gtg ttg atg gtg atg ggt tcc gcc cta tcc ctg caa ttt ggt 163
Ala Ala Val Leu Met Val Met Gly Ser Ala Leu Ser Leu Gln Phe Gly
10 15 20

gct gcc att gga acg cag ctt ttc ccc ctg aac ggc ccc tgg gct gtc 211
Ala Ala Ile Gly Thr Gln Leu Phe Pro Leu Asn Gly Pro Trp Ala Val
25 30 35

acc tct tta agg ctg ttc atc gca ggc ttg atc atg tgc ctg gtg atc 259
Thr Ser Leu Arg Leu Phe Ile Ala Gly Leu Ile Met Cys Leu Val Ile
40 45 50

cgc ccg cga ctt cgt tcc tgg act aaa aaa caa tgg atc gcc gtg ctg 307
Arg Pro Arg Leu Arg Ser Trp Thr Lys Lys Gln Trp Ile Ala Val Leu
55 60 65

ctg ttg gga tta tct ctt ggc gga atg aac agc ctg ttt tac gca tcc 355
Leu Leu Gly Leu Ser Leu Gly Gly Met Asn Ser Leu Phe Tyr Ala Ser
70 75 80 85

atc gaa ctg atc ccg ctg ggt acc gcc gtg acc att gag ttc ctg ggc 403
Ile Glu Leu Ile Pro Leu Gly Thr Ala Val Thr Ile Glu Phe Leu Gly
90 95 100

ccc ctg att ttc tcc gcg gtg tta gcc cgc acg ctg aaa aac gga ttg 451
Pro Leu Ile Phe Ser Ala Val Leu Ala Arg Thr Leu Lys Asn Gly Leu
105 110 115

tgc gtg gct tta gcg ttt ctg gcc atg gca cta ctg ggt atc gat tcc 499
Cys Val Ala Leu Ala Phe Leu Gly Met Ala Leu Leu Gly Ile Asp Ser
120 125 130

ctc agc ggc gaa acc ctt gac cca ctg gcc gtc att ttc gca gcc gtc 547
Leu Ser Gly Glu Thr Leu Asp Pro Leu Gly Val Ile Phe Ala Ala Val
135 140 145

gca gga atc ttc tgg gtg tgc tac atc ctg gca tca aag aaa atc ggc 595
Ala Gly Ile Phe Trp Val Cys Tyr Ile Leu Ala Ser Lys Lys Ile Gly
150 155 160 165

caa ctc atc ccc gga aca agc ggc ctg gcc gtc gca ctg att atc ggc 643
 Gln Leu Ile Pro Gly Thr Ser Gly Leu Ala Val Ala Leu Ile Ile Gly
 170 175 180

gca gtg gca gta ttt cca ctg ggt gct aca cac atg ggc cgg att ttc 691
 Ala Val Ala Val Phe Pro Leu Gly Ala Thr His Met Gly Pro Ile Phe
 185 190 195

cag acc cca acc cta ctc atc ctg gcg ctt ggc aca gca ctt ctc ggg 739
 Gln Thr Pro Thr Leu Leu Ile Leu Ala Leu Gly Thr Ala Leu Leu Gly
 200 205 210

tcg ctt atc ccc tat tcg ctg gaa tta tcg gca ctg cgc cga ctc ccc 787
 Ser Leu Ile Pro Tyr Ser Leu Glu Leu Ser Ala Leu Arg Arg Leu Pro
 215 220 225

gcc ccc att ttc agt att ctg ctc agc ctc gaa cgg gca ttc gcc gcc 835
 Ala Pro Ile Phe Ser Ile Leu Leu Ser Leu Glu Pro Ala Phe Ala Ala
 230 235 240 245

gcc gtc ggc tgg atc ctg ctt gat caa acc ccc acc gcg ctc aag tgg 883
 Ala Val Gly Trp Ile Leu Leu Asp Gln Thr Pro Thr Ala Leu Lys Trp
 250 255 260

gcc gcg atc atc ctt gtc atc gcg gcc agc atc ggc gtc acg tgg gag 931
 Ala Ala Ile Ile Leu Val Ile Ala Ala Ser Ile Gly Val Thr Trp Glu
 265 270 275

cct aaa aag atg ctt gtc gac gcg ccc ctc cac tca aaa tgc aac gcg 979
 Pro Lys Lys Met Leu Val Asp Ala Pro Leu His Ser Lys Cys Asn Ala
 280 285 290

aag agg cga gta cac aca cct agt taacgtgcag gcttaccttt tgg 1026
 Lys Arg Arg Val His Thr Pro Ser
 295 300

<210> 1786
 <211> 301
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 1786
 Met Asn Lys Gln Ser Ala Ala Val Leu Met Val Met Gly Ser Ala Leu
 1 5 10 15
 Ser Leu Gln Phe Gly Ala Ala Ile Gly Thr Gln Leu Phe Pro Leu Asn
 20 25 30
 Gly Pro Trp Ala Val Thr Ser Leu Arg Leu Phe Ile Ala Gly Leu Ile
 35 40 45
 Met Cys Leu Val Ile Arg Pro Arg Leu Arg Ser Trp Thr Lys Lys Gln
 50 55 60
 Trp Ile Ala Val Leu Leu Leu Gly Leu Ser Leu Gly Gly Met Asn Ser
 65 70 75 80
 Leu Phe Tyr Ala Ser Ile Glu Leu Ile Pro Leu Gly Thr Ala Val Thr
 85 90 95

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Ile Glu Phe Leu Gly Pro Leu Ile Phe Ser Ala Val Leu Ala Arg Thr
    100                      105                      110

Leu Lys Asn Gly Leu Cys Val Ala Leu Ala Phe Leu Gly Met Ala Leu
    115                      120                      125

Leu Gly Ile Asp Ser Leu Ser Gly Glu Thr Leu Asp Pro Leu Gly Val
    130                      135                      140

Ile Phe Ala Ala Val Ala Gly Ile Phe Trp Val Cys Tyr Ile Leu Ala
    145                      150                      155                      160

Ser Lys Lys Ile Gly Gln Leu Ile Pro Gly Thr Ser Gly Leu Ala Val
    165                      170                      175

Ala Leu Ile Ile Gly Ala Val Ala Val Phe Pro Leu Gly Ala Thr His
    180                      185                      190

Met Gly Pro Ile Phe Gln Thr Pro Thr Leu Leu Ile Leu Ala Leu Gly
    195                      200                      205

Thr Ala Leu Leu Gly Ser Leu Ile Pro Tyr Ser Leu Glu Leu Ser Ala
    210                      215                      220

Leu Arg Arg Leu Pro Ala Pro Ile Phe Ser Ile Leu Leu Ser Leu Glu
    225                      230                      235                      240

Pro Ala Phe Ala Ala Ala Val Gly Trp Ile Leu Leu Asp Gln Thr Pro
    245                      250                      255

Thr Ala Leu Lys Trp Ala Ala Ile Ile Leu Val Ile Ala Ala Ser Ile
    260                      265                      270

Gly Val Thr Trp Glu Pro Lys Lys Met Leu Val Asp Ala Pro Leu His
    275                      280                      285

Ser Lys Cys Asn Ala Lys Arg Arg Val His Thr Pro Ser
    290                      295                      300

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<210> 1787

<211> 543

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(520)

<223> RXA00491

<400> 1787

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gctgcagctc acacgctatt ccacaaccgg aaatctggca gtg tat tgg gtt tta 115
Val Tyr Trp Val Leu
1 5

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gca acc tct gcc aat agg gtg gaa gat gtg aac ttt gat gcg atg atg 163
Ala Thr Ser Ala Asn Arg Val Glu Asp Val Asn Phe Asp Ala Met Met
10 15 20

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ccc cgc gac ccg ttt gcc gat gat ccc aat gac ccg gca tgc ttt att 211
Pro Arg Asp Pro Phe Ala Asp Asp Pro Asn Asp Pro Ala Ser Phe Ile
      25              30              35

acc gac gat gac cct tat gat cat ccc gaa ccg ctt tct gaa gaa gag 259
Thr Asp Asp Asp Pro Tyr Asp His Pro Glu Pro Leu Ser Glu Glu Glu
      40              45              50

cga atc cac gtg agc caa gac ctt cgc ctc gtg atg gaa ttt aaa aaa 307
Arg Ile His Val Ser Gln Asp Leu Arg Leu Val Met Glu Phe Lys Lys
      55              60              65

gtt tta ggt ccc cga gga atc gaa ggc gtg ttc atg tgc gaa gac 355
Val Leu Gly Pro Arg Gly Ile Glu Gly Val Phe Phe Met Cys Glu Asp
      70              75              80              85

tgc gaa gag ttc cac tac tac gac tgg gac atc atg gca gca aac atg 403
Cys Glu Glu Phe His Tyr Tyr Asp Trp Asp Ile Met Ala Ala Asn Met
      90              95              100

cgc gcc acc ttg gct ggg gaa ctc agc ccc gtg cat gaa cca agt gcg 451
Arg Ala Thr Leu Ala Gly Glu Leu Ser Pro Val His Glu Pro Ser Ala
      105              110              115

caa ccc aat att gat gcc tat gtg ccg tgg gac tac tgc att ggt tac 499
Gln Pro Asn Ile Asp Ala Tyr Val Pro Trp Asp Tyr Cys Ile Gly Tyr
      120              125              130

cta gac gga ctt gaa gcc aaa taaaaactgc tagcaactaa aga 543
Leu Asp Gly Leu Glu Ala Lys
      135              140

<210> 1788
<211> 140
<212> PRT
<213> Corynebacterium glutamicum

<400> 1788
Val Tyr Trp Val Leu Ala Thr Ser Ala Asn Arg Val Glu Asp Val Asn
  1              5              10              15

Phe Asp Ala Met Met Pro Arg Asp Pro Phe Ala Asp Asp Pro Asn Asp
      20              25              30

Pro Ala Ser Phe Ile Thr Asp Asp Pro Tyr Asp His Pro Glu Pro
      35              40              45

Leu Ser Glu Glu Glu Arg Ile His Val Ser Gln Asp Leu Arg Leu Val
      50              55              60

Met Glu Phe Lys Lys Val Leu Gly Pro Arg Gly Ile Glu Gly Val Phe
      65              70              75              80

Phe Met Cys Glu Asp Cys Glu Glu Phe His Tyr Tyr Asp Trp Asp Ile
      85              90              95

Met Ala Ala Asn Met Arg Ala Thr Leu Ala Gly Glu Leu Ser Pro Val
      100              105              110

```

His Glu Pro Ser Ala Gln Pro Asn Ile Asp Ala Tyr Val Pro Trp Asp
115 120 125

Tyr Cys Ile Gly Tyr Leu Asp Gly Leu Glu Ala Lys
130 135 140

<210> 1789

<211> 347

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1) .. (324)

<223> RXA00493

<400> 1789

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Phe Glu Gly Asp Gln Lys Val Gly Val Arg Ala Leu Ala Thr Ala Leu
1 5 10 15

ggc aag cca gcg tac tgg atc gcc tcc aac gca ggt ctt gac ggc tct 96
Gly Lys Pro Ala Tyr Trp Ile Ala Ser Asn Ala Gly Leu Asp Gly Ser
20 25 30

ggt gtt gtt gca cgc act gct gct ctg cca aac ggc gag ggc ttc aac 144
Val Val Val Val Ala Arg Thr Ala Ala Leu Pro Asn Gly Glu Gly Phe Asn
35 40 45

gct gca act ttg gaa tac gga aac ctg atc aac gac ggt gtc atc gac 192
Ala Ala Thr Leu Glu Tyr Gly Asn Leu Ile Asn Asp Gly Val Ile Asp
50 55 60

cca gtc aag gtc acc cat tcc gca gta gtg aat gca acc tct gtt gca 240
Pro Val Lys Val Thr His Ser Ala Val Val Asn Ala Thr Ser Val Ala
65 70 75 80

cgc atg gtt ctg acc act gag gct tct gtt gtt gag aag cct gca gaa 288
Arg Met Val Leu Thr Thr Glu Ala Ser Val Val Glu Lys Pro Ala Glu
85 90 95

gaa gca gcc gat gca cat gca gga cat cat cac cac taaagttctg 334
Glu Ala Ala Asp Ala His Ala Gly His His His His
100 105

tgaaaaacac cgt 347

<210> 1790

<211> 108

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1790

Phe Glu Gly Asp Gln Lys Val Gly Val Arg Ala Leu Ala Thr Ala Leu
1 5 10 15

Gly Lys Pro Ala Tyr Trp Ile Ala Ser Asn Ala Gly Leu Asp Gly Ser
20 25 30

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Val Val Val Ala Arg Thr Ala Ala Leu Pro Asn Gly Glu Gly Phe Asn
   35                               40               45

Ala Ala Thr Leu Glu Tyr Gly Asn Leu Ile Asn Asp Gly Val Ile Asp
   50                               55               60

Pro Val Lys Val Thr His Ser Ala Val Val Asn Ala Thr Ser Val Ala
   65                               70               75               80

Arg Met Val Leu Thr Thr Glu Ala Ser Val Val Glu Lys Pro Ala Glu
           85                               90               95

Glu Ala Ala Asp Ala His Ala Gly His His His His
   100                               105

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<210> 1791
<211> 536
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (1)..(513)
<223> RXA00519

<400> 1791
atg gct ggc ggc gga ctg ttc gag acc ggt gct ggt gga tct gct cct 48
Met Ala Gly Gly Gly Leu Phe Glu Thr Gly Ala Gly Gly Ser Ala Pro
   1                               5                               10          15

aag cac gtc cag cag gtt cag gaa gaa aac cac ctg cgt tgg gat tcc 96
Lys His Val Gln Gln Val Gln Glu Glu Asn His Leu Arg Trp Asp Ser
           20                               25          30

ctc ggt gag ttc ctc gca ctg gct gag tcc ttc cgc cac gag ctc aac 144
Leu Gly Glu Phe Leu Ala Leu Ala Glu Ser Phe Arg His Glu Leu Asn
           35                               40          45

aac aac ggc aac acc aag gcc ggc gtt ctg gct gac gct ctg gac aag 192
Asn Asn Gly Asn Thr Lys Ala Gly Val Leu Ala Asp Ala Leu Asp Lys
   50                               55          60

gca act gag aag ctg ctg aac gaa gag aag tcc cca tcc cgc aag gtt 240
Ala Thr Glu Lys Leu Leu Asn Glu Glu Lys Ser Pro Ser Arg Lys Val
   65                               70          75          80

ggc gag atc gac aac cgt ggc tcc cac ttc tgg ctg acc aag ttc tgg 288
Gly Glu Ile Asp Asn Arg Gly Ser His Phe Trp Leu Thr Lys Phe Trp
           85                               90          95

gct gac gag ctc gct gct cag acc gag gac gca gat ctg gct gct acc 336
Ala Asp Glu Leu Ala Ala Gln Thr Glu Asp Ala Asp Leu Ala Ala Thr
   100                               105          110

ttc gca cca gtc gca gaa gca ctg aac aca ggc gct gca gac atc gat 384
Phe Ala Pro Val Ala Glu Ala Leu Asn Thr Gly Ala Ala Asp Ile Asp
   115                               120          125

gct gca ctg ctc gca gtt cag ggt gga gca act gac ctt ggt ggc tac 432
Ala Ala Leu Leu Ala Val Gln Gly Gly Ala Thr Asp Leu Gly Gly Tyr

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130

135

140

tac tcc cct aac gag gag aag ctc acc aac atc atg cgc cca gtc gca 480
 Tyr Ser Pro Asn Glu Glu Lys Leu Thr Asn Ile Met Arg Pro Val Ala
 145 150 155 160

cag ttc aac gag atc gtt gac gca ctg aag aag taaagtctct tcacaaaaag 533
 Gln Phe Asn Glu Ile Val Asp Ala Leu Lys Lys
 165 170

cgc 536

<210> 1792

<211> 171

<212> PRT

<213> Corynebacterium glutamicum

<400> 1792

Met Ala Gly Gly Leu Phe Glu Thr Gly Ala Gly Gly Ser Ala Pro
 1 5 10 15

Lys His Val Gln Gln Val Gln Glu Glu Asn His Leu Arg Trp Asp Ser
 20 25 30

Leu Gly Glu Phe Leu Ala Leu Ala Glu Ser Phe Arg His Glu Leu Asn
 35 40 45

Asn Asn Gly Asn Thr Lys Ala Gly Val Leu Ala Asp Ala Leu Asp Lys
 50 55 60

Ala Thr Glu Lys Leu Leu Asn Glu Glu Lys Ser Pro Ser Arg Lys Val
 65 70 75 80

Gly Glu Ile Asp Asn Arg Gly Ser His Phe Trp Leu Thr Lys Phe Trp
 85 90 95

Ala Asp Glu Leu Ala Ala Gln Thr Glu Asp Ala Asp Leu Ala Ala Thr
 100 105 110

Phe Ala Pro Val Ala Glu Ala Leu Asn Thr Gly Ala Ala Asp Ile Asp
 115 120 125

Ala Ala Leu Leu Ala Val Gln Gly Gly Ala Thr Asp Leu Gly Gly Tyr
 130 135 140

Tyr Ser Pro Asn Glu Glu Lys Leu Thr Asn Ile Met Arg Pro Val Ala
 145 150 155 160

Gln Phe Asn Glu Ile Val Asp Ala Leu Lys Lys
 165 170

<210> 1793

<211> 1212

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1189)

<223> RXA00528

<400> 1793

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tcggtcgcgcg ccggttatctt ttttaagagga gaaatttttag atg agc acg tcc acc 115
Met Ser Thr Ser Thr
1 5
atc agg gtt gcc att gcc gga gtc gga aac tgc gcg acc tcc ctc att 163
Ile Arg Val Ala Ile Ala Gly Val Gly Asn Cys Ala Thr Ser Leu Ile
10 15 20
cag ggt gtg gaa tat tac cga aat gcg gat cct tcc gaa act gtc ccg 211
Gln Gly Val Glu Tyr Tyr Arg Asn Ala Asp Pro Ser Glu Thr Val Pro
25 30 35
ggg ttg atg cac gtc aaa ttc ggt gat tac cac gtt ggc gac att gaa 259
Gly Leu Met His Val Lys Phe Gly Asp Tyr His Val Gly Asp Ile Glu
40 45 50
ttc gtg gcc gcg ttc gac gtc gac gcc gaa aaa gta ggc atc gat ctt 307
Phe Val Ala Ala Phe Asp Val Asp Ala Glu Lys Val Gly Ile Asp Leu
55 60 65
gcc gac gcc acc gag gct tca caa aac tgc act atc aaa atc gcc gat 355
Ala Asp Ala Thr Glu Ala Ser Gln Asn Cys Thr Ile Lys Ile Ala Asp
70 75 80 85
gtc cca cag acc ggc atc aac gtg ctg cgt ggc ccg act ctc gac ggc 403
Val Pro Gln Thr Gly Ile Asn Val Leu Arg Gly Pro Thr Leu Asp Gly
90 95 100
ctg ggc gat cat tac cgc gcg acc atc gac gag tcc acc gcc gag cca 451
Leu Gly Asp His Tyr Arg Ala Thr Ile Asp Glu Ser Thr Ala Glu Pro
105 110 115
gtc gac gtt gtc cag gcg ctt atc gac gca aaa gcc gat gtt ttg gtg 499
Val Asp Val Val Gln Ala Leu Ile Asp Ala Lys Ala Asp Val Leu Val
120 125 130
tcc tac ctc cca gtg ggc tcc gaa gaa gcc gac aaa ttc tac gca caa 547
Ser Tyr Leu Pro Val Gly Ser Glu Glu Ala Asp Lys Phe Tyr Ala Gln
135 140 145
gcc gcc atc gat gca ggc tgc gcc ttt gtc aac gct ctc cca gta ttc 595
Ala Ala Ile Asp Ala Gly Cys Ala Phe Val Asn Ala Leu Pro Val Phe
150 155 160 165
atc gcc tcc gac cct gag tgg gct aag aag ttc act gac gct ggc atc 643
Ile Ala Ser Asp Pro Glu Trp Ala Lys Lys Phe Thr Asp Ala Gly Ile
170 175 180
cca att gtt ggc gat gac atc aaa tcc cag atc ggt gca acc atc acc 691
Pro Ile Val Gly Asp Asp Ile Lys Ser Gln Ile Gly Ala Thr Ile Thr
185 190 195
cac cgt gtc ctc gca cgc ctt ttt gaa gaa cgt ggc gtt cgc gta gat 739
His Arg Val Leu Ala Arg Leu Phe Glu Glu Arg Gly Val Arg Val Asp
200 205 210

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cgc acc atg cag ctc aac gtc ggc ggc aac atg gac ttc aaa aac atg 787
 Arg Thr Met Gln Leu Asn Val Gly Gly Asn Met Asp Phe Lys Asn Met
 215 220 225

 ctt gac cgc aat cgc ttg gaa tcc aag aag gtc tcc aaa acc caa gca 835
 Leu Asp Arg Asn Arg Leu Glu Ser Lys Lys Val Ser Lys Thr Gln Ala
 230 235 240 245

 gtg acc tcc aac att cca gat ggt cca ctg tct gga aag gtg gaa gac 883
 Val Thr Ser Asn Ile Pro Asp Gly Pro Leu Ser Gly Lys Val Glu Asp
 250 255 260

 cgc aac gtc cac atc gga cca tcc gac cac gtc caa tgg ctc gat gac 931
 Arg Asn Val His Ile Gly Pro Ser Asp His Val Gln Trp Leu Asp Asp
 265 270 275

 cgc aag tgg gct tat gtc cgc ctc gaa ggc acc gca ttc ggt gga gtt 979
 Arg Lys Trp Ala Tyr Val Arg Leu Glu Gly Thr Ala Phe Gly Gly Val
 280 285 290

 ccc ctc aac ctt gag tac aaa ctc gag gtg tgg gat tca ccc aac tct 1027
 Pro Leu Asn Leu Glu Tyr Lys Leu Glu Val Trp Asp Ser Pro Asn Ser
 295 300 305

 gcc ggc atc atc atc gac gct gtt cgc gcc gcc aag atc gcc ctc gat 1075
 Ala Gly Ile Ile Ile Asp Ala Val Arg Ala Lys Ile Ala Leu Asp
 310 315 320 325

 cgc ggt atc ggc gga ccg atc atg cca gca agc tcc tac ctg atg aag 1123
 Arg Gly Ile Gly Gly Pro Ile Met Pro Ala Ser Ser Tyr Leu Met Lys
 330 335 340

 tcc cca cct gag cag ctt cca gac gat gtt gct tgt gaa cgc cta gag 1171
 Ser Pro Pro Glu Gln Leu Pro Asp Asp Val Ala Cys Glu Arg Leu Glu
 345 350 355

 gca ttc atc atc gag gcg taaaattagg ctaaaaattt ggg 1212
 Ala Phe Ile Ile Glu Ala
 360

<210> 1794

<211> 363

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1794

Met Ser Thr Ser Thr Ile Arg Val Ala Ile Ala Gly Val Gly Asn Cys
 1 5 10 15

 Ala Thr Ser Leu Ile Gln Gly Val Glu Tyr Tyr Arg Asn Ala Asp Pro
 20 25 30

 Ser Glu Thr Val Pro Gly Leu Met His Val Lys Phe Gly Asp Tyr His
 35 40 45

 Val Gly Asp Ile Glu Phe Val Ala Ala Phe Asp Val Asp Ala Glu Lys
 50 55 60

 Val Gly Ile Asp Leu Ala Asp Ala Thr Glu Ala Ser Gln Asn Cys Thr
 65 70 75 80


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Ile Lys Ile Ala Asp Val Pro Gln Thr Gly Ile Asn Val Leu Arg Gly
      85                      90                      95
Pro Thr Leu Asp Gly Leu Gly Asp His Tyr Arg Ala Thr Ile Asp Glu
      100                    105
Ser Thr Ala Glu Pro Val Asp Val Val Gln Ala Leu Ile Asp Ala Lys
      115                    120                    125
Ala Asp Val Leu Val Ser Tyr Leu Pro Val Gly Ser Glu Glu Ala Asp
      130                    135                    140
Lys Phe Tyr Ala Gln Ala Ala Ile Asp Ala Gly Cys Ala Phe Val Asn
      145                    150                    155                    160
Ala Leu Pro Val Phe Ile Ala Ser Asp Pro Glu Trp Ala Lys Lys Phe
      165                    170                    175
Thr Asp Ala Gly Ile Pro Ile Val Gly Asp Asp Ile Lys Ser Gln Ile
      180                    185
Gly Ala Thr Ile Thr His Arg Val Leu Ala Arg Leu Phe Glu Glu Arg
      195                    200                    205
Gly Val Arg Val Asp Arg Thr Met Gln Leu Asn Val Gly Gly Asn Met
      210                    215                    220
Asp Phe Lys Asn Met Leu Asp Arg Asn Arg Leu Glu Ser Lys Lys Val
      225                    230                    235                    240
Ser Lys Thr Gln Ala Val Thr Ser Asn Ile Pro Asp Gly Pro Leu Ser
      245                    250                    255
Gly Lys Val Glu Asp Arg Asn Val His Ile Gly Pro Ser Asp His Val
      260                    265                    270
Gln Trp Leu Asp Asp Arg Lys Trp Ala Tyr Val Arg Leu Glu Gly Thr
      275                    280                    285
Ala Phe Gly Gly Val Pro Leu Asn Leu Glu Tyr Lys Leu Glu Val Trp
      290                    295                    300
Asp Ser Pro Asn Ser Ala Gly Ile Ile Ile Asp Ala Val Arg Ala Ala
      305                    310                    315                    320
Lys Ile Ala Leu Asp Arg Gly Ile Gly Gly Pro Ile Met Pro Ala Ser
      325                    330                    335
Ser Tyr Leu Met Lys Ser Pro Pro Glu Gln Leu Pro Asp Asp Val Ala
      340                    345                    350
Cys Glu Arg Leu Glu Ala Phe Ile Ile Glu Ala
      355                    360

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<210> 1795

<211> 666

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(643)

<223> RXA00529

<400> 1795

gcaaaagcttt gtaccggaag cgtaaagcca ctggatatttg tcgagcagtt tcaggctgtt 60

tagcggcgca gttcttatag agatgtataa ggtgaagctc atg aag ttg aag tgg 115
 Met Lys Leu Lys Trp
 1 5

att gca cca att ctt ccg gtt ttg gcc ctt gca gcc tgc gga aac tac 163
 Ile Ala Pro Ile Leu Pro Val Leu Ala Leu Ala Gly Cys Gly Asn Tyr
 10 15 20

gtc aac gta gag tcg caa ggg aaa tct gga att tcc cat gat gag gac 211
 Val Asn Val Glu Ser Gln Gly Lys Ser Gly Ile Ser His Asp Glu Asp
 25 30 35

gga aat ata agc gtt cac atg tac atc tgt ggt gat aat gcg gtg gat 259
 Gly Asn Ile Ser Val His Met Tyr Ile Cys Gly Asp Asn Ala Val Asp
 40 45 50

gaa ctg ata ctt agc ggt ggt ttt tac gat gcc cca cct ggg aca aac 307
 Glu Leu Ile Leu Ser Gly Gly Phe Tyr Asp Gly Pro Pro Gly Thr Asn
 55 60 65

aac cca gcc ctt ggg atg ttg aaa act tcc aac cct gag tcg ggt tat 355
 Asn Pro Ala Leu Gly Met Leu Lys Thr Ser Asn Pro Glu Ser Gly Tyr
 70 75 80 85

gtt gta gtc aac atc gct gat cca gca ccg tgg gaa gtt gtt gag cca 403
 Val Val Val Asn Ile Ala Asp Pro Ala Pro Trp Glu Val Val Glu Pro
 90 95 100

atc aat ttg ccc acg gaa cag gga aag tac att att gcc aat ccg agg 451
 Ile Asn Leu Pro Thr Glu Gln Gly Lys Tyr Ile Ile Ala Asn Pro Arg
 105 110 115

ttg gta gat aaa ggt tgg ccg att cct ttc gca aaa gaa aag tat atg 499
 Leu Val Asp Lys Gly Trp Pro Ile Pro Phe Ala Lys Glu Lys Tyr Met
 120 125 130

ccg agt gtt tcc aca tca gta gga atg ctt gaa gga ata gat cca ggt 547
 Pro Ser Val Ser Thr Ser Val Gly Met Leu Glu Gly Ile Asp Pro Gly
 135 140 145

cta gtc atg cgg gat atg tat acc gag tcg act cat gtg ttc ggt act 595
 Leu Val Met Arg Asp Met Tyr Thr Glu Ser Thr His Val Phe Gly Thr
 150 155 160 165

gcc gaa gac ttt gtt gaa gcc ggt caa cag tgg tgc gag gat tat ttc 643
 Ala Glu Asp Phe Val Glu Ala Gly Gln Trp Cys Glu Asp Tyr Phe
 170 175 180

taaaacgtga atctggcaaa aga 666

<210> 1796

<211> 181

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1796

Met Lys Leu Lys Trp Ile Ala Pro Ile Leu Pro Val Leu Ala Leu Ala
 1 5 10 15

Gly Cys Gly Asn Tyr Val Asn Val Glu Ser Gln Gly Lys Ser Gly Ile
 20 25 30

Ser His Asp Glu Asp Gly Asn Ile Ser Val His Met Tyr Ile Cys Gly
 35 40 45

Asp Asn Ala Val Asp Glu Leu Ile Leu Ser Gly Gly Phe Tyr Asp Gly
 50 55 60

Pro Pro Gly Thr Asn Asn Pro Ala Leu Gly Met Leu Lys Thr Ser Asn
 65 70 75 80

Pro Glu Ser Gly Tyr Val Val Val Asn Ile Ala Asp Pro Ala Pro Trp
 85 90 95

Glu Val Val Glu Pro Ile Asn Leu Pro Thr Glu Gln Gly Lys Tyr Ile
 100 105 110

Ile Ala Asn Pro Arg Leu Val Asp Lys Gly Trp Pro Ile Pro Phe Ala
 115 120 125

Lys Glu Lys Tyr Met Pro Ser Val Ser Thr Ser Val Gly Met Leu Glu
 130 135 140

Gly Ile Asp Pro Gly Leu Val Met Arg Asp Met Tyr Thr Glu Ser Thr
 145 150 155 160

His Val Phe Gly Thr Ala Glu Asp Phe Val Glu Ala Gly Gln Gln Trp
 165 170 175

Cys Glu Asp Tyr Phe
 180

<210> 1797

<211> 1404

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1381)

<223> RXA00530

<400> 1797

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ggggtagat ttcagctgaa gcaactgggg agttggcgct atg agc atc gga ttc 115
 Met Ser Ile Gly Phe
 1 5

gac cgc gac ctt tat att aag atg cag tcg cag cac atc aat gag cgc 163
 Asp Arg Asp Leu Tyr Ile Lys Met Gln Ser Gln His Ile Asn Glu Arg
 10 15 20

cgc gag cag atc ggc ggc aag ctg tat ctg gaa atg ggc ggc aag ctt 211
 Arg Glu Gln Ile Gly Gly Lys Leu Tyr Leu Glu Met Gly Gly Lys Leu
 25 30 35

ttc gac gac atg cac gct tcc cgt gtg ctg cca ggt ttc acg cct gac 259
 Phe Asp Asp Met His Ala Ser Arg Val Leu Pro Gly Phe Thr Pro Asp
 40 45 50

aac aag atc gct atg ctc act gag ctt aaa gat gag ctg gaa atc ctc 307
 Asn Lys Ile Ala Met Leu Thr Glu Leu Lys Asp Glu Leu Glu Ile Leu
 55 60 65

gtc gca atc aat gcg aag gat ctg gag cgc aag aaa acc cgc gcc gac 355
 Val Ala Ile Asn Ala Lys Asp Leu Glu Arg Lys Lys Thr Arg Ala Asp
 70 75 80 85

ctc gac att tct tat gag gaa gat gtt tta cgc ctc att gat gtg ttc 403
 Leu Asp Ile Ser Tyr Glu Glu Asp Val Leu Arg Leu Ile Asp Val Phe
 90 95 100

cgt gag ctg ggc ttt ttg gcg gag cat gtg gtg ctc aca cag ttg gag 451
 Arg Glu Leu Gly Phe Leu Ala Glu His Val Val Leu Thr Gln Leu Glu
 105 110 115

gat gac aac tat cag gca ctc gcg ttc aag cag cgc cta gag cgc ctt 499
 Asp Asp Asn Tyr Gln Ala Leu Ala Phe Lys Gln Arg Leu Glu Arg Leu
 120 125 130

ggc ctg aag gtt gct gtt cac cgc gtg att cca ggt tac cca act gat 547
 Gly Leu Lys Val Ala Val His Arg Val Ile Pro Gly Tyr Pro Thr Asp
 135 140 145

gct cgc cgc att gtt agc gag gaa ggt ttc ggc atc aac gag tat gtg 595
 Ala Arg Arg Ile Val Ser Glu Glu Gly Phe Gly Ile Asn Glu Tyr Val
 150 155 160 165

gaa acc acc cgc aat ttg gtt gtt gtg acc gca ccg ggc cca ggt tct 643
 Glu Thr Thr Arg Asn Leu Val Val Val Thr Ala Pro Gly Pro Gly Ser
 170 175 180

gga aag ctc gct acc tgc ttg agc cag att tat ggc gat cac cag cgc 691
 Gly Lys Leu Ala Thr Cys Leu Ser Gln Ile Tyr Gly Asp His Gln Arg
 185 190 195

gga atc aag tcc ggc tac gca aag ttt gaa act ttc ccc att tgg aac 739
 Gly Ile Lys Ser Gly Tyr Ala Lys Phe Glu Thr Phe Pro Ile Trp Asn
 200 205 210

ctg cct ctt gag cac cca gtt aac ttg gct tat gag gct gcc acg gca 787
 Leu Pro Leu Glu His Pro Val Asn Leu Ala Tyr Glu Ala Ala Thr Ala
 215 220 225

gat ctc gat gac atc aac atc atc gat cct ttc cac ctc gcc gcc tat 835
 Asp Leu Asp Asp Ile Asn Ile Ile Asp Phe His Leu Ala Ala Tyr
 230 235 240 245

gac acc aaa gcc acc agc tac aac cgc gac gtg gaa gtc ttc ccg ctg 883
 Asp Thr Lys Ala Thr Ser Tyr Asn Arg Asp Val Glu Val Phe Pro Leu
 250 255 260

ctg aaa acc atg ctg gaa atg ctg tgc ggc tca tgc ccg tac aaa tcc 931
 Leu Lys Thr Met Leu Glu Met Leu Ser Gly Ser Ser Pro Tyr Lys Ser
 265 270 275

 ccc acc gac atg ggt gtc aac atg gtc gga agc gca att atc gac gac 979
 Pro Thr Asp Met Gly Val Asn Met Val Gly Ser Ala Ile Asp Asp
 280 285 290

 gcc gcg tgc cag gaa gcc gcc cgc caa gaa att gtt cgg cgt tac ttc 1027
 Ala Ala Cys Gln Glu Ala Ala Arg Gln Glu Ile Val Arg Arg Tyr Phe
 295 300 305

 aag gcg ctt gtc gac gag cgt cgc gag gag cag gac gat acc att tca 1075
 Lys Ala Leu Val Asp Glu Arg Arg Glu Glu Gln Asp Asp Thr Ile Ser
 310 315 320 325

 gcg cgc atc gcc att gtc atg agc aag gcc ggt tgc acc gtt gaa gac 1123
 Ala Arg Ile Ala Ile Val Met Ser Lys Ala Gly Cys Thr Val Glu Asp
 330 335 340

 cgc cgc gtg gtt gcc cga gca ctt gat gtt gaa gaa tcc acc ggc gcg 1171
 Arg Arg Val Val Ala Arg Ala Leu Asp Val Glu Glu Ser Thr Gly Ala
 345 350 355

 ccg ggt tgt gcc att gaa ctt aac gat ggt cga ctc gtc acc ggc aag 1219
 Pro Gly Cys Ala Ile Glu Leu Asn Asp Gly Arg Leu Val Thr Gly Lys
 360 365 370

 act tca gaa ctt ctc gga tgc tcc gca gcg atg gtg ctt aat gca ctg 1267
 Thr Ser Glu Leu Leu Gly Cys Ser Ala Ala Met Val Leu Asn Ala Leu
 375 380 385

 aag gaa ctc gct gcc att gat cgc agc gtg gat ctc ctc tcc cct gaa 1315
 Lys Glu Leu Ala Gly Ile Asp Arg Ser Val Asp Leu Leu Ser Pro Glu
 390 395 400 405

 tcc atc gag cca atc caa tgc ctg aag acc cag cac ctg gga tcc cgc 1363
 Ser Ile Glu Pro Ile Gln Ser Leu Lys Thr Gln His Leu Gly Ser Arg
 410 415 420

 aac ccc tgc cct gca cac tgaatgaagt cttattgctt tgt 1404
 Asn Pro Ser Pro Ala His
 425

<210> 1798

<211> 427

<212> PRT

<213> Corynebacterium glutamicum

<400> 1798

Met Ser Ile Gly Phe Asp Arg Asp Leu Tyr Ile Lys Met Gln Ser Gln
 1 5 10 15

His Ile Asn Glu Arg Arg Glu Gln Ile Gly Gly Lys Leu Tyr Leu Glu
 20 25 30

Met Gly Gly Lys Leu Phe Asp Asp Met His Ala Ser Arg Val Leu Pro
 35 40 45

Gly Phe Thr Pro Asp Asn Lys Ile Ala Met Leu Thr Glu Leu Lys Asp

50	55	60
Glu Leu Glu Ile Leu Val 65	Ala Ile Asn Ala Lys Asp 70	Leu Glu Arg Lys 80
Lys Thr Arg Ala Asp Leu Asp Ile Ser Tyr Glu Glu Asp Val Leu Arg 85	90	95
Leu Ile Asp Val Phe Arg Glu Leu Gly Phe Leu Ala Glu His Val Val 100	105	110
Leu Thr Gln Leu Glu Asp Asp Asn Tyr Gln Ala Leu Ala Phe Lys Gln 115	120	125
Arg Leu Glu Arg Leu Gly Leu Lys Val Ala Val His Arg Val Ile Pro 130	135	140
Gly Tyr Pro Thr Asp Ala Arg Arg Ile Val Ser Glu Glu Gly Phe Gly 145	150	155
Ile Asn Glu Tyr Val Glu Thr Thr Arg Asn Leu Val Val Val Thr Ala 165	170	175
Pro Gly Pro Gly Ser Gly Lys Leu Ala Thr Cys Leu Ser Gln Ile Tyr 180	185	190
Gly Asp His Gln Arg Gly Ile Lys Ser Gly Tyr Ala Lys Phe Glu Thr 195	200	205
Phe Pro Ile Trp Asn Leu Pro Leu Glu His Pro Val Asn Leu Ala Tyr 210	215	220
Glu Ala Ala Thr Ala Asp Leu Asp Asp Ile Asn Ile Ile Asp Pro Phe 225	230	235
His Leu Ala Ala Tyr Asp Thr Lys Ala Thr Ser Tyr Asn Arg Asp Val 245	250	255
Glu Val Phe Pro Leu Leu Lys Thr Met Leu Glu Met Leu Ser Gly Ser 260	265	270
Ser Pro Tyr Lys Ser Pro Thr Asp Met Gly Val Asn Met Val Gly Ser 275	280	285
Ala Ile Ile Asp Asp Ala Ala Cys Gln Glu Ala Ala Arg Gln Glu Ile 290	295	300
Val Arg Arg Tyr Phe Lys Ala Leu Val Asp Glu Arg Arg Glu Glu Gln 305	310	315
Asp Asp Thr Ile Ser Ala Arg Ile Ala Ile Val Met Ser Lys Ala Gly 325	330	335
Cys Thr Val Glu Asp Arg Arg Val Val Ala Arg Ala Leu Asp Val Glu 340	345	350
Glu Ser Thr Gly Ala Pro Gly Cys Ala Ile Glu Leu Asn Asp Gly Arg 355	360	365
Leu Val Thr Gly Lys Thr Ser Glu Leu Leu Gly Cys Ser Ala Ala Met 370	375	380

Val Leu Asn Ala Leu Lys Glu Leu Ala Gly Ile Asp Arg Ser Val Asp
385 390 395 400

Leu Leu Ser Pro Glu Ser Ile Glu Pro Ile Gln Ser Leu Lys Thr Gln
405 410 415

His Leu Gly Ser Arg Asn Pro Ser Pro Ala His
420 425

<210> 1799

<211> 840

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(817)

<223> RXA00535

<400> 1799

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cctaaggagc tcacctttac tcaatgctct gatgacaccg atg tgg tgg gca ggc 115
Met Trp Trp Ala Gly
1 5

atg agt acc gcg atg ctg gca tat ttc tta caa aca gta gca ctt ggt 163
Met Ser Thr Ala Met Leu Ala Tyr Phe Leu Gln Thr Val Ala Leu Gly
10 15 20

ttc ggc acc ctc ttg gta gtg caa cca gtg ctt gtc ctg tgg ctg atg 211
Phe Gly Thr Leu Leu Val Val Gln Pro Val Leu Val Leu Ser Leu Met
25 30 35

ttc acg ctg ccg ctc tca gca cga ttc aat ggc tac cga cta cgc cga 259
Phe Thr Leu Pro Leu Ser Ala Arg Phe Asn Gly Tyr Arg Leu Arg Arg
40 45 50

act gaa atc ttc tgg gct acc ctc ctc acc gta gcc gtg ggc atc atg 307
Thr Glu Ile Phe Trp Ala Thr Leu Leu Thr Val Ala Val Gly Ile Met
55 60 65

atc gtt ttg gga cgc ccc ctt ccc gga aac ccc cac ccc cca ctc gat 355
Ile Val Leu Gly Arg Pro Leu Pro Gly Asn Pro His Pro Pro Leu Asp
70 75 80 85

cga tgg att cca gta ctt tta gtc ggc gtt gca gta atg ggt gga atg 403
Arg Trp Ile Pro Val Leu Leu Val Gly Val Ala Val Met Gly Gly Met
90 95 100

tgg ctg ctt gcg gaa tac gta tta aag aag gac aaa gcc ctc atc ctt 451
Trp Leu Leu Ala Glu Tyr Val Leu Lys Lys Asp Lys Ala Leu Ile Leu
105 110 115

ggc ctt gtg acg ggt gca ttg ttt ggc tac gta gca gtg atg tcc aaa 499
Gly Leu Val Thr Gly Ala Leu Phe Gly Tyr Val Ala Val Met Ser Lys
120 125 130

gcc gcg gtg gat ctt ttt gtc cat caa gcc ata acg gga ctc atc ttg 547

Ala Ala Val Asp Leu Phe Val His Gln Gly Ile Thr Gly Leu Ile Leu
135 140 145

aac tgg gaa ggc tac ggc cta atc ctc acc gca tta ctt gga aca atc 595
Asn Trp Glu Gly Tyr Gly Leu Ile Leu Thr Ala Leu Leu Gly Thr Ile
150 155 160 165

gtg cag cag tat tcc ttt aac gct ggc gaa cta caa aaa tcg cta ccc 643
Val Gln Gln Tyr Ser Phe Asn Ala Gly Glu Leu Gln Lys Ser Leu Pro
170 175 180

gcc atg acc att gcc gaa cca att gtt gcc ttc agt ttg ggc tac ttg 691
Ala Met Thr Ile Ala Glu Pro Ile Val Ala Phe Ser Leu Gly Tyr Leu
185 190 195

gtt ctg ggc gaa aaa ttc caa gtc gtg gac tgg gaa tgg atc gcc atg 739
Val Leu Gly Glu Lys Phe Gln Val Val Asp Trp Glu Trp Ile Ala Met
200 205 210

ggc atc gca cta ctg gtg atg att gtt tcc acc att gca ctg tct cgt 787
Gly Ile Ala Leu Leu Val Met Ile Val Ser Thr Ile Ala Leu Ser Arg
215 220 225

aca agc aca atg ccg gcc gga tcg aaa agg taaaactcca aagttccccc 837
Thr Ser Thr Met Pro Ala Gly Ser Lys Arg
230 235

cga 840

<210> 1800
<211> 239
<212> PRT
<213> Corynebacterium glutamicum

<400> 1800
Met Trp Trp Ala Gly Met Ser Thr Ala Met Leu Ala Tyr Phe Leu Gln
1 5 10 15

Thr Val Ala Leu Gly Phe Gly Thr Leu Leu Val Val Gln Pro Val Leu
20 25 30

Val Leu Ser Leu Met Phe Thr Leu Pro Leu Ser Ala Arg Phe Asn Gly
35 40 45

Tyr Arg Leu Arg Arg Thr Glu Ile Phe Trp Ala Thr Leu Leu Thr Val
50 55 60

Ala Val Gly Ile Met Ile Val Leu Gly Arg Pro Leu Pro Gly Asn Pro
65 70 75 80

His Pro Pro Leu Asp Arg Trp Ile Pro Val Leu Leu Val Gly Val Ala
85 90 95

Val Met Gly Gly Met Trp Leu Leu Ala Glu Tyr Val Leu Lys Lys Asp
100 105 110

Lys Ala Leu Ile Leu Gly Leu Val Thr Gly Ala Leu Phe Gly Tyr Val
115 120 125

Ala Val Met Ser Lys Ala Ala Val Asp Leu Phe Val His Gln Gly Ile

130	135	140
Thr Gly Leu Ile Leu Asn Trp Glu Gly Tyr Gly Leu Ile Leu Thr Ala		
145	150	155
Leu Leu Gly Thr Ile Val Gln Gln Tyr Ser Phe Asn Ala Gly Glu Leu		
	165	170
Gln Lys Ser Leu Pro Ala Met Thr Ile Ala Glu Pro Ile Val Ala Phe		
	180	185
Ser Leu Gly Tyr Leu Val Leu Gly Glu Lys Phe Gln Val Val Asp Trp		
	195	200
Glu Trp Ile Ala Met Gly Ile Ala Leu Leu Val Met Ile Val Ser Thr		
	210	215
Ile Ala Leu Ser Arg Thr Ser Thr Met Pro Ala Gly Ser Lys Arg		
225	230	235

<210> 1801
 <211> 366
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(343)
 <223> RXA00540

<400> 1801
 tctccctatc taagggtcgg ctagggttga ccagtggtcaa cagttacact tgtgctcgta 60
 aaacattgtc ctccccattt ctgagtaag ggaaaataacc gtg gcc cgt gta gtt 115
 Val Ala Arg Val Val
 1 5
 gtc aat gtc atg cct aag gct gag att ctg gat ccc cag ggg cag gcg 163
 Val Asn Val Met Pro Lys Ala Glu Ile Leu Asp Pro Gln Gly Gln Ala
 10 15 20
 gta cac cgc gcc ctc gga cgt atc gga gtt tct gcc gtt tcc gat gtc 211
 Val His Arg Ala Leu Gly Arg Ile Gly Val Ser Gly Val Ser Asp Val
 25 30 35
 cgt cag gga aag cgc ttc gag ctt gag gta gat gat tcc gtc acc gaa 259
 Arg Gln Gly Lys Arg Phe Glu Leu Glu Val Asp Asp Ser Val Thr Glu
 40 45 50
 gct gac cta aag aaa att gct gaa acc ctc ctc gca aac acc gtc atc 307
 Ala Asp Leu Lys Lys Ile Ala Glu Thr Leu Leu Ala Asn Thr Val Ile
 55 60 65
 gaa gac ttc gat gtg gtg gga gtt gag gtc gcg aag tgagcgccaa 353
 Glu Asp Phe Asp Val Val Gly Val Glu Val Ala Lys
 70 75 80
 aatcggtgctc att 366

<210> 1802

<211> 81

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1802

Val Ala Arg Val Val Val Asn Val Met Pro Lys Ala Glu Ile Leu Asp
 1 5 10 15

Pro Gln Gly Gln Ala Val His Arg Ala Leu Gly Arg Ile Gly Val Ser
 20 25 30

Gly Val Ser Asp Val Arg Gln Gly Lys Arg Phe Glu Leu Glu Val Asp
 35 40 45

Asp Ser Val Thr Glu Ala Asp Leu Lys Lys Ile Ala Glu Thr Leu Leu
 50 55 60

Ala Asn Thr Val Ile Glu Asp Phe Asp Val Val Gly Val Glu Val Ala
 65 70 75 80

Lys

<210> 1803

<211> 519

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(496)

<223> RXA00549

<400> 1803

attcggttgc agcaggatct ggaaaatggt tcacaggata ctgctggacat ggcgcgatct 60

ttgggtatcg cgaagtcctt gccaaactatc cctgagacac ttg act gaa aac gga 115
 Leu Thr Glu Asn Gly
 1 5

gag acc cct tat gag ggc atc atc ttg ggt cag tat gag tcc cgc cca 163
 Glu Thr Pro Tyr Glu Gly Ile Ile Leu Gly Gln Tyr Glu Ser Arg Pro
 10 15 20

ctt gat atg gct tct gcg atg gca act atc gct aat gaa ggt gtc tgg 211
 Leu Asp Met Ala Ser Ala Met Ala Thr Ile Ala Asn Glu Gly Val Trp
 25 30 35

cac cgc ccg cac ttc gtg tcc aag gtg gag act gtc agc ggt gag gtt 259
 His Arg Pro His Phe Val Ser Lys Val Glu Thr Val Ser Gly Glu Val
 40 45 50

ctc tac gag ttc gag gat ggc gac ggc gag cgt cgt gtt tct gaa aag 307
 Leu Tyr Glu Phe Glu Asp Gly Asp Gly Glu Arg Arg Val Ser Glu Lys
 55 60 65

gtt gca ctg aat ctg ctc aag gcc atg ggg cca atc gct gca tac tcc 355
 Val Ala Leu Asn Leu Leu Lys Ala Met Gly Pro Ile Ala Ala Tyr Ser
 70 75 80 85

```

aac gga aac gct ctg gct gat ggc cag gtt tct gca tcc aag act ggt 403
Asn Gly Asn Ala Leu Ala Asp Gly Gln Val Ser Ala Ser Lys Thr Gly
          90                      95                      100

```

```

acc act cag ctt ggt gat acc ggt gca aac aag gat gcg tgg atg ttg 451
Thr Thr Gln Leu Gly Asp Thr Gly Ala Asn Lys Asp Ala Trp Met Leu
          105                      110                      115

```

```

ggt gcg gca cct cag cta gct act gcg gtg tgg gtc gga act gct 496
Gly Ala Ala Pro Gln Leu Ala Thr Ala Val Trp Val Gly Thr Ala
          120                      125                      130

```

```

tgataacact gcattgtata aca 519

```

<210> 1804

<211> 132

<212> PRT

<213> Corynebacterium glutamicum

<400> 1804

```

Leu Thr Glu Asn Gly Glu Thr Pro Tyr Glu Gly Ile Ile Leu Gly Gln
 1                      5                      10                      15

```

```

Tyr Glu Ser Arg Pro Leu Asp Met Ala Ser Ala Met Ala Thr Ile Ala
          20                      25                      30

```

```

Asn Glu Gly Val Trp His Arg Pro His Phe Val Ser Lys Val Glu Thr
          35                      40                      45

```

```

Val Ser Gly Glu Val Leu Tyr Glu Phe Glu Asp Gly Asp Gly Glu Arg
          50                      55                      60

```

```

Arg Val Ser Glu Lys Val Ala Leu Asn Leu Leu Lys Ala Met Gly Pro
          65                      70                      75                      80

```

```

Ile Ala Ala Tyr Ser Asn Gly Asn Ala Leu Ala Asp Gly Gln Val Ser
          85                      90                      95

```

```

Ala Ser Lys Thr Gly Thr Thr Gln Leu Gly Asp Thr Gly Ala Asn Lys
          100                      105                      110

```

```

Asp Ala Trp Met Leu Gly Ala Ala Pro Gln Leu Ala Thr Ala Val Trp
          115                      120                      125

```

```

Val Gly Thr Ala
          130

```

<210> 1805

<211> 444

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(421)

<223> RXA00550

<400> 1805

aaggatgcgt ggaatgttggg tgcggcacct cagctagcta ctgcggtgtg ggtcggaaact 60
gcttgataac actgcattgt ataacacctg ggttggcagt atg tat ggt tct aac 115
Met Tyr Gly Ser Asn
1 5
tcc cct gcc acg atc tgg aag cag acc atg gat aac gcc ctc gag aac 163
Ser Pro Ala Thr Ile Trp Lys Gln Thr Met Asp Asn Ala Leu Glu Asn
10 15 20
tcc cct ctc gaa act tgg gat atc gct cca gca ttg ggg tac ggt aac 211
Ser Pro Leu Glu Thr Trp Asp Ile Ala Pro Ala Leu Gly Tyr Gly Asn
25 30 35
cca cca gtt ccg gaa tat gtg tgg act cca agt cca aac atc gcg act 259
Pro Pro Val Pro Glu Tyr Val Trp Thr Pro Ser Pro Asn Ile Ala Thr
40 45 50
aat gat cca gaa gga gca acc gag gaa gct cca gtg gag gat cca aat 307
Asn Asp Pro Glu Gly Ala Thr Glu Glu Ala Pro Val Glu Asp Pro Asn
55 60 65
gca gta atc gat acc cct gct gta gat ccc act gca cct gca gag gag 355
Ala Val Ile Asp Thr Pro Ala Val Asp Pro Thr Ala Pro Ala Glu Glu
70 75 80 85
acc ggt aac ggt cag gta gaa atc ctg ccg ggg ctg act atc ccg gga 403
Thr Gly Asn Gly Gln Val Glu Ile Leu Pro Gly Leu Thr Ile Pro Gly
90 95 100
gat ctc tta ggg atc ggc taaaatccgg tcgtagccta aac 444
Asp Leu Leu Gly Ile Gly
105
<210> 1806
<211> 107
<212> PRT
<213> *Corynebacterium glutamicum*
<400> 1806
Met Tyr Gly Ser Asn Ser Pro Ala Thr Ile Trp Lys Gln Thr Met Asp
1 5 10 15
Asn Ala Leu Glu Asn Ser Pro Leu Glu Thr Trp Asp Ile Ala Pro Ala
20 25 30
Leu Gly Tyr Gly Asn Pro Pro Val Pro Glu Tyr Val Trp Thr Pro Ser
35 40 45
Pro Asn Ile Ala Thr Asn Asp Pro Glu Gly Ala Thr Glu Glu Ala Pro
50 55 60
Val Glu Asp Pro Asn Ala Val Ile Asp Thr Pro Ala Val Asp Pro Thr
65 70 75 80
Ala Pro Ala Glu Glu Thr Gly Asn Gly Gln Val Glu Ile Leu Pro Gly
85 90 95
Leu Thr Ile Pro Gly Asp Leu Leu Gly Ile Gly
100 105

<210> 1807

<211> 444

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(421)

<223> RXA00553

<400> 1807

gtcattgcaa gcggaacgc tgtgcagcaa ttgctgcgga ttctgctgag caaggaattg 60

atcgcctcgt	tactttcttaa	aaagggtatg	gtggctgggt	atg	agc	atc	ggt	aag	115
				Met	Ser	Ile	Val	Lys	
				1				5	

atc	aac	gca	att	tcc	gta	ccc	gaa	ggc	gct	ggt	gaa	gag	ctt	gag	aag	163
Ile	Asn	Ala	Ile	Ser	Val	Pro	Glu	Gly	Ala	Gly	Glu	Glu	Leu	Glu	Lys	
				10				15					20			

cg	ttc	gca	gcc	cg	caa	aat	gcc	gtg	gat	tcc	gct	ccg	gga	ttt	gag	211
Arg	Phe	Ala	Ala	Arg	Gln	Asn	Ala	Val	Asp	Ser	Ala	Pro	Gly	Phe	Glu	
			25				30						35			

ggc	ttt	caa	ctg	tta	cg	cct	gtt	tcc	ggt	gaa	gac	cg	tac	ttt	gta	259
Gly	Phe	Gln	Leu	Leu	Arg	Pro	Val	Ser	Gly	Glu	Asp	Arg	Tyr	Phe	Val	
		40				45					50					

gtc	acc	cag	tg	gct	gat	gaa	gac	agc	tat	aac	gc	tg	cg	gat	gcc	307
Val	Thr	Gln	Trp	Ala	Asp	Glu	Asp	Ser	Tyr	Asn	Ala	Trp	Arg	Asp	Ala	
		55			60				65							

gaa	aag	gcc	aag	ggc	ggt	cat	ggc	cag	gga	gcc	cac	ggc	tca	gat	aag	355
Glu	Lys	Ala	Lys	Gly	Gly	His	Gly	Gln	Gly	Ala	His	Gly	Ser	Asp	Lys	
	70				75				80					85		

aag	cct	gtc	gct	tcc	ggc	gct	tcc	ctg	ctg	gag	ttc	gaa	gta	gtc	cta	403
Lys	Pro	Val	Ala	Ser	Gly	Ala	Ser	Leu	Leu	Glu	Phe	Glu	Val	Val	Leu	
			90					95					100			

gga	tct	acc	ggc	gct	aag	tagggaaaga	gaaaagtcgg	aac								444
Gly	Ser	Thr	Gly	Ala	Lys											
			105													

<210> 1808

<211> 107

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1808

Met	Ser	Ile	Val	Lys	Ile	Asn	Ala	Ile	Ser	Val	Pro	Glu	Gly	Ala	Gly
1				5					10					15	

Glu	Glu	Leu	Glu	Lys	Arg	Phe	Ala	Ala	Arg	Gln	Asn	Ala	Val	Asp	Ser
		20					25					30			

Ala	Pro	Gly	Phe	Glu	Gly	Phe	Gln	Leu	Leu	Arg	Pro	Val	Ser	Gly	Glu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35	40	45
Asp Arg Tyr Phe Val Val Thr Gln Trp Ala Asp Glu Asp Ser Tyr Asn		
50	55	60
Ala Trp Arg Asp Ala Glu Lys Ala Lys Gly Gly His Gly Gln Gly Ala		
65	70	75
His Gly Ser Asp Lys Lys Pro Val Ala Ser Gly Ala Ser Leu Leu Glu		
85	90	95
Phe Glu Val Val Leu Gly Ser Thr Gly Ala Lys		
100	105	

<210> 1809

<211> 594

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(571)

<223> RXA00554

<400> 1809

atccgaaact ctccgtgtacc gaccatcatt tatcccggtc tttaggctct ccaacagcag 60

aggactagac ttaagtatgac ctgcaaaagga ggacaacttc atg aac acc caa cca 115

Met Asn Thr Gln Pro

1

5

gag cat cca gaa aat gat cta gtc gac gaa gcc gat ttt tct aac cgg 163

Glu His Pro Glu Asn Asp Leu Val Asp Glu Ala Asp Phe Ser Asn Arg

10

15

20

ccc agg atc tac tgc gac gat cct gat tcc ttg gct gat gcg cca gac 211

Pro Arg Ile Tyr Ser Asp Asp Pro Asp Ser Leu Ala Asp Ala Pro Asp

25

30

35

cca gcg ctg gag cat gag aag aac aag aaa tct tca cgc caa gca ctc 259

Pro Ala Leu Glu His Glu Lys Asn Lys Lys Ser Ser Arg Gln Ala Leu

40

45

50

att tat ctg ttg cag gtt cca cta gtt aca ttc gtt tct gca tac gta 307

Ile Tyr Leu Leu Gln Val Pro Leu Val Thr Phe Val Ser Ala Tyr Val

55

60

65

ttg gcc tgg gtg tca cga ctc cag ggc ggt ccc atc tgt gac gcc ggt 355

Leu Ala Trp Val Ser Arg Leu Gln Gly Gly Pro Ile Cys Asp Ala Gly

70

75

80

85

gag gct gtg tgg att tgt tcc cgt gct gca gaa ctg tgg tgg cca att 403

Glu Ala Val Trp Ile Cys Ser Arg Ala Ala Glu Leu Trp Trp Pro Ile

90

95

100

acc act agc gtc atc gca ttt ggt ggc atg ctt gga tct gca tgg atc 451

Thr Thr Ser Val Ile Ala Phe Gly Gly Met Leu Gly Ser Ala Trp Ile

105

110

115

ctc tat gac aaa tac cga aat tac cta cgc tgg cgt cct tgg atg ggc 499

```

Leu Tyr Asp Lys Tyr Arg Asn Tyr Leu Arg Trp Arg Pro Trp Met Gly
    120                      125                      130

gtg ttg tgg att ttg att cca ttc agc atg ctg tgg gga acc tcg gtg   547
Val Leu Trp Ile Leu Ile Pro Phe Ser Met Leu Trp Gly Thr Ser Val
    135                      140                      145

ctc acc ttg tcc atc ttg ggg cac taaaaacttc acataaatga caa       594
Leu Thr Leu Ser Ile Leu Gly His
    150                      155

```

<210> 1810

<211> 157

<212> PRT

<213> Corynebacterium glutamicum

<400> 1810

```

Met Asn Thr Gln Pro Glu His Pro Glu Asn Asp Leu Val Asp Glu Ala
    1                      5                      10                      15

Asp Phe Ser Asn Arg Pro Arg Ile Tyr Ser Asp Asp Pro Asp Ser Leu
    20                      25                      30

Ala Asp Ala Pro Asp Pro Ala Leu Glu His Glu Lys Asn Lys Lys Ser
    35                      40                      45

Ser Arg Gln Ala Leu Ile Tyr Leu Leu Gln Val Pro Leu Val Thr Phe
    50                      55                      60

Val Ser Ala Tyr Val Leu Ala Trp Val Ser Arg Leu Gln Gly Gly Pro
    65                      70                      75                      80

Ile Cys Asp Ala Gly Glu Ala Val Trp Ile Cys Ser Arg Ala Ala Gly
    85                      90                      95

Leu Trp Trp Pro Ile Thr Thr Ser Val Ile Ala Phe Gly Gly Met Leu
    100                     105                     110

Gly Ser Ala Trp Ile Leu Tyr Asp Lys Tyr Arg Asn Tyr Leu Arg Trp
    115                     120                     125

Arg Pro Trp Met Gly Val Leu Trp Ile Leu Ile Pro Phe Ser Met Leu
    130                     135                     140

Trp Gly Thr Ser Val Leu Thr Leu Ser Ile Leu Gly His
    145                     150                     155

```

<210> 1811

<211> 2762

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(2739)

<223> RXA00563

<400> 1811

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ttc tac aag gat ctc tac gca cgt tcc gca cgc ggc acg gca gca ctg   48

```

Phe	Tyr	Lys	Asp	Leu	Tyr	Ala	Arg	Ser	Ala	Arg	Gly	Thr	Ala	Ala	Leu		
1				5					10					15			
tgg	atc	gtg	gcg	gct	aac	ttg	agc	tcc	tac	tca	gac	atc	gac	gcc	atc	96	
Trp	Ile	Val	Ala	Ala	Asn	Leu	Ser	Ser	Tyr	Ser	Asp	Ile	Asp	Ala	Ile		
			20				25					30					
atc	aac	tggt	gtc	gga	tcc	gag	cag	acc	acc	acc	gtc	aac	ggc	gca	tcc	144	
Ile	Asn	Trp	Val	Gly	Ser	Glu	Gln	Thr	Thr	Thr	Val	Asn	Gly	Ala	Ser		
		35				40					45						
aag	ctg	gtc	aag	cca	gct	ttg	gtc	cct	acc	ttg	ctg	ttc	cca	ttc	gcg	192	
Lys	Leu	Val	Lys	Pro	Ala	Leu	Val	Pro	Thr	Leu	Leu	Phe	Pro	Phe	Ala		
	50				55					60							
gca	cct	cg	gtg	tcc	gga	tcc	atg	gca	gat	gca	ggc	cca	cag	gca	gaa	240	
Ala	Pro	Arg	Val	Ser	Gly	Ser	Met	Ala	Asp	Ala	Gly	Pro	Gln	Ala	Glu		
	65				70					75				80			
tcc	cag	atg	cga	ctt	ctg	ctc	tgg	tct	gtt	gag	cg	ctc	atc	gca	ggt	288	
Ser	Gln	Met	Arg	Leu	Leu	Leu	Trp	Ser	Val	Glu	Arg	Leu	Ile	Ala	Gly		
				85				90					95				
ctt	gcg	cca	ttg	ggc	tcc	tcc	atc	aac	gtg	ggg	cac	cg	ctg	cac	gtg	336	
Leu	Ala	Pro	Leu	Gly	Ser	Ser	Ile	Asn	Val	Gly	His	Arg	Leu	His	Val		
		100					105					110					
gtc	atc	cca	ggg	tca	cca	aac	cg	gga	cg	ttc	ggg	ggc	gat	ggg	gca	384	
Val	Ile	Pro	Gly	Ser	Pro	Asn	Arg	Gly	Arg	Phe	Gly	Gly	Asp	Gly	Ala		
		115				120					125						
tac	ggg	gaa	tcc	aag	gca	gct	ctc	gac	gcc	gtg	gtt	acc	cg	tg	aac	432	
Tyr	Gly	Glu	Ser	Lys	Ala	Ala	Leu	Asp	Ala	Val	Val	Thr	Arg	Trp	Asn		
	130				135					140							
gca	gag	caa	gct	gca	tgg	gga	gca	cac	acc	tcc	ctc	gtg	cac	gct	cac	480	
Ala	Glu	Gln	Ala	Ala	Trp	Gly	Ala	His	Thr	Ser	Leu	Val	His	Ala	His		
	145			150						155				160			
atc	ggg	tg	gtt	cg	ggc	acc	ggc	ctc	atg	ggc	ggc	aac	gat	cct	ttg	528	
Ile	Gly	Trp	Val	Arg	Gly	Thr	Gly	Leu	Met	Gly	Gly	Asn	Asp	Pro	Leu		
			165				170						175				
gtc	aag	gca	gct	gaa	gaa	gca	ggc	gtg	gaa	acc	tac	tcc	acc	caa	gaa	576	
Val	Lys	Ala	Ala	Glu	Glu	Ala	Gly	Val	Glu	Thr	Tyr	Ser	Thr	Gln	Glu		
		180					185					190					
att	gca	gag	aaa	ctg	ctg	tcc	cag	gca	act	tcc	act	gtt	cg	gag	cag	624	
Ile	Ala	Glu	Lys	Leu	Leu	Ser	Gln	Ala	Thr	Ser	Thr	Val	Arg	Glu	Gln		
		195				200						205					
gca	gca	tcc	gcg	cca	atc	acc	gtc	gac	ttc	act	ggc	gga	ctt	ggg	gaa	672	
Ala	Ala	Ser	Ala	Pro	Ile	Thr	Val	Asp	Phe	Thr	Gly	Gly	Leu	Gly	Glu		
		210			215					220							
tct	gat	ctg	aac	ctg	gcg	gaa	atg	gca	cg	gca	gaa	gca	gct	aag	gca	720	
Ser	Asp	Leu	Asn	Leu	Ala	Glu	Met	Ala	Arg	Ala	Glu	Ala	Ala	Lys	Ala		
	225			230						235			240				
gct	aac	gca	cca	gtg	gtt	gag	gct	cca	cg	aca	gtg	gca	gca	ctg	cca	768	
Ala	Asn	Ala	Pro	Val	Val	Glu	Ala	Pro	Arg	Thr	Val	Ala	Ala	Leu	Pro		

245										250										255										
act	cct	tac	cga	cca	gtg	gtt	caa	acc	acc	cct	gat	ttc	gca	ggc	caa	816														
Thr	Pro	Tyr	Arg	Pro	Val	Val	Gln	Thr	Thr	Pro	Asp	Phe	Ala	Gly	Gln															
260										265										270										
gtc	acc	caa	aac	ctt	gac	gag	atg	gtc	gtc	atc	gtt	ggc	gcc	ggc	gag	864														
Val	Thr	Gln	Asn	Leu	Asp	Glu	Met	Val	Val	Ile	Val	Gly	Ala	Gly	Glu															
275										280										285										
ctc	ggc	cca	ctg	ggc	tct	gca	cgt	acg	cgt	ttc	gac	gcc	gaa	ctc	aac	912														
Leu	Gly	Pro	Leu	Gly	Ser	Ala	Arg	Thr	Arg	Phe	Asp	Ala	Glu	Leu	Asn															
290										295										300										
ggt	tcc	ctc	tcc	gcc	gcg	ggc	gtc	atc	gaa	ctt	gca	tgg	acg	atg	gga	960														
Gly	Ser	Leu	Ser	Ala	Ala	Gly	Val	Ile	Glu	Leu	Ala	Trp	Thr	Met	Gly															
305										310										315										
ctt	atc	cac	tgg	gat	gaa	gat	cca	aag	cca	ggc	tgg	tac	gac	gac	tcc	1008														
Leu	Ile	His	Trp	Asp	Glu	Asp	Pro	Lys	Pro	Gly	Trp	Tyr	Asp	Asp	Ser															
325										330										335										
gac	gac	gca	gtg	gcc	gaa	gaa	gac	atc	ttc	gac	cgc	tac	cac	gac	gaa	1056														
Asp	Asp	Ala	Val	Ala	Glu	Glu	Asp	Ile	Phe	Asp	Arg	Tyr	His	Asp	Glu															
340										345										350										
gtc	atg	gca	cgc	gtt	ggc	gtc	cgc	aag	tac	aat	gac	atg	cct	gag	tac	1104														
Val	Met	Ala	Arg	Val	Gly	Val	Arg	Lys	Tyr	Asn	Asp	Met	Pro	Glu	Tyr															
355										360										365										
ggc	atg	atc	gac	aac	ttt	gca	cca	gag	ctg	acc	acc	gtc	tac	ctc	gac	1152														
Gly	Met	Ile	Asp	Asn	Phe	Ala	Pro	Glu	Leu	Thr	Thr	Val	Tyr	Leu	Asp															
370										375										380										
cag	gac	ctc	acc	ttc	aac	gtg	gga	tcc	cgc	gaa	gag	gca	ctg	acc	tac	1200														
Gln	Asp	Leu	Thr	Phe	Asn	Val	Gly	Ser	Arg	Glu	Glu	Ala	Leu	Thr	Tyr															
385										390										395										
gtc	gac	tcc	gag	cca	gaa	ctc	acc	ttt	gct	tct	ttc	gac	gaa	gca	gca	1248														
Val	Asp	Ser	Glu	Pro	Glu	Leu	Thr	Phe	Ala	Ser	Phe	Asp	Glu	Ala	Ala															
405										410										415										
ggg	gag	tgg	aag	gtc	act	cgc	aag	gca	ggc	tcc	gca	atc	cgc	gta	cct	1296														
Gly	Glu	Trp	Lys	Val	Thr	Arg	Lys	Ala	Gly	Ser	Ala	Ile	Arg	Val	Pro															
420										425										430										
cgc	cgc	atg	gcg	atg	acc	cgc	ttc	gtt	ggc	gga	cag	gtt	cct	aag	gac	1344														
Arg	Arg	Met	Ala	Met	Thr	Arg	Phe	Val	Gly	Gly	Gln	Val	Pro	Lys	Asp															
435										440										445										
ttc	gac	cca	gct	gtg	tgg	ggc	att	cca	gct	gac	atg	gtg	gac	aac	ctg	1392														
Phe	Asp	Pro	Ala	Val	Trp	Gly	Ile	Pro	Ala	Asp	Met	Val	Asp	Asn	Leu															
450										455										460										
gac	acc	gtc	gcg	ctg	tgg	aac	att	gtc	tgt	act	gtc	gac	gcc	ttc	ctg	1440														
Asp	Thr	Val	Ala	Leu	Trp	Asn	Ile	Val	Cys	Thr	Val	Asp	Ala	Phe	Leu															
465										470										475										
tcc	gct	gga	ttc	acc	cca	gca	gag	ctg	ctt	gct	tcc	gtt	cac	cca	gca	1488														
Ser	Ala	Gly	Phe	Thr	Pro	Ala	Glu	Leu	Leu	Ala	Ser	Val	His	Pro	Ala															
485										490										495										

cgc gtg tcc tct acc caa ggc acc ggc atg ggc ggc atg gaa tcc ctc Arg Val Ser Ser Thr Gln Gly Thr Gly Met Gly Gly Met Glu Ser Leu 500 505 510	1536
cgt ggc atc tac gtc gac cgc att ctg gca gag cca cgc gcc aac gac Arg Gly Ile Tyr Val Asp Arg Ile Leu Ala Glu Pro Arg Ala Asn Asp 515 520 525	1584
gtt ctg cag gaa gca ctg ccc aac gtt gtt gca gct cac gtc atg cag Val Leu Gln Glu Ala Leu Pro Asn Val Val Ala Ala His Val Met Gln 530 535 540	1632
tcc tac gtc ggt ggc tac gga cag atg atc cac cca gtc gca gct tgt Ser Tyr Val Gly Gly Tyr Gly Gln Met Ile His Pro Val Ala Ala Cys 545 550 555 560	1680
gca acc gca gct gtt tct gtg gaa gaa gca ctg gac aag atc cgc atc Ala Thr Ala Ala Val Ser Val Glu Glu Ala Leu Asp Lys Ile Arg Ile 565 570 575	1728
ggc aag tcc gac ttc gtt gtc gca ggt ggc ttc gat gcc ctg tcc gtt Gly Lys Ser Asp Phe Val Val Ala Gly Gly Phe Asp Ala Leu Ser Val 580 585 590	1776
gaa ggc atc acc ggc ttc ggc gac atg gca gca acc gcc gac tcc gca Glu Gly Ile Thr Gly Phe Gly Asp Met Ala Ala Thr Ala Asp Ser Ala 595 600 605	1824
gag atg gaa ggc aag gga att gag cac cgc ttc ttc tcc cgc gcc aac Glu Met Glu Gly Lys Gly Ile Glu His Arg Phe Phe Ser Arg Ala Asn 610 615 620	1872
gac cgg cgc cgc ggt gga ttc atc gaa tcc gaa ggt ggc gga acc gtc Asp Arg Arg Arg Gly Gly Phe Ile Glu Ser Glu Gly Gly Gly Thr Val 625 630 635 640	1920
ctt ctg gca cgc gga tca ctc gca gct gac ctg ggc ctt cca gta ctc Leu Leu Ala Arg Gly Ser Leu Ala Ala Asp Leu Gly Leu Pro Val Leu 645 650 655	1968
ggt gtc atc gga ttc gca gag tcc ttt gca gat ggt gcc cac acc tcc Gly Val Ile Gly Phe Ala Glu Ser Phe Ala Asp Gly Ala His Thr Ser 660 665 670	2016
atc cca gcc cca ggc ctc ggt gcc ctt ggt gct gct cgc gat ggt gtg Ile Pro Ala Pro Gly Leu Gly Ala Leu Gly Ala Ala Arg Asp Gly Val 675 680 685	2064
gaa tct cgc ctt gca gta gca ctg cgt tcc gtc ggt gtc tct gct gat Glu Ser Arg Leu Ala Val Ala Leu Arg Ser Val Gly Val Ser Ala Asp 690 695 700	2112
gag atc tcc att atc tcc aag cac gac acc tcc acc aac cgc aat gat Glu Ile Ser Ile Ile Ser Lys His Asp Thr Ser Thr Asn Ala Asn Asp 705 710 715 720	2160
cca aac gag tcc gac ctg cac gag cgc atc gca tcc gct atc ggt cgt Pro Asn Glu Ser Asp Leu His Glu Arg Ile Ala Ser Ala Ile Gly Arg 725 730 735	2208

gca gac ggc aac ccg atg tac gtg att tcc cag aag tca ctc acc gga 2256
 Ala Asp Gly Asn Pro Met Tyr Val Ile Ser Gln Lys Ser Leu Thr Gly
 740 745 750

cac gcc aag ggt ggt gca gca gca ttc cag atg atc ggt ctc acc cag 2304
 His Ala Lys Gly Gly Ala Ala Ala Phe Gln Met Ile Gly Leu Thr Gln
 755 760 765

gtc ctc cga tcc gga ctg gtg cca gcc aac cgc gca ctc gac tgc gtt 2352
 Val Leu Arg Ser Gly Leu Val Pro Ala Asn Arg Ala Leu Asp Cys Val
 770 775 780

gac cca gta ctg tcc aag cat tcc cac ctc gtc tgg ctg cgc aag cca 2400
 Asp Pro Val Leu Ser Lys His Ser His Leu Val Trp Leu Arg Lys Pro
 785 790 795 800

cta gac ctt cgt gcg aag gca cca aag gca ggt ctt gtt acc tcc ctt 2448
 Leu Asp Leu Arg Ala Lys Ala Pro Lys Ala Gly Leu Val Thr Ser Leu
 805 810 815

ggc ttc gga cac gtc tcc gct ctg gtt gcg att gtt cac cca gac gcc 2496
 Gly Phe Gly His Val Ser Ala Leu Val Ala Ile Val His Pro Asp Ala
 820 825 830

ttc tat gag gca gtt cgt gtg gca cgt ggt gct gag gca gct gac gta 2544
 Phe Tyr Glu Ala Val Arg Val Ala Arg Gly Ala Glu Ala Ala Asp Val
 835 840 845

tgg cgc gca tcc gcg atc gct cgc gaa gaa gca ggc ctt cgt acc atc 2592
 Trp Arg Ala Ser Ala Ile Ala Arg Glu Glu Ala Gly Leu Arg Thr Ile
 850 855 860

gtc gcc ggt atg cac ggt ggc gta ctg tac gaa cgc cca gtc gag cgc 2640
 Val Ala Gly Met His Gly Gly Val Leu Tyr Glu Arg Pro Val Glu Arg
 865 870 875 880

aac ctc ggt gtc cac gga gac gca gct aag gaa gtt gaa gct gca gtc 2688
 Asn Leu Gly Val His Gly Asp Ala Ala Lys Glu Val Glu Ala Ala Val
 885 890 895

ctc ctg gat tcc cgc gcc cgc cta gtt gac ggt gtc ctc cgc gcc gaa 2736
 Leu Leu Asp Ser Arg Ala Arg Leu Val Asp Gly Val Leu Arg Ala Glu
 900 905 910

ggc tagttggtta ttgcgttgag ccc 2762
 Gly

<210> 1812

<211> 913

<212> PRT

<213> Corynebacterium glutamicum

<400> 1812

Phe Tyr Lys Asp Leu Tyr Ala Arg Ser Ala Arg Gly Thr Ala Ala Leu
 1 5 10 15

Trp Ile Val Ala Ala Asn Leu Ser Ser Tyr Ser Asp Ile Asp Ala Ile
 20 25 30

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Ile Asn Trp Val Gly Ser Glu Gln Thr Thr Thr Val Asn Gly Ala Ser
   35                               40                               45

Lys Leu Val Lys Pro Ala Leu Val Pro Thr Leu Leu Phe Pro Phe Ala
   50                               55                               60

Ala Pro Arg Val Ser Gly Ser Met Ala Asp Ala Gly Pro Gln Ala Glu
   65                               70                               75                               80

Ser Gln Met Arg Leu Leu Leu Trp Ser Val Glu Arg Leu Ile Ala Gly
           85                               90                               95

Leu Ala Pro Leu Gly Ser Ser Ile Asn Val Gly His Arg Leu His Val
   100                               105                               110

Val Ile Pro Gly Ser Pro Asn Arg Gly Arg Phe Gly Gly Asp Gly Ala
   115                               120                               125

Tyr Gly Glu Ser Lys Ala Ala Leu Asp Ala Val Val Thr Arg Trp Asn
   130                               135                               140

Ala Glu Gln Ala Ala Trp Gly Ala His Thr Ser Leu Val His Ala His
   145                               150                               155                               160

Ile Gly Trp Val Arg Gly Thr Gly Leu Met Gly Gly Asn Asp Pro Leu
           165                               170                               175

Val Lys Ala Ala Glu Glu Ala Gly Val Glu Thr Tyr Ser Thr Gln Glu
           180                               185                               190

Ile Ala Glu Lys Leu Leu Ser Gln Ala Thr Ser Thr Val Arg Glu Gln
   195                               200                               205

Ala Ala Ser Ala Pro Ile Thr Val Asp Phe Thr Gly Gly Leu Gly Glu
   210                               215                               220

Ser Asp Leu Asn Leu Ala Glu Met Ala Arg Ala Glu Ala Ala Lys Ala
   225                               230                               235                               240

Ala Asn Ala Pro Val Val Glu Ala Pro Arg Thr Val Ala Ala Leu Pro
           245                               250                               255

Thr Pro Tyr Arg Pro Val Val Gln Thr Thr Pro Asp Phe Ala Gly Gln
   260                               265                               270

Val Thr Gln Asn Leu Asp Glu Met Val Val Ile Val Gly Ala Gly Glu
   275                               280                               285

Leu Gly Pro Leu Gly Ser Ala Arg Thr Arg Phe Asp Ala Glu Leu Asn
   290                               295                               300

Gly Ser Leu Ser Ala Ala Gly Val Ile Glu Leu Ala Trp Thr Met Gly
   305                               310                               315                               320

Leu Ile His Trp Asp Glu Asp Pro Lys Pro Gly Trp Tyr Asp Asp Ser
           325                               330                               335

Asp Asp Ala Val Ala Glu Glu Asp Ile Phe Asp Arg Tyr His Asp Glu
           340                               345                               350

Val Met Ala Arg Val Gly Val Arg Lys Tyr Asn Asp Met Pro Glu Tyr

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355										360										365										
Gly	Met	Ile	Asp	Asn	Phe	Ala	Pro	Glu	Leu	Thr	Thr	Val	Tyr	Leu	Asp															
370							375							380																
Gln	Asp	Leu	Thr	Phe	Asn	Val	Gly	Ser	Arg	Glu	Glu	Ala	Leu	Thr	Tyr															
385							390							395							400									
Val	Asp	Ser	Glu	Pro	Glu	Leu	Thr	Phe	Ala	Ser	Phe	Asp	Glu	Ala	Ala															
							405							410							415									
Gly	Glu	Trp	Lys	Val	Thr	Arg	Lys	Ala	Gly	Ser	Ala	Ile	Arg	Val	Pro															
							420							425							430									
Arg	Arg	Met	Ala	Met	Thr	Arg	Phe	Val	Gly	Gly	Gln	Val	Pro	Lys	Asp															
							435							440							445									
Phe	Asp	Pro	Ala	Val	Trp	Gly	Ile	Pro	Ala	Asp	Met	Val	Asp	Asn	Leu															
							450							455							460									
Asp	Thr	Val	Ala	Leu	Trp	Asn	Ile	Val	Cys	Thr	Val	Asp	Ala	Phe	Leu															
							465							470							475									
Ser	Ala	Gly	Phe	Thr	Pro	Ala	Glu	Leu	Leu	Ala	Ser	Val	His	Pro	Ala															
							485							490							495									
Arg	Val	Ser	Ser	Thr	Gln	Gly	Thr	Gly	Met	Gly	Gly	Met	Glu	Ser	Leu															
							500							505							510									
Arg	Gly	Ile	Tyr	Val	Asp	Arg	Ile	Leu	Ala	Glu	Pro	Arg	Ala	Asn	Asp															
							515							520							525									
Val	Leu	Gln	Glu	Ala	Leu	Pro	Asn	Val	Val	Ala	Ala	His	Val	Met	Gln															
							530							535							540									
Ser	Tyr	Val	Gly	Gly	Tyr	Gly	Gln	Met	Ile	His	Pro	Val	Ala	Ala	Cys															
							545							550							555									
Ala	Thr	Ala	Ala	Val	Ser	Val	Glu	Glu	Ala	Leu	Asp	Lys	Ile	Arg	Ile															
							565							570							575									
Gly	Lys	Ser	Asp	Phe	Val	Val	Ala	Gly	Gly	Phe	Asp	Ala	Leu	Ser	Val															
							580							585							590									
Glu	Gly	Ile	Thr	Gly	Phe	Gly	Asp	Met	Ala	Ala	Thr	Ala	Asp	Ser	Ala															
							595							600							605									
Glu	Met	Glu	Gly	Lys	Gly	Ile	Glu	His	Arg	Phe	Phe	Ser	Arg	Ala	Asn															
							610							615							620									
Asp	Arg	Arg	Arg	Gly	Gly	Phe	Ile	Glu	Ser	Glu	Gly	Gly	Gly	Thr	Val															
							625							630							635									
Leu	Leu	Ala	Arg	Gly	Ser	Leu	Ala	Ala	Asp	Leu	Gly	Leu	Pro	Val	Leu															
							645							650							655									
Gly	Val	Ile	Gly	Phe	Ala	Glu	Ser	Phe	Ala	Asp	Gly	Ala	His	Thr	Ser															
							660							665							670									
Ile	Pro	Ala	Pro	Gly	Leu	Gly	Ala	Leu	Gly	Ala	Ala	Arg	Asp	Gly	Val															
							675							680							685									

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Glu Ser Arg Leu Ala Val Ala Leu Arg Ser Val Gly Val Ser Ala Asp
690                      695                      700

Glu Ile Ser Ile Ile Ser Lys His Asp Thr Ser Thr Asn Ala Asn Asp
705                      710                      715                      720

Pro Asn Glu Ser Asp Leu His Glu Arg Ile Ala Ser Ala Ile Gly Arg
725                      730                      735

Ala Asp Gly Asn Pro Met Tyr Val Ile Ser Gln Lys Ser Leu Thr Gly
740                      745                      750

His Ala Lys Gly Gly Ala Ala Ala Phe Gln Met Ile Gly Leu Thr Gln
755                      760                      765

Val Leu Arg Ser Gly Leu Val Pro Ala Asn Arg Ala Leu Asp Cys Val
770                      775                      780

Asp Pro Val Leu Ser Lys His Ser His Leu Val Trp Leu Arg Lys Pro
785                      790                      795                      800

Leu Asp Leu Arg Ala Lys Ala Pro Lys Ala Gly Leu Val Thr Ser Leu
805                      810                      815

Gly Phe Gly His Val Ser Ala Leu Val Ala Ile Val His Pro Asp Ala
820                      825                      830

Phe Tyr Glu Ala Val Arg Val Ala Arg Gly Ala Glu Ala Ala Asp Val
835                      840                      845

Trp Arg Ala Ser Ala Ile Ala Arg Glu Glu Ala Gly Leu Arg Thr Ile
850                      855                      860

Val Ala Gly Met His Gly Gly Val Leu Tyr Glu Arg Pro Val Glu Arg
865                      870                      875                      880

Asn Leu Gly Val His Gly Asp Ala Ala Lys Glu Val Glu Ala Ala Val
885                      890                      895

Leu Leu Asp Ser Arg Ala Arg Leu Val Asp Gly Val Leu Arg Ala Glu
900                      905                      910

Gly

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<210> 1813
<211> 528
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(505)
<223> RXA00564

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<400> 1813
caacgatgga gtgctattcg taacgagggtg acattcccac cggcaccttg atccagatag 60
aaaaacggat ggaaccagta ttgggaaaag gatggttgcg atg aaa tac aac gtc 115

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Met Lys Tyr Asn Val
1 5

gat gtc tct cgt gaa agc gag gac tgg ctc gcc acc gtc acc aat ctc 163
Asp Val Ser Arg Glu Ser Glu Asp Trp Leu Ala Thr Val Thr Asn Leu
10 15 20

gaa ggc gta tcc acg tgg gcg aca acc ttc gcc aac ctt gat cgc aac 211
Glu Gly Val Ser Thr Trp Ala Thr Thr Phe Ala Asn Leu Asp Arg Asn
25 30 35

ggc cgg gaa gcc att gct cta gct gaa gat ctc ccc gaa ggt gcg gaa 259
Gly Arg Glu Ala Ile Ala Leu Ala Glu Asp Leu Pro Glu Gly Ala Glu
40 45 50

agc tca ctg acc atc tct tgg tcg gtt cct aca gat tcc cac ccc gaa 307
Ser Ser Leu Thr Ile Ser Trp Ser Val Pro Thr Asp Ser His Pro Glu
55 60 65

ctg gac act gca att caa att gct caa cag cgt cgc tat cta gtg caa 355
Leu Asp Thr Ala Ile Gln Ile Ala Gln Gln Arg Tyr Leu Val Gln
70 75 80 85

gcc caa caa gac tta gag ccc aaa gtt cga tcc gct att tcc gct ctc 403
Ala Gln Gln Asp Leu Glu Pro Lys Val Arg Ser Ala Ile Ser Ala Leu
90 95 100

acc caa gct gcg ctg cta ggt atg act gca ggt cga gta tcc cca act 451
Thr Gln Ala Ala Leu Leu Gly Met Thr Ala Gly Arg Val Ser Pro Thr
105 110 115

cac aac ccg ggt agc aga gct atc tca ttg gat cag gtg tca gga gtt 499
His Asn Pro Gly Ser Arg Ala Ile Ser Leu Asp Gln Val Ser Gly Val
120 125 130

tta aac tagcgtgcgc aattcccgtg tga 528
Leu Asn
135

<210> 1814

<211> 135

<212> PRT

<213> Corynebacterium glutamicum

<400> 1814

Met Lys Tyr Asn Val Asp Val Ser Arg Glu Ser Glu Asp Trp Leu Ala
1 5 10 15

Thr Val Thr Asn Leu Glu Gly Val Ser Thr Trp Ala Thr Thr Phe Ala
20 25 30

Asn Leu Asp Arg Asn Gly Arg Glu Ala Ile Ala Leu Ala Glu Asp Leu
35 40 45

Pro Glu Gly Ala Glu Ser Ser Leu Thr Ile Ser Trp Ser Val Pro Thr
50 55 60

Asp Ser His Pro Glu Leu Asp Thr Ala Ile Gln Ile Ala Gln Gln Arg
65 70 75 80

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Arg Tyr Leu Val Gln Ala Gln Gln Asp Leu Glu Pro Lys Val Arg Ser
      85                      90                      95
Ala Ile Ser Ala Leu Thr Gln Ala Ala Leu Leu Gly Met Thr Ala Gly
      100                    105                    110
Arg Val Ser Pro Thr His Asn Pro Gly Ser Arg Ala Ile Ser Leu Asp
      115                    120                    125
Gln Val Ser Gly Val Leu Asn
      130                    135

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<210> 1815

<211> 774

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(751)

<223> RXA00573

<400> 1815

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atcgtgacca ccattgcagc tcatgaggtt caggtttccc atg ctc gtt agg cca 115
                                     Met Leu Val Arg Pro
                                     1                      5
tgt ggt gag caa gca gtc atc atc gat ttg ctt gct gaa gat gcc gaa 163
Cys Gly Glu Gln Ala Val Ile Ile Asp Leu Leu Ala Glu Asp Ala Glu
      10                    15                    20
gcc gtc caa ggc agc atc ttg gat gct gtt ctt gca ctc aac cgc tct 211
Ala Val Gln Gly Ser Ile Leu Asp Ala Val Leu Ala Leu Asn Arg Ser
      25                    30                    35
ttg gtg ggc atg cag gtc cct gga atc atc gat act att ccc gct gcg 259
Leu Val Gly Met Gln Val Pro Gly Ile Ile Asp Thr Ile Pro Ala Ala
      40                    45                    50
caa aca ctg tta gtg acg ttt gac acc aag cag atc acc ccg aat cgt 307
Gln Thr Leu Leu Val Thr Phe Asp Thr Lys Gln Ile Thr Pro Asn Arg
      55                    60                    65
ttc gca gag atc gtt gat tca att gcg ctg acc cca gcc gca aag ggc 355
Phe Ala Glu Ile Val Asp Ser Ile Ala Leu Thr Pro Ala Ala Lys Gly
      70                    75                    80                    85
gca gca gag ctt acc gac acc att gag att ccc gtg gtc tac gac ggc 403
Ala Ala Glu Leu Thr Asp Thr Ile Glu Ile Pro Val Val Tyr Asp Gly
      90                    95                    100
cct gat cta gaa acc gta gct caa cac aca ggt ctg agc gtg gag gaa 451
Pro Asp Leu Glu Thr Val Ala Gln His Thr Gly Leu Ser Val Glu Glu
      105                    110                    115
gtt atc gcc acg cat tct ggc acc gtg tgg act gct gct ttc ggt gga 499
Val Ile Ala Thr His Ser Gly Thr Val Trp Thr Ala Ala Phe Gly Gly
      120                    125                    130

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ttt gca cca ggt ttt tac tat ctg atc ccc cag act ccc ctg tgg gat 547
Phe Ala Pro Gly Phe Tyr Tyr Leu Ile Pro Gln Thr Pro Leu Trp Asp
135 140 145

att ccc cgc ttg gaa tcg cca cgc acc aag att cct gca ggt tct gtc 595
Ile Pro Arg Leu Glu Ser Pro Arg Thr Lys Ile Pro Ala Gly Ser Val
150 155 160 165

gca gtg gcc ggt gaa ttc agc gct gtg tac ccg cag cag tcc cct ggt 643
Ala Val Ala Gly Glu Phe Ser Ala Val Tyr Pro Gln Gln Ser Pro Gly
170 175 180

ggt tgg caa ctg ctg ggc act act gag att ccc atg tgg gat gtg gac 691
Gly Trp Gln Leu Leu Gly Thr Thr Glu Ile Pro Met Trp Asp Val Asp
185 190 195

cgg tgg caa cca tcg ctt ctc aag ccc ggt gat tca gtt cga ttt gtg 739
Arg Trp Gln Pro Ser Leu Leu Lys Pro Gly Asp Ser Val Arg Phe Val
200 205 210

cag gtg aag aaa tgagcttcaa agtaatttcc act 774
Gln Val Lys Lys
215

<210> 1816
<211> 217
<212> PRT
<213> Corynebacterium glutamicum

<400> 1816
Met Leu Val Arg Pro Cys Gly Glu Gln Ala Val Ile Ile Asp Leu Leu
1 5 10 15

Ala Glu Asp Ala Glu Ala Val Gln Gly Ser Ile Leu Asp Ala Val Leu
20 25 30

Ala Leu Asn Arg Ser Leu Val Gly Met Gln Val Pro Gly Ile Ile Asp
35 40 45

Thr Ile Pro Ala Ala Gln Thr Leu Leu Val Thr Phe Asp Thr Lys Gln
50 55 60

Ile Thr Pro Asn Arg Phe Ala Glu Ile Val Asp Ser Ile Ala Leu Thr
65 70 75 80

Pro Ala Ala Lys Gly Ala Ala Glu Leu Thr Asp Thr Ile Glu Ile Pro
85 90 95

Val Val Tyr Asp Gly Pro Asp Leu Glu Thr Val Ala Gln His Thr Gly
100 105 110

Leu Ser Val Glu Glu Val Ile Ala Thr His Ser Gly Thr Val Trp Thr
115 120 125

Ala Ala Phe Gly Gly Phe Ala Pro Gly Phe Tyr Tyr Leu Ile Pro Gln
130 135 140

Thr Pro Leu Trp Asp Ile Pro Arg Leu Glu Ser Pro Arg Thr Lys Ile
145 150 155 160

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Pro Ala Gly Ser Val Ala Val Ala Gly Glu Phe Ser Ala Val Tyr Pro
 165 170 175
 Gln Gln Ser Pro Gly Gly Trp Gln Leu Leu Gly Thr Thr Glu Ile Pro
 180 185 190
 Met Trp Asp Val Asp Arg Trp Gln Pro Ser Leu Leu Lys Pro Gly Asp
 195 200 205
 Ser Val Arg Phe Val Gln Val Lys Lys
 210 215

<210> 1817
 <211> 795
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(772)
 <223> RXA00576

<400> 1817
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 cagattcttc gtccaagccc acaacggtag cattgttttc atg ctg acc tta agt 115
 Met Leu Thr Leu Ser
 1 5
 ttc atc act ggc acg gag cca gga aag tgg ttt acc cga ttc cga gat 163
 Phe Ile Thr Gly Thr Glu Pro Gly Lys Trp Phe Thr Arg Phe Arg Asp
 10 15 20
 cgg act cat cac ggt gga ctt gag acc ctt gat tcg gac gac gcc cta 211
 Arg Thr His His Gly Gly Leu Glu Thr Leu Asp Ser Asp Ala Leu
 25 30 35
 ggc ctg atg ctg gct ggc cag gca caa ctg gcc tta acc agg ctt cca 259
 Gly Leu Met Leu Ala Gly Gln Ala Gln Leu Ala Leu Thr Arg Leu Pro
 40 45 50
 gat gcg cgt atc gac gcc tcc ctg cac gtg gtc act ctt tat cag gaa 307
 Asp Ala Arg Ile Asp Ala Ser Leu His Val Val Thr Leu Tyr Gln Glu
 55 60 65
 caa ccc gga gtc gct ttt cca aaa gac ttt ttc ctg agt gcc gaa gaa 355
 Gln Pro Gly Val Ala Phe Pro Lys Asp Phe Phe Leu Ser Ala Glu Glu
 70 75 80 85
 ggc gcg gtg gac ctt gcg gac tta gat ggg gag atc atc aac tgg tcc 403
 Gly Ala Val Asp Leu Ala Asp Leu Asp Gly Glu Ile Ile Asn Trp Ser
 90 95 100
 atg ccc gat agt ggg gaa gtc gat gcc gct gct gtt cgc gat gct ctg 451
 Met Pro Asp Ser Gly Glu Val Asp Ala Ala Ala Val Arg Asp Ala Leu
 105 110 115
 caa atc gtg gca gcg aac gtc ggt gtg gtg atc gcc ccc agg cca ctt 499
 Gln Ile Val Ala Ala Asn Val Gly Val Val Ile Ala Pro Arg Pro Leu

120	125	130	
ctc aag gtg ttg agc aag aaa ttg gtg gag cac cgg gac atc aag ggt			547
Leu Lys Val Leu Ser Lys Lys Leu Val Glu His Arg Asp Ile Lys Gly			
135	140	145	
gga act gaa aca tct atc gcc ctg gta tgg aag aaa gat gag gat tct			595
Gly Thr Glu Thr Ser Ile Ala Leu Val Trp Lys Asp Glu Asp Ser			
150	155	160	165
gaa gag att caa gac ttc gtc ggt att gct cgc ggt cga acg cgg aat			643
Glu Glu Ile Gln Asp Phe Val Gly Ile Ala Arg Gly Arg Thr Arg Asn			
170	175	180	
tcc agc agg cag caa acg gta aag ctc agt gct cgt gaa aaa aca ctg			691
Ser Ser Arg Gln Gln Thr Val Lys Leu Ser Ala Arg Glu Lys Thr Leu			
185	190	195	
gca aaa caa gcc cgc agg cag ggg gag aaa cca aaa act ccg aag cgt			739
Ala Lys Gln Ala Arg Arg Gln Gly Glu Lys Pro Lys Thr Pro Lys Arg			
200	205	210	
ccg cag gca aga aaa cgt ccc gga aaa cgg cga taggggtcac ccgcgcatgt			792
Pro Gln Ala Arg Lys Arg Pro Gly Lys Arg Arg			
215	220		
ccg			795
<210> 1818			
<211> 224			
<212> PRT			
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<400> 1818			
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Thr Arg Phe Arg Asp Arg Thr His His Gly Gly Leu Glu Thr Leu Asp			
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Ser Asp Asp Ala Leu Gly Leu Met Leu Ala Gly Gln Ala Gln Leu Ala			
35	40	45	
Leu Thr Arg Leu Pro Asp Ala Arg Ile Asp Ala Ser Leu His Val Val			
50	55	60	
Thr Leu Tyr Gln Glu Gln Pro Gly Val Ala Phe Pro Lys Asp Phe Phe			
65	70	75	80
Leu Ser Ala Glu Glu Gly Ala Val Asp Leu Ala Asp Leu Asp Gly Glu			
85	90	95	
Ile Ile Asn Trp Ser Met Pro Asp Ser Gly Glu Val Asp Ala Ala Ala			
100	105	110	
Val Arg Asp Ala Leu Gln Ile Val Ala Ala Asn Val Gly Val Val Ile			
115	120	125	
Ala Pro Arg Pro Leu Leu Lys Val Leu Ser Lys Lys Leu Val Glu His			
130	135	140	

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Arg Asp Ile Lys Gly Gly Thr Glu Thr Ser Ile Ala Leu Val Trp Lys
145                150                155                160

Lys Asp Glu Asp Ser Glu Glu Ile Gln Asp Phe Val Gly Ile Ala Arg
                165                170                175

Gly Arg Thr Arg Asn Ser Ser Arg Gln Gln Thr Val Lys Leu Ser Ala
                180                185                190

Arg Glu Lys Thr Leu Ala Lys Gln Ala Arg Arg Gln Gly Glu Lys Pro
195                200                205

Lys Thr Pro Lys Arg Pro Gln Ala Arg Lys Arg Pro Gly Lys Arg Arg
210                215                220

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<210> 1819
<211> 471
<212> DNA
<213> Corynebacterium glutamicum

```

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<220>
<221> CDS
<222> (101)..(448)
<223> RXA00577

```

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<400> 1819
ctggctccgt gccagtgatg aaacttaagg tcagcatgaa aacaatgcta ccgttgtggg 60

cgtgaacgaa gaatctgtac gccagccatc gggcagggct atg aag cca cag acc 115
                Met Lys Pro Gln Thr
                1                5

gcc gct aag aag ctc gga ctg ttt ttg ccc gcc acg cca gag gag ttc 163
Ala Ala Lys Lys Leu Gly Leu Phe Leu Pro Ala Thr Pro Glu Glu Phe
                10                15                20

caa aca ggt gca ttg act cac caa gag ttc aag aac ctg cag gaa aac 211
Gln Thr Gly Ala Leu Thr His Gln Gln Phe Lys Asn Leu Gln Glu Asn
                25                30                35

cca ccg gag tgg ctc caa acc cta cgc cgc gag ggc cca cac cct cgt 259
Pro Pro Glu Trp Leu Gln Thr Leu Arg Arg Glu Gly Pro His Pro Arg
                40                45                50

cca gtg gtc gcc caa aaa ttg ggc atc acc atc gcg gct ctg aaa aag 307
Pro Val Val Ala Gln Lys Leu Gly Ile Thr Ile Ala Ala Leu Lys Lys
                55                60                65

aac gac atg gac aaa cca ctg acc acc gcc gag atc aag gca ctt ctg 355
Asn Asp Met Asp Lys Pro Leu Thr Thr Ala Glu Ile Lys Ala Leu Leu
                70                75                80                85

gaa aac cag cca gaa tgg ttg cgc acc gca cgc aca cag ctt gct gaa 403
Glu Asn Gln Pro Glu Trp Leu Arg Thr Ala Arg Thr Gln Leu Ala Glu
                90                95                100

```

ggt cgc gaa acc gca aag aaa gaa act gaa gaa act acc gaa gac 448
 Gly Arg Glu Thr Ala Lys Lys Glu Thr Glu Glu Thr Thr Glu Asp
 105 110 115

taaattctca caaagactgc gct 471

<210> 1820

<211> 116

<212> PRT

<213> Corynebacterium glutamicum

<400> 1820

Met Lys Pro Gln Thr Ala Ala Lys Lys Leu Gly Leu Phe Leu Pro Ala
 1 5 10 15

Thr Pro Glu Glu Phe Gln Thr Gly Ala Leu Thr His Gln Glu Phe Lys
 20 25 30

Asn Leu Gln Glu Asn Pro Pro Glu Trp Leu Gln Thr Leu Arg Arg Glu
 35 40 45

Gly Pro His Pro Arg Pro Val Val Ala Gln Lys Leu Gly Ile Thr Ile
 50 55 60

Ala Ala Leu Lys Lys Asn Asp Met Asp Lys Pro Leu Thr Thr Ala Glu
 65 70 75 80

Ile Lys Ala Leu Leu Glu Asn Gln Pro Glu Trp Leu Arg Thr Ala Arg
 85 90 95

Thr Gln Leu Ala Glu Gly Arg Glu Thr Ala Lys Lys Glu Thr Glu Glu
 100 105 110

Thr Thr Glu Asp
 115

<210> 1821

<211> 846

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(823)

<223> RXA00578

<400> 1821

tggcgggtgc acttcttgcct ctgtctgcatc cggaggctga gtgggaggaa atccgcgtta 60

aatcacggcc tctgctgaat ttgtttgggg ttgaattccc atg acg tac ctc gtg 115
 Met Thr Tyr Leu Val
 1 5

tgg gac ggt gca aca ctc gta gaa ggc gcg ctg gaa tca aca ccc aca 163
 Trp Asp Gly Ala Thr Leu Val Glu Gly Ala Leu Glu Ser Thr Pro Thr
 10 15 20

gtt gtt gat tcc tac cta gcc aaa gac cac cgc gtg gtg cgc tgg gat 211
 Val Val Asp Ser Tyr Leu Ala Lys Asp His Arg Val Val Arg Trp Asp

	25	30	35	
ctt cat gaa cag cgc ttc gcc act agc gtg gac gtg gac ccg tgg gat	259			
Leu His Glu Gln Arg Phe Ala Thr Ser Val Asp Val Asp Pro Trp Asp				
40 45 50				
ttt ctc cac gca gta agg gaa gca att cca cgc cag ggc tca tgg ttt	307			
Phe Leu His Ala Val Arg Glu Ala Ile Pro Arg Gln Gly Ser Trp Phe				
55 60 65				
ccc aaa gtt gaa tgg cat ggc gat gat ctt ttc gca gtc aat att cgc	355			
Pro Lys Val Glu Trp His Gly Asp Asp Leu Phe Ala Val Asn Ile Arg				
70 75 80 85				
ccg gca cca aca ctg cga aag gcc aca tca ttg tgg ctt tcc gaa gac	403			
Pro Ala Pro Thr Leu Arg Lys Ala Thr Ser Leu Trp Leu Ser Glu Asp				
90 95 100				
cca gat cca cgc aca cag cca acc att aaa ggc cca gac cta gat gtg	451			
Pro Asp Pro Arg Thr Gln Pro Thr Ile Lys Gly Pro Asp Leu Asp Val				
105 110 115				
ctt gct cac ctt cgc agt cgc gcc aac gat aac ggc tgc gat gat gcg	499			
Leu Ala His Leu Arg Ser Arg Ala Asn Asp Asn Gly Cys Asp Asp Ala				
120 125 130				
ctg ttg atc agc gcg gat ggg ttc att ctg gaa gct gcc aac gcc acc	547			
Leu Leu Ile Ser Ala Asp Gly Phe Ile Leu Glu Ala Ala Asn Ala Thr				
135 140 145				
gtg gtg ttt tgg gcg gat cca cag acg gtc atc gtg ccc agg gga gat	595			
Val Val Phe Trp Ala Asp Pro Gln Thr Val Ile Val Pro Arg Gly Asp				
150 155 160 165				
gtg ctc cca tcg gtg aca ctc gcc gca acc att ccg ctg tgg gaa aaa	643			
Val Leu Pro Ser Val Thr Leu Ala Ala Thr Ile Pro Leu Trp Glu Lys				
170 175 180				
gcc gga atc aca ttg cgc tat caa aac att ccg cac att ggt ttt ccc	691			
Ala Gly Ile Thr Leu Arg Tyr Gln Asn Ile Arg His Ile Gly Phe Pro				
185 190 195				
gcg tgg tgc ggt agt tcg ctg cat ggt tgg aca cct gtg gtc agt tgg	739			
Ala Trp Cys Gly Ser Ser Leu His Gly Trp Thr Pro Val Val Ser Trp				
200 205 210				
ggc agg gga ttg ggc aaa att gca gca gcg aaa gct cca tcg gtg aag	787			
Gly Arg Gly Leu Gly Lys Ile Ala Ala Ala Lys Ala Pro Ser Val Lys				
215 220 225				
ccc tgg aat gaa aaa ttg cgc cca acc att ttt ctg tgaggaag	833			
Pro Trp Asn Glu Lys Leu Arg Pro Thr Ile Phe Leu				
230 235 240				
gttgagcgca gtc	846			

<210> 1822

<211> 241

<212> PRT

<213> Corynebacterium glutamicum

<400> 1822

```

Met Thr Tyr Leu Val Trp Asp Gly Ala Thr Leu Val Glu Gly Ala Leu
 1          5          10          15

Glu Ser Thr Pro Thr Val Val Asp Ser Tyr Leu Ala Lys Asp His Arg
          20          25          30

Val Val Arg Trp Asp Leu His Glu Gln Arg Phe Ala Thr Ser Val Asp
          35          40          45

Val Asp Pro Trp Asp Phe Leu His Ala Val Arg Glu Ala Ile Pro Arg
          50          55          60

Gln Gly Ser Trp Phe Pro Lys Val Glu Trp His Gly Asp Asp Leu Phe
          65          70          75          80

Ala Val Asn Ile Arg Pro Ala Pro Thr Leu Arg Lys Ala Thr Ser Leu
          85          90          95

Trp Leu Ser Glu Asp Pro Asp Pro Arg Thr Gln Pro Thr Ile Lys Gly
          100          105          110

Pro Asp Leu Asp Val Leu Ala His Leu Arg Ser Arg Ala Asn Asp Asn
          115          120          125

Gly Cys Asp Asp Ala Leu Leu Ile Ser Ala Asp Gly Phe Ile Leu Glu
          130          135          140

Ala Ala Asn Ala Thr Val Val Phe Trp Ala Asp Pro Gln Thr Val Ile
          145          150          155          160

Val Pro Arg Gly Asp Val Leu Pro Ser Val Thr Leu Ala Ala Thr Ile
          165          170          175

Pro Leu Trp Glu Lys Ala Gly Ile Thr Leu Arg Tyr Gln Asn Ile Arg
          180          185          190

His Ile Gly Phe Pro Ala Trp Cys Gly Ser Ser Leu His Gly Trp Thr
          195          200          205

Pro Val Val Ser Trp Gly Arg Gly Leu Gly Lys Ile Ala Ala Ala Lys
          210          215          220

Ala Pro Ser Val Lys Pro Trp Asn Glu Lys Leu Arg Pro Thr Ile Phe
          225          230          235          240

Leu

```

<210> 1823

<211> 642

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(619)

<223> RXA00582

<400> 1823

```

actggccagc cttccgacgc atcgacttcc tccgcgccat tgcgcactac tgcgacgcga 60
gcagaagatt cggtaaataa cttattctcc aaggagagac atg tct gac tac atc 115
                               Met Ser Asp Tyr Ile
                               1           5

gtc gca ttt gaa tcc gca tac ggc tct acc aag cag tac gca gaa tct 163
Val Ala Phe Glu Ser Ala Tyr Gly Ser Thr Lys Gln Tyr Ala Glu Ser
                10                15                20

ctg gcg caa cgc ctc ggc gta gat gcc tta aat ttt gaa caa gcg tgt 211
Leu Ala Gln Arg Leu Gly Val Asp Ala Leu Asn Phe Glu Gln Ala Cys
                25                30                35

gcg gaa ctc gcg gcg aac ccg acc gca gca atc gtg gtt ttg agc ttt 259
Ala Glu Leu Ala Ala Asn Pro Thr Thr Val Ile Val Leu Ser Phe
                40                45                50

gtt cac ggc cca tcc cat cca ggt gcg aaa ttc att acc gat acc gat 307
Val His Gly Pro Ser His Pro Gly Ala Lys Phe Ile Thr Asp Thr Asp
                55                60                65

ctc tcc ggc cac cgc gtc gca ctg tgc acc gtc ggc atg acg ctt gat 355
Leu Ser Gly His Arg Val Ala Leu Cys Thr Val Gly Met Thr Leu Asp
                70                75                80                85

gat gtc gtg caa aag aag gac ggc gca gct cga tca ctg gga aac aag 403
Asp Val Val Gln Lys Lys Asp Gly Ala Ala Arg Ser Leu Gly Asn Lys
                90                95                100

gca gac gat gtc acc cgt ttc tac ctt ccg gga cgc ctt aat tac tca 451
Ala Asp Asp Val Thr Arg Phe Tyr Leu Pro Gly Arg Leu Asn Tyr Ser
                105                110                115

gag ctc tgc acc gcg cac cgc acc acc atg tgg acg atc gtc aac atg 499
Glu Leu Ser Thr Ala His Arg Thr Thr Met Trp Thr Ile Val Asn Met
                120                125                130

ctg aaa gcg aag ccg ttg aag aat gac aac gac aaa atg atg atc aac 547
Leu Lys Ala Lys Pro Leu Lys Asn Asp Asn Asp Lys Met Met Ile Asn
                135                140                145

act ttt gat acc gat gtt gac cgc gtc gat gag tcc cgc ctg gac gca 595
Thr Phe Asp Thr Asp Val Asp Arg Val Asp Glu Ser Arg Leu Asp Ala
                150                155                160                165

gtg gag gag tgg gcg agg ggc ctc tagagtgggc gttgcaaaaa ctc 642
Val Glu Glu Trp Ala Arg Gly Leu
                170

```

<210> 1824

<211> 173

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1824

```

Met Ser Asp Tyr Ile Val Ala Phe Glu Ser Ala Tyr Gly Ser Thr Lys
1           5           10           15

```


Gln Tyr Ala Glu Ser Leu Ala Gln Arg Leu Gly Val Asp Ala Leu Asn
20 25 30

Phe Glu Gln Ala Cys Ala Glu Leu Ala Ala Asn Pro Thr Ala Ala Ile
35 40 45

Val Val Leu Ser Phe Val His Gly Pro Ser His Pro Gly Ala Lys Phe
50 55 60

Ile Thr Asp Thr Asp Leu Ser Gly His Arg Val Ala Leu Cys Thr Val
65 70 75 80

Gly Met Thr Leu Asp Asp Val Val Gln Lys Lys Asp Gly Ala Ala Arg
85 90 95

Ser Leu Gly Asn Lys Ala Asp Asp Val Thr Arg Phe Tyr Leu Pro Gly
100 105 110

Arg Leu Asn Tyr Ser Glu Leu Ser Thr Ala His Arg Thr Thr Met Trp
115 120 125

Thr Ile Val Asn Met Leu Lys Ala Lys Pro Leu Lys Asn Asp Asn Asp
130 135 140

Lys Met Met Ile Asn Thr Phe Asp Thr Asp Val Asp Arg Val Asp Glu
145 150 155 160

Ser Arg Leu Asp Ala Val Glu Glu Trp Ala Arg Gly Leu
165 170

<210> 1825

<211> 441

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(418)

<223> RXA00585

<400> 1825

tgatgaagacg tcgatccacg aagatgacct gtttgccgga atcacacccg atgcagaata 60

atgcagtttag accacatcct ttaggaagga ccttttcggc gtg att gac ctc agc 115
Val Ile Asp Leu Ser
1 5

cct gta ttc aat aca gct gcc ggc gta tac aac gac acc aac gca atc 163
Pro Val Phe Asn Thr Ala Ala Gly Val Tyr Asn Asp Thr Asn Ala Ile
10 15 20

atc ttg gct cag cag cag caa ggt gga cca ctt gga cct gag ttt gga 211
Ile Leu Ala Gln Gln Gln Gly Gly Pro Leu Gly Pro Glu Phe Gly
25 30 35

aag gcc tcg ccg gtt ggt ttg cta ctg atc gtc gcg atg ctc gtt gcc 259
Lys Ala Ser Pro Val Gly Leu Leu Leu Ile Val Ala Met Leu Val Ala
40 45 50

att ctt gtt ctc ggc tgg gcg ttc cac cga cgc tgg tca cgg atg aat 307

```

Ile Leu Val Leu Gly Trp Ala Phe His Arg Arg Trp Ser Arg Met Asn
 55                      60                      65

cgt cgt cgt att ttc gca gag cgc aac ggc ctt gat ccc ttc gat att   355
Arg Arg Arg Ile Phe Ala Glu Arg Asn Gly Leu Asp Pro Phe Asp Ile
 70                      75                      80                      85

gag ggt gtt cgc aag gca atg gct gag gcc ggc ttg aat gaa aag tcc   403
Glu Gly Val Arg Lys Ala Met Ala Glu Ala Gly Leu Asn Glu Lys Ser
                      90                      95                      100

aaa aag ggc ttc ctt taaaaagaaa gtgtgttaag gtt                     441
Lys Lys Gly Phe Leu
                      105

```

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<210> 1826
<211> 106
<212> PRT
<213> Corynebacterium glutamicum

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```

<400> 1826
Val Ile Asp Leu Ser Pro Val Phe Asn Thr Ala Ala Gly Val Tyr Asn
 1                      5                      10                      15

Asp Thr Asn Ala Ile Ile Leu Ala Gln Gln Gln Gln Gly Gly Pro Leu
                      20                      25                      30

Gly Pro Glu Phe Gly Lys Ala Ser Pro Val Gly Leu Leu Leu Ile Val
                      35                      40                      45

Ala Met Leu Val Ala Ile Leu Val Leu Gly Trp Ala Phe His Arg Arg
 50                      55                      60

Trp Ser Arg Met Asn Arg Arg Arg Ile Phe Ala Glu Arg Asn Gly Leu
 65                      70                      75                      80

Asp Pro Phe Asp Ile Glu Gly Val Arg Lys Ala Met Ala Glu Ala Gly
                      85                      90                      95

Leu Asn Glu Lys Ser Lys Lys Gly Phe Leu
                      100                      105

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<210> 1827
<211> 1005
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(982)
<223> RXA00586

```

```

<400> 1827
tcatccaaagg ggtaaatagg tatgacggcg gaaacgacta tcatgaatgc aatacacatc 60

aactaaaccc tgcggaagca tataaagctt caaggaaagg atg aaa cac gtg agt   115
                      Met Lys His Val Ser
                      1                      5

```

ggt cta cgc cta atg gcg atc cac gcc cac cct gac gac gag tca agc 163
 Gly Leu Arg Leu Met Ala Ile His Ala His Pro Asp Asp Glu Ser Ser
 10 15 20

aag ggc gca gca acc atg gcg cgc tat gca gct gag ggc aat caa gta 211
 Lys Gly Ala Ala Thr Met Ala Arg Tyr Ala Ala Glu Gly Asn Gln Val
 25 30 35

atg gtt gtt acc tgc act ggt ggt gag cgt gga gac att ctc aac cct 259
 Met Val Val Thr Cys Thr Gly Gly Glu Arg Gly Asp Ile Leu Asn Pro
 40 45 50

gct atg gat aag cca gga atc ctg gac aat att ttt gct gtg cgt cag 307
 Ala Met Asp Lys Pro Gly Ile Leu Asp Asn Ile Phe Ala Val Arg Gln
 55 60 65

gaa gag atg gcg aag gcc atg gaa att ctt ggc act gag cac aga tgg 355
 Glu Glu Met Ala Lys Ala Met Glu Ile Leu Gly Thr Glu His Arg Trp
 70 75 80 85

cta ggt tat gag gac tct ggg ctg ccc caa ggt gat cct ttg cct cct 403
 Leu Gly Tyr Glu Asp Ser Gly Leu Pro Gln Gly Asp Pro Leu Pro Pro
 90 95 100

ctg cct gag ggc tgt ttt gct tta gaa gac tgg gat aaa gtc acc caa 451
 Leu Pro Glu Gly Cys Phe Ala Leu Glu Asp Ser Asp Lys Val Thr Gln
 105 110 115

gat tta gtg aag att ctg cgc gag ttc cgc cca cac gtc atc att acc 499
 Asp Leu Val Lys Ile Leu Arg Glu Phe Arg Pro His Val Ile Ile Thr
 120 125 130

tat gat gag aac ggc ggt tac cca cac ccg gat cac ctc aag gtt cat 547
 Tyr Asp Glu Asn Gly Gly Tyr Pro His Pro Asp His Leu Lys Val His
 135 140 145

gag gtg tcg atg ctt gca tgg gag aag tcc ggc gat gca gcg tat gca 595
 Glu Val Ser Met Leu Ala Trp Glu Lys Ser Gly Asp Ala Ala Tyr Ala
 150 155 160 165

cct gag ttg ggc gca ccg tgg gag cca ctg aag ctt tat tac acc cac 643
 Pro Glu Leu Gly Ala Pro Trp Glu Pro Leu Lys Leu Tyr Tyr Thr His
 170 175 180

ggc ttt atc cgt cag cgc atg gaa atg ttc cat gat ctg ctc att gaa 691
 Gly Phe Ile Arg Gln Arg Met Glu Met Phe His Asp Leu Leu Ile Glu
 185 190 195

cag ggc aag ccc agc cca tac acc ccg atg ctt gag cgt tgg aag gca 739
 Gln Gly Lys Pro Ser Pro Tyr Thr Pro Met Leu Glu Arg Trp Lys Ala
 200 205 210

aat gag gct gat gtg atg gct cga gtt acc act cag gtt cct tgt gag 787
 Asn Glu Ala Asp Val Met Ala Arg Val Thr Thr Gln Val Pro Cys Glu
 215 220 225

cgc ttc ttt gat cag cgt gat gac gcc ctg cgt gcg cac gca act cag 835
 Arg Phe Phe Asp Gln Arg Asp Asp Ala Leu Arg Ala His Ala Thr Gln
 230 235 240 245

att gat cct gcg ggt gct ttc ttt gga act ccc gtt gag gtg cag cgt 883

```

Ile Asp Pro Ala Gly Ala Phe Phe Gly Thr Pro Val Glu Val Gln Arg
      250                      255                      260

cgc ctg tgg ccg act gaa gag ttc gaa tta gct aaa act cgt gtg aag   931
Arg Leu Trp Pro Thr Glu Glu Phe Glu Leu Ala Lys Thr Arg Val Lys
      265                      270                      275

acg tcg atc cca gaa gat gac ctg ttt gcc gga atc aca ccc gat gca   979
Thr Ser Ile Pro Glu Asp Asp Leu Phe Ala Gly Ile Thr Pro Asp Ala
      280                      285                      290

gaa taatgcagtt agaccacatc ctt                               1005
Glu

```

<210> 1828

<211> 294

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1828

```

Met Lys His Val Ser Gly Leu Arg Leu Met Ala Ile His Ala His Pro
  1                      5                      10                      15

Asp Asp Glu Ser Ser Lys Gly Ala Ala Thr Met Ala Arg Tyr Ala Ala
      20                      25                      30

Glu Gly Asn Gln Val Met Val Val Thr Cys Thr Gly Gly Glu Arg Gly
      35                      40                      45

Asp Ile Leu Asn Pro Ala Met Asp Lys Pro Gly Ile Leu Asp Asn Ile
      50                      55                      60

Phe Ala Val Arg Gln Glu Glu Met Ala Lys Ala Met Glu Ile Leu Gly
      65                      70                      75                      80

Thr Glu His Arg Trp Leu Gly Tyr Glu Asp Ser Gly Leu Pro Gln Gly
      85                      90                      95

Asp Pro Leu Pro Pro Leu Pro Glu Gly Cys Phe Ala Leu Glu Asp Ser
      100                      105                      110

Asp Lys Val Thr Gln Asp Leu Val Lys Ile Leu Arg Glu Phe Arg Pro
      115                      120                      125

His Val Ile Ile Thr Tyr Asp Glu Asn Gly Gly Tyr Pro His Pro Asp
      130                      135                      140

His Leu Lys Val His Glu Val Ser Met Leu Ala Trp Glu Lys Ser Gly
      145                      150                      155                      160

Asp Ala Ala Tyr Ala Pro Glu Leu Gly Ala Pro Trp Glu Pro Leu Lys
      165                      170                      175

Leu Tyr Tyr Thr His Gly Phe Ile Arg Gln Arg Met Glu Met Phe His
      180                      185                      190

Asp Leu Leu Ile Glu Gln Gly Lys Pro Ser Pro Tyr Thr Pro Met Leu
      195                      200                      205

```

Glu Arg Trp Lys Ala Asn Glu Ala Asp Val Met Ala Arg Val Thr Thr
210 215 220

Gln Val Pro Cys Glu Arg Phe Phe Asp Gln Arg Asp Asp Ala Leu Arg
225 230 235 240

Ala His Ala Thr Gln Ile Asp Pro Ala Gly Ala Phe Phe Gly Thr Thr
245 250 255

Val Glu Val Gln Arg Arg Leu Trp Pro Thr Glu Glu Phe Glu Leu Ala
260 265 270

Lys Thr Arg Val Lys Thr Ser Ile Pro Glu Asp Asp Leu Phe Ala Gly
275 280 285

Ile Thr Pro Asp Ala Glu
290

<210> 1829

<211> 606

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(583)

<223> RXA00587

<400> 1829

cccttggtg acctcgggta acagtttttc ctgaggtgac taagatgtat aggtgaccaa 60

ctcgattcgg ctttgaagag gatgcagaca gacttccatc atg agt aca aat tcc 115
Met Ser Thr Asn Ser
1 5

aac tct cca tcc aac gca tca ggc gct tgc aac att cca aac acc caa 163
Asn Ser Pro Ser Asn Ala Ser Gly Ala Ser Asn Ile Pro Asn Thr Gln
10 15 20

cgt ccg gct agc cga tac aat tgc cct cgc ccg gaa gct gct gca ggc 211
Arg Pro Ala Ser Arg Tyr Asn Ser Pro Arg Pro Glu Ala Ala Ala Gly
25 30 35

agg aac atc agc gga aaa atc atc gca gtc att ggc gtg ctg ctg gtg 259
Arg Asn Ile Ser Gly Lys Ile Ile Ala Val Ile Gly Val Leu Leu Val
40 45 50

atc gcc att gtg att gtt ggc gca aac ttc ctc aaa aac cgc gat gca 307
Ile Ala Ile Val Ile Val Gly Ala Asn Phe Leu Lys Asn Arg Asp Ala
55 60 65

caa aca gtg tcc ggc caa atg ggt tca ttt gaa cgc atc gac gac gac 355
Gln Thr Val Ser Gly Gln Met Gly Ser Phe Glu Arg Ile Asp Asp Asp
70 75 80 85

acc ttc cgc ttt gaa gtt gac gtc acc cgc gat gac cca agc caa gtc 403
Thr Phe Arg Phe Glu Val Asp Val Thr Arg Asp Asp Pro Ser Gln Val
90 95 100

gcc tac tgc atc gtg acc gca aag gac tac tgc cac gca gaa gtc ggg 451

Ala Tyr Cys Ile Val Thr Ala Lys Asp Tyr Ser His Ala Glu Val Gly
 105 110 115

cgt cga gaa gtg ctt gtg gag ccc agc gac cac tca acg gtg cgt atc 499
 Arg Arg Glu Val Leu Val Glu Pro Ser Asp His Ser Thr Val Arg Ile
 120 125 130

tcc acg ctg atc ccc acc cgc gaa cca gca gtt tcc ggt ggt gtt tac 547
 Ser Thr Leu Ile Pro Thr Arg Glu Pro Ala Val Ser Gly Gly Val Tyr
 135 140 145

ggt tgt tca acc gtg atc cca tca cat atg aac ctg taaaactaga 593
 Gly Cys Ser Thr Val Ile Pro Ser His Met Asn Leu
 150 155 160

aaattttgct gtg 606

<210> 1830

<211> 161

<212> PRT

<213> Corynebacterium glutamicum

<400> 1830

Met Ser Thr Asn Ser Asn Ser Pro Ser Asn Ala Ser Gly Ala Ser Asn
 1 5 10 15

Ile Pro Asn Thr Gln Arg Pro Ala Ser Arg Tyr Asn Ser Pro Arg Pro
 20 25 30

Glu Ala Ala Ala Gly Arg Asn Ile Ser Gly Lys Ile Ile Ala Val Ile
 35 40 45

Gly Val Leu Leu Val Ile Ala Ile Val Ile Val Gly Ala Asn Phe Leu
 50 55 60

Lys Asn Arg Asp Ala Gln Thr Val Ser Gly Gln Met Gly Ser Phe Glu
 65 70 75 80

Arg Ile Asp Asp Asp Thr Phe Arg Phe Glu Val Asp Val Thr Arg Asp
 85 90 95

Asp Pro Ser Gln Val Ala Tyr Cys Ile Val Thr Ala Lys Asp Tyr Ser
 100 105 110

His Ala Glu Val Gly Arg Arg Glu Val Leu Val Glu Pro Ser Asp His
 115 120 125

Ser Thr Val Arg Ile Ser Thr Leu Ile Pro Thr Arg Glu Pro Ala Val
 130 135 140

Ser Gly Gly Val Tyr Gly Cys Ser Thr Val Ile Pro Ser His Met Asn
 145 150 155 160

Leu

<210> 1831

<211> 353

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(330)

<223> RXA00595

<400> 1831

cgc	aat	att	gca	gca	tgg	atc	gca	atc	gcc	gcc	atc	atc	atc	gcc	agc	48
Arg	Asn	Ile	Ala	Ala	Trp	Ile	Ala	Ile	Ala	Ala	Ile	Ile	Ile	Ala	Ser	
1				5					10					15		

ctg	ggc	gca	ctg	ctc	tgc	atg	atc	cgc	gtg	tgg	cgt	gaa	gtc	ttc	tgg	96
Leu	Gly	Ala	Leu	Leu	Ser	Met	Ile	Arg	Val	Trp	Arg	Glu	Val	Phe	Trp	
			20					25					30			

ggc	ggc	gca	atg	cac	cag	cgc	ggc	gtc	tgc	ccg	cag	ctg	cgc	atc	agc	144
Gly	Gly	Ala	Met	His	Gln	Arg	Gly	Val	Ser	Pro	Gln	Leu	Arg	Ile	Ser	
		35					40					45				

cca	gca	aaa	atc	gcc	cca	gcg	ctc	agc	ctg	atc	att	tta	tgc	gta	ggc	192
Pro	Ala	Lys	Ile	Ala	Pro	Ala	Leu	Ser	Leu	Ile	Ile	Leu	Ser	Val	Gly	
		50				55					60					

atg	ttc	atc	ttc	gcg	ggc	ccg	ctt	atc	gac	gcg	acc	ctc	acc	gcc	acc	240
Met	Phe	Ile	Phe	Ala	Gly	Pro	Leu	Ile	Asp	Ala	Thr	Leu	Thr	Ala	Thr	
		65			70					75				80		

gac	ggc	ctc	ttg	aac	acc	gat	gca	tac	caa	cag	gct	gtg	ctc	ggc	gaa	288
Asp	Gly	Leu	Leu	Asn	Thr	Asp	Ala	Tyr	Gln	Gln	Ala	Val	Leu	Gly	Glu	
				85				90					95			

aat	gcc	atc	gga	gtg	cca	agc	cct	agc	tac	cag	gga	gga	aac			330
Asn	Ala	Ile	Gly	Val	Pro	Ser	Pro	Ser	Tyr	Gln	Gly	Gly	Asn			
			100					105					110			

taatgcttaa	cgccctgaaa	ttc														353
------------	------------	-----	--	--	--	--	--	--	--	--	--	--	--	--	--	-----

<210> 1832

<211> 110

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1832

Arg	Asn	Ile	Ala	Ala	Trp	Ile	Ala	Ile	Ala	Ala	Ile	Ile	Ile	Ala	Ser
1				5					10					15	

Leu	Gly	Ala	Leu	Leu	Ser	Met	Ile	Arg	Val	Trp	Arg	Glu	Val	Phe	Trp
			20					25					30		

Gly	Gly	Ala	Met	His	Gln	Arg	Gly	Val	Ser	Pro	Gln	Leu	Arg	Ile	Ser
		35					40					45			

Pro	Ala	Lys	Ile	Ala	Pro	Ala	Leu	Ser	Leu	Ile	Ile	Leu	Ser	Val	Gly
		50				55					60				

Met	Phe	Ile	Phe	Ala	Gly	Pro	Leu	Ile	Asp	Ala	Thr	Leu	Thr	Ala	Thr
	65				70				75					80	

Asp	Gly	Leu	Leu	Asn	Thr	Asp	Ala	Tyr	Gln	Gln	Ala	Val	Leu	Gly	Glu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

85

90

95

Asn Ala Ile Gly Val Pro Ser Pro Ser Tyr Gln Gly Gly Asn
 100 105 110

<210> 1833

<211> 393

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(370)

<223> RXA00597

<400> 1833

caaggagatc cgccccagcg atgctgagtg gccaaagtcgc gagatcgctg acaccgcccc 60

aaacaccgtc agccaagaca agaggagatt ttaaacaac atg act gct ttt gga 115
 Met Thr Ala Phe Gly
 1 5

att gtc acc aca gtt ggc atc tgc atg ttt gcg ttc tcc ctc tta tct 163
 Ile Val Thr Thr Val Gly Ile Cys Met Phe Ala Phe Ser Leu Leu Ser
 10 15 20

gcc ctg gtc ctt att ctg cgc acc aaa gat ttc ctc acc cgc gtg gtg 211
 Ala Leu Val Leu Ile Leu Arg Thr Lys Asp Phe Leu Thr Arg Val Val
 25 30 35

ctt tcc gac atg gtt ttc tac tct atg atc gcg atc tac ctc atc tgg 259
 Leu Ser Asp Met Val Phe Tyr Ser Met Ile Ala Ile Tyr Leu Ile Trp
 40 45 50

gtg ctc aac aac cca acc tca atc gcc ttt gag att gct ctt ctc gca 307
 Val Leu Asn Asn Pro Thr Ser Ile Ala Phe Glu Ile Ala Leu Leu Ala
 55 60 65

gca gtc ctc ggc ggc gta ctt cca acc ctg tcc atg gct cgc atc att 355
 Ala Val Leu Gly Gly Val Leu Pro Thr Leu Ser Met Ala Arg Ile Ile
 70 75 80 85

tcg aag gga cgc agg taaatgacca ttccagagat cat 393
 Ser Lys Gly Arg Arg
 90

<210> 1834

<211> 90

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1834

Met Thr Ala Phe Gly Ile Val Thr Thr Val Gly Ile Cys Met Phe Ala
 1 5 10 15

Phe Ser Leu Leu Ser Ala Leu Val Leu Ile Leu Arg Thr Lys Asp Phe
 20 25 30

Leu Thr Arg Val Val Leu Ser Asp Met Val Phe Tyr Ser Met Ile Ala

35

40

45

Ile Tyr Leu Ile Trp Val Leu Asn Asn Pro Thr Ser Ile Ala Phe Glu
50 55 60

Ile Ala Leu Leu Ala Ala Val Leu Gly Gly Val Leu Pro Thr Leu Ser
65 70 75 80

Met Ala Arg Ile Ile Ser Lys Gly Arg Arg
85 90

<210> 1835

<211> 441

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(418)

<223> RXA00598

<400> 1835

aacctcaatc gccttttgaga ttgctcttct cgcagcagtc ctcggcggcg tacttccaac 60

cctgtccatg gctcgcatca ttctgaaggg acgcaggtaa atg acc att cca gag 115
Met Thr Ile Pro Glu
1 5

atc atc gtc tcc atc ctc gtg atc ctc gca ggc ctg ttt tct cta ggt 163
Ile Ile Val Ser Ile Leu Val Ile Leu Ala Gly Leu Phe Ser Leu Gly
10 15 20

act gca atc gct ttg tgg cgc gca ccg gat ctc acc cga gcc aac 211
Thr Ala Ile Ala Leu Trp Arg Ala Pro Asp Pro Leu Thr Arg Ala Asn
25 30 35

ctg ctt ggc acc acc gtg ggt gtc tcc ata ccg ctg ctc atc att gcg 259
Leu Leu Gly Thr Thr Val Gly Val Ser Ile Pro Leu Leu Ile Ile Ala
40 45 50

ctg ctg att cac acc tgg tcc gtc gac gga ttt aac ccc aac aat ttc 307
Leu Leu Ile His Thr Trp Ser Val Asp Gly Phe Asn Pro Asn Asn Phe
55 60 65

atc cga gcg atc atc gcc atc atc ggc gtc tgg gtc atc ggt tcc gtt 355
Ile Arg Ala Ile Ile Ala Ile Ile Gly Val Trp Val Ile Gly Ser Val
70 75 80 85

ggc tcc tac tac atg gga cgc gcc atc tat ggt gtg acc gta gtg gat 403
Gly Ser Tyr Tyr Met Gly Arg Ala Ile Tyr Gly Val Thr Val Val Asp
90 95 100

aac aga cga tcc aaa taaactgctt ttagaaaaaa agg 441
Asn Arg Arg Ser Lys
105

<210> 1836

<211> 106

<212> PRT

<213> Corynebacterium glutamicum

<400> 1836

Met Thr Ile Pro Glu Ile Ile Val Ser Ile Leu Val Ile Leu Ala Gly
 1 5 10 15

Leu Phe Ser Leu Gly Thr Ala Ile Ala Leu Trp Arg Ala Pro Asp Pro
 20 25 30

Leu Thr Arg Ala Asn Leu Leu Gly Thr Thr Val Gly Val Ser Ile Pro
 35 40 45

Leu Leu Ile Ile Ala Leu Leu Ile His Thr Trp Ser Val Asp Gly Phe
 50 55 60

Asn Pro Asn Asn Phe Ile Arg Ala Ile Ile Ala Ile Ile Gly Val Trp
 65 70 75 80

Val Ile Gly Ser Val Gly Ser Tyr Tyr Met Gly Arg Ala Ile Tyr Gly
 85 90 95

Val Thr Val Val Asp Asn Arg Arg Ser Lys
 100 105

<210> 1837

<211> 414

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(391)

<223> RXA00601

<400> 1837

tagatataga acacattcta ttgcagggaa ttatcaagtt tcatacattg tctctgtagg 60

ggcaagtata ttcccatgc aatatttttt aggagtcacca atg cgt ttc aag tca 115
 Met Arg Phe Lys Ser
 1 5

gtt gca gct atc gca ctt tcc acc gca atg atc agg ggt gga acc gca 163
 Val Ala Ala Ile Ala Leu Ser Thr Ala Met Ile Arg Gly Gly Thr Ala
 10 15 20

agc gtt gct aat gct cag cag gtt agc cct agt tcc acg att gag atc 211
 Ser Val Ala Asn Ala Gln Gln Val Ser Pro Ser Ser Thr Ile Glu Ile
 25 30 35

cct caa gaa ttc gtc cac acc gtg cag aac ttc gtg cca ggt atg act 259
 Pro Gln Glu Phe Val His Thr Val Gln Asn Phe Val Pro Gly Met Thr
 40 45 50

tac ggc gat gca ggg tcc gct atc cag agc acc gct ggt tct gtg gca 307
 Tyr Gly Asp Ala Gly Ser Ala Ile Gln Ser Thr Ala Gly Ser Val Ala
 55 60 65

ctg aac agt acc gct gga atc atc ctt cca atc gtt ctt cca ttc ctt 355
 Leu Asn Ser Thr Ala Gly Ile Ile Leu Pro Ile Val Leu Pro Phe Leu
 70 75 80 85

ggt ctg gga gct gtt ggt tct gca gcg ctg tct gct taagcctttt 401
Gly Leu Gly Ala Val Gly Ser Ala Ala Leu Ser Ala
90 95

ctaggttcct taa 414

<210> 1838

<211> 97

<212> PRT

<213> Corynebacterium glutamicum

<400> 1838

Met Arg Phe Lys Ser Val Ala Ala Ile Ala Leu Ser Thr Ala Met Ile
1 5 10 15

Arg Gly Gly Thr Ala Ser Val Ala Asn Ala Gln Gln Val Ser Pro Ser
20 25 30

Ser Thr Ile Glu Ile Pro Gln Glu Phe Val His Thr Val Gln Asn Phe
35 40 45

Val Pro Gly Met Thr Tyr Gly Asp Ala Gly Ser Ala Ile Gln Ser Thr
50 55 60

Ala Gly Ser Val Ala Leu Asn Ser Thr Ala Gly Ile Ile Leu Pro Ile
65 70 75 80

Val Leu Pro Phe Leu Gly Leu Gly Ala Val Gly Ser Ala Ala Leu Ser
85 90 95

Ala

<210> 1839

<211> 876

<212> DNA

<213> *Corynebacterium glutamicum*

 $\langle 220 \rangle$

<221> CDS

<222> (101) .. (853)

<223> RXA00602

<400> 1839

gcgcgatcaa tggaatctag cttcatatat tgcacaatag cctagttgag gtgcgcaaac 60

tggcaacaaa actaccggc aattgtgtga tgattgtagt gtg caa aaa acg caa 115
 Val Gln Lys Thr Gln
 1 5

gag att cat tca agc ctg gag gtg tcg cca tcc aag gca gcc ctg gaa 163
Glu Ile His Ser Ser Leu Glu Val Ser Pro Ser Lys Ala Ala Leu Glu
10 15 20

cca gat gat aaa ggt tat cgg cgc tac gaa atc gcg caa ggt cta aaa 211
Pro Asp Asp Lys Gly Tyr Arg Arg Tyr Glu Ile Ala Gln Gly Leu Lys
25 30 35

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acc tcc ctt gct gca ggt ttg ggc atg tac ccg att ggt att gcg ttt 259
Thr Ser Leu Ala Ala Gly Leu Gly Met Tyr Pro Ile Gly Ile Ala Phe
      40                45                50

ggg ctc ttg gtt att caa tac ggc tac gaa tgg tgg gca gcc cca ctg 307
Gly Leu Leu Val Ile Gln Tyr Gly Tyr Glu Trp Trp Ala Ala Pro Leu
      55                60                65

ttt tcc ggc ctg att ttc gcg ggc tcc acc gaa atg ctg gtc atc gcc 355
Phe Ser Gly Leu Ile Phe Ala Gly Ser Thr Glu Met Leu Val Ile Ala
      70                75                80                85

ctc gtt gtg ggc gca gcg ccc ctg ggc gcc atc gcg ctc acc aca ttg 403
Leu Val Val Gly Ala Ala Pro Leu Gly Ala Ile Ala Leu Thr Thr Leu
      90                95                100

ctg gtg aac ttc cgc cac gta ttc tat gcg ttt tca ttc ccg ctg cat 451
Leu Val Asn Phe Arg His Val Phe Tyr Ala Phe Ser Phe Pro Leu His
      105                110                115

gtg gtc aaa aac ccc att gcc cgt ttc tat tcg gtt ttc gcg ctt atc 499
Val Val Lys Asn Pro Ile Ala Arg Phe Tyr Ser Val Phe Ala Leu Ile
      120                125                130

gac gaa gcc tac gca gtc act gcg gcc agg ccc gca ggc tgg tcg gcg 547
Asp Glu Ala Tyr Ala Val Thr Ala Ala Arg Pro Ala Gly Trp Ser Ala
      135                140                145

tgg cga ctt atc tca atg caa ata gcg ttt cac tcc tac tgg gta ttc 595
Trp Arg Leu Ile Ser Met Gln Ile Ala Phe His Ser Tyr Trp Val Phe
      150                155                160                165

ggc ggt ctc acc gga gtg gcg atc gca gag ttg att cct ttt gaa att 643
Gly Gly Leu Thr Gly Val Ala Ile Ala Glu Leu Ile Pro Phe Glu Ile
      170                175                180

aag ggc ctc gag ttc gcc ctt tgc tct ctc ttt gtc acg ctg act ttg 691
Lys Gly Leu Glu Phe Ala Leu Cys Ser Leu Phe Val Thr Leu Thr Leu
      185                190                195

gat tcc tgc cga acg aaa aag cag atc cct tct ctg ctg ctc gca ggt 739
Asp Ser Cys Arg Thr Lys Lys Gln Ile Pro Ser Leu Leu Leu Ala Gly
      200                205                210

ttg agc ttc acc att gct ctt gtg gta att cca ggt cag gcc cta ttt 787
Leu Ser Phe Thr Ile Ala Leu Val Val Ile Pro Gly Gln Ala Leu Phe
      215                220                225

gcg gcg ctg ctg atc ttc ttg ggt ctg ttg acc atc cgg tac ttc ttc 835
Ala Ala Leu Leu Ile Phe Leu Gly Leu Leu Thr Ile Arg Tyr Phe Phe
      230                235                240                245

ttg gga aag gct gct aaa tgacaactga tttctcctgt att 876
Leu Gly Lys Ala Ala Lys
      250

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<210> 1840

<211> 251

<212> PRT

<213> Corynebacterium glutamicum

<400> 1840

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Val Gln Lys Thr Gln Glu Ile His Ser Ser Leu Glu Val Ser Pro Ser
  1              5              10              15

Lys Ala Ala Leu Glu Pro Asp Asp Lys Gly Tyr Arg Arg Tyr Glu Ile
      20              25              30

Ala Gln Gly Leu Lys Thr Ser Leu Ala Ala Gly Leu Gly Met Tyr Pro
      35              40              45

Ile Gly Ile Ala Phe Gly Leu Leu Val Ile Gln Tyr Gly Tyr Glu Trp
      50              55              60

Trp Ala Ala Pro Leu Phe Ser Gly Leu Ile Phe Ala Gly Ser Thr Glu
      65              70              75              80

Met Leu Val Ile Ala Leu Val Val Gly Ala Ala Pro Leu Gly Ala Ile
      85              90              95

Ala Leu Thr Thr Leu Leu Val Asn Phe Arg His Val Phe Tyr Ala Phe
      100             105             110

Ser Phe Pro Leu His Val Val Lys Asn Pro Ile Ala Arg Phe Tyr Ser
      115             120             125

Val Phe Ala Leu Ile Asp Glu Ala Tyr Ala Val Thr Ala Ala Arg Pro
      130             135             140

Ala Gly Trp Ser Ala Trp Arg Leu Ile Ser Met Gln Ile Ala Phe His
      145             150             155             160

Ser Tyr Trp Val Phe Gly Gly Leu Thr Gly Val Ala Ile Ala Glu Leu
      165             170             175

Ile Pro Phe Glu Ile Lys Gly Leu Glu Phe Ala Leu Cys Ser Leu Phe
      180             185             190

Val Thr Leu Thr Leu Asp Ser Cys Arg Thr Lys Lys Gln Ile Pro Ser
      195             200             205

Leu Leu Leu Ala Gly Leu Ser Phe Thr Ile Ala Leu Val Val Ile Pro
      210             215             220

Gly Gln Ala Leu Phe Ala Ala Leu Leu Ile Phe Leu Gly Leu Leu Thr
      225             230             235             240

Ile Arg Tyr Phe Phe Leu Gly Lys Ala Ala Lys
      245             250

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<210> 1841

<211> 414

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(391)

<223> RXA00604

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<400> 1841
atcacgtttt gctatgaaag tgggtgaaacc agctcgcccc cagggtgtgaa gcattgcattt 60

tgaagcatga atcttttttca tctagtgaag gactgatccc atg cgt atg aaa tca 115
Met Arg Met Lys Ser
1 5

atc gca gca att gca atc gct acc gcc gcc ctg gct ggt ggc act gga 163
Ile Ala Ala Ile Ala Ile Ala Thr Ala Ala Leu Ala Gly Gly Thr Gly
10 15 20

gtc gct agc gca cag gaa gct ggc tcg act gct ggt tcc tcc aac ctc 211
Val Ala Ser Ala Gln Glu Ala Gly Ser Thr Ala Gly Ser Ser Asn Leu
25 30 35

agc tct ggg atc cag ctt cca caa gaa gcc acc gat ctg ttg agc ttc 259
Ser Ser Gly Ile Gln Leu Pro Gln Glu Ala Thr Asp Leu Leu Ser Phe
40 45 50

ctg cct gct gct cag gct gcg cag gtt gaa gga gca att cag agc acc 307
Leu Pro Ala Ala Gln Ala Ala Gln Val Glu Gly Ala Ile Gln Ser Thr
55 60 65

gct ggt ttc ttt gcc gtt gga ctc ggc tcg acc gcc att ggt tcc act 355
Ala Gly Phe Phe Ala Val Gly Leu Gly Ser Thr Ala Ile Gly Ser Thr
70 75 80 85

gca gtg acc ttg gga att gcg gat ctg ctg tct agc taatttcctc 401
Ala Val Thr Leu Gly Ile Ala Asp Leu Leu Ser Ser
90 95

tcaatagctt caa 414

<210> 1842
<211> 97
<212> PRT
<213> Corynebacterium glutamicum

<400> 1842
Met Arg Met Lys Ser Ile Ala Ala Ile Ala Ile Ala Thr Ala Ala Leu
1 5 10 15

Ala Gly Gly Thr Gly Val Ala Ser Ala Gln Glu Ala Gly Ser Thr Ala
20 25 30

Gly Ser Ser Asn Leu Ser Ser Gly Ile Gln Leu Pro Gln Glu Ala Thr
35 40 45

Asp Leu Leu Ser Phe Leu Pro Ala Ala Gln Ala Ala Gln Val Glu Gly
50 55 60

Ala Ile Gln Ser Thr Ala Gly Phe Phe Ala Val Gly Leu Gly Ser Thr
65 70 75 80

Ala Ile Gly Ser Thr Ala Val Thr Leu Gly Ile Ala Asp Leu Leu Ser
85 90 95

Ser

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<210> 1843
 <211> 987
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(964)
 <223> RXA00610

<400> 1843
 caagcactcc caggggaacg ttcattcgaa aaactcgacg ccttatacga gcttctagag 60
 cctcggaacc aattgctcga gatcgcgatc taactagagt atg gaa cgg aaa aaa 115
 Met Glu Pro Lys Lys
 1 5
 cct gtc aca tat aaa gaa ctt gcc cac gaa tat tca aga aga acg ttt 163
 Pro Val Thr Tyr Lys Glu Leu Ala His Glu Tyr Ser Arg Arg Thr Phe
 10 15 20
 aac aaa ctc ttc acc aaa att act ggc ttc gtc tat cta aaa aac gat 211
 Asn Lys Leu Phe Thr Lys Ile Thr Gly Phe Val Tyr Leu Lys Asn Asp
 25 30 35
 cta atc aac gat ccc aac tta gtg acc caa gca ctg ctc aaa aga tgc 259
 Leu Ile Asn Asp Pro Asn Leu Val Thr Gln Ala Leu Leu Lys Arg Cys
 40 45 50
 cca gaa gga gta ctt cgc gga tat gca gca tta aag caa cgt ggc tat 307
 Pro Glu Gly Val Leu Arg Gly Tyr Ala Ala Leu Lys Gln Arg Gly Tyr
 55 60 65
 cag ctt tta gac gat cag tgg atg cca atc atc agt gtt tcc gga gat 355
 Gln Leu Leu Asp Asp Gln Trp Met Pro Ile Ile Ser Val Ser Gly Asp
 70 75 80 85
 cta aac agg agg gac tgc tca cga ggt gaa att ctc agg cgg att gaa 403
 Leu Asn Arg Arg Asp Cys Ser Arg Gly Glu Ile Leu Arg Arg Ile Glu
 90 95 100
 cca gaa aac acc ctg ctc agt ggc aac att agg ttc gtt aat gat gtt 451
 Pro Glu Asn Thr Leu Leu Ser Gly Asn Ile Arg Phe Val Asn Asp Val
 105 110 115
 caa gcg atc caa gac gtc ttc gac ctg cat tct ctc aac gac ttt gaa 499
 Gln Ala Ile Gln Asp Val Phe Asp Leu His Ser Leu Asn Asp Phe Glu
 120 125 130
 gac caa gta gct ctc atc gat cat ctc atc agg cag cgc ccc gaa tta 547
 Asp Gln Val Ala Leu Ile Asp His Leu Ile Arg Gln Arg Pro Glu Leu
 135 140 145
 ttc caa gaa ctc ata caa gag cca aaa ctt aag aaa cac act caa tac 595
 Phe Gln Glu Leu Ile Gln Glu Pro Lys Leu Lys Lys His Thr Gln Tyr
 150 155 160 165
 gcc aat cct ttt gct gaa tct ccg caa gaa tca cga ctt cgg gtc aga 643
 Ala Asn Pro Phe Ala Glu Ser Pro Gln Glu Ser Arg Leu Arg Val Arg
 170 175 180

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ctt cat tca ctg ggt tac cac ggc ttc atc cca cag att cat gtt gaa 691
Leu His Ser Leu Gly Tyr His Gly Phe Ile Pro Gln Ile His Val Glu
      185                      190                      195

tac gac ggt caa tcc tat ttt cta gat ctc gca gat ccg ctg tgg cag 739
Tyr Asp Gly Gln Ser Tyr Phe Leu Asp Leu Ala Asp Pro Leu Trp Gln
      200                      205                      210

gtt gcc ctc gaa tac aac ggc gga tgg cac tac acc tct gag cag cga 787
Val Ala Leu Glu Tyr Asn Gly Gly Trp His Tyr Thr Ser Glu Gln Arg
      215                      220                      225

gag aaa gat tct cat ccg aag aat gct ctg aaa agt gcg gga tgg gat 835
Glu Lys Asp Ser His Arg Lys Asn Ala Leu Lys Ser Ala Gly Trp Asp
      230                      235                      240                      245

gtc cta gaa gtg aca tca aaa act ctg cag aat ccg aat tcc tgg aac 883
Val Leu Glu Val Thr Ser Lys Thr Leu Gln Asn Pro Asn Ser Trp Asn
      250                      255                      260

aac ctg ata caa cag atc aat agc tct ctc cgc cga aag cag gct cag 931
Asn Leu Ile Gln Gln Ile Asn Ser Ser Leu Arg Arg Lys Gln Ala Gln
      265                      270                      275

cga cgc cga agg tta ccc atg caa acg gtg ggc taacggcatc actgaaaaag 984
Arg Arg Arg Arg Leu Pro Met Gln Thr Val Gly
      280                      285

acc 987

<210> 1844
<211> 288
<212> PRT
<213> Corynebacterium glutamicum

<400> 1844
Met Glu Pro Lys Lys Pro Val Thr Tyr Lys Glu Leu Ala His Glu Tyr
  1                      5                      10                      15

Ser Arg Arg Thr Phe Asn Lys Leu Phe Thr Lys Ile Thr Gly Phe Val
  20                      25                      30

Tyr Leu Lys Asn Asp Leu Ile Asn Asp Pro Asn Leu Val Thr Gln Ala
  35                      40                      45

Leu Leu Lys Arg Cys Pro Glu Gly Val Leu Arg Gly Tyr Ala Ala Leu
  50                      55                      60

Lys Gln Arg Gly Tyr Gln Leu Leu Asp Asp Gln Trp Met Pro Ile Ile
  65                      70                      75                      80

Ser Val Ser Gly Asp Leu Asn Arg Arg Asp Cys Ser Arg Gly Glu Ile
  85                      90                      95

Leu Arg Arg Ile Glu Pro Glu Asn Thr Leu Leu Ser Gly Asn Ile Arg
  100                     105                     110

Phe Val Asn Asp Val Gln Ala Ile Gln Asp Val Phe Asp Leu His Ser
  115                     120                     125

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Leu Asn Asp Phe Glu Asp Gln Val Ala Leu Ile Asp His Leu Ile Arg
130 135 140

Gln Arg Pro Glu Leu Phe Gln Glu Leu Ile Gln Glu Pro Lys Leu Lys
145 150 155 160

Lys His Thr Gln Tyr Ala Asn Pro Phe Ala Glu Ser Pro Gln Glu Ser
165 170 175

Arg Leu Arg Val Arg Leu His Ser Leu Gly Tyr His Gly Phe Ile Pro
180 185 190

Gln Ile His Val Glu Tyr Asp Gly Gln Ser Tyr Phe Leu Asp Leu Ala
195 200 205

Asp Pro Leu Trp Gln Val Ala Leu Glu Tyr Asn Gly Gly Trp His Tyr
210 215 220

Thr Ser Glu Gln Arg Glu Lys Asp Ser His Arg Lys Asn Ala Leu Lys
225 230 235 240

Ser Ala Gly Trp Asp Val Leu Glu Val Thr Ser Lys Thr Leu Gln Asn
245 250 255

Pro Asn Ser Trp Asn Asn Leu Ile Gln Gln Ile Asn Ser Ser Leu Arg
260 265 270

Arg Lys Gln Ala Gln Arg Arg Arg Arg Leu Pro Met Gln Thr Val Gly
275 280 285

<210> 1845

<211> 1599

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1576)

<223> RXA00611

<400> 1845

ctttaaattg actatttaca aaactacttg atgagttagc aagagcaccat ttccggtgcgc 60

ctccctgcta aacctcgaaa caataactag attgcacact atg tct gcc gct gct 115
Met Ser Ala Ala Ala
1 5

tct cga tca aga aac atc ttg act gcc ctc ctg cta ttg gtc ccg ctc 163
Ser Arg Ser Arg Asn Ile Leu Thr Ala Leu Leu Leu Val Pro Leu
10 15 20

atc gca ggt acc atc tac gcc tcc gcc atg ggc ttg gac gtc tcc cgc 211
Ile Ala Gly Thr Ile Tyr Ala Ser Ala Met Gly Leu Asp Val Ser Arg
25 30 35

gca tgg tcc tca gca gat gaa gta acg ggg gca cct gca gcc tcc gta 259

Ala	Trp	Ser	Ser	Ala	Asp	Glu	Val	Thr	Gly	Ala	Pro	Ala	Ala	Ser	Val	
		40					45					50				
gcc	acc	aac	aac	cag	gag	ctt	atc	gaa	gcc	cgt	cgc	gcc	gcc	gga	gaa	307
Ala	Thr	Asn	Asn	Gln	Glu	Leu	Ile	Glu	Ala	Arg	Arg	Ala	Ala	Gly	Glu	
		55				60				65						
gcc	ggc	gcc	caa	gcg	ggg	ttc	ctc	acc	tca	gga	act	gaa	gag	cta	acc	355
Ala	Gly	Ala	Gln	Ala	Gly	Phe	Leu	Thr	Ser	Gly	Thr	Glu	Glu	Leu	Thr	
	70				75					80				85		
agc	gga	aca	caa	gag	ctt	atc	gac	ggc	gca	gcc	cca	ctc	gaa	gaa	ggc	403
Ser	Gly	Thr	Gln	Glu	Leu	Ile	Asp	Gly	Ala	Ala	Pro	Leu	Glu	Glu	Gly	
			90					95					100			
gtc	tca	gcc	gcg	gct	gac	ggc	gca	gcg	caa	ctc	cac	gat	ggc	ctc	atc	451
Val	Ser	Ala	Ala	Ala	Asp	Gly	Ala	Ala	Gln	Leu	His	Asp	Gly	Leu	Ile	
			105				110						115			
caa	ctc	cag	gcc	ggc	act	gga	caa	atg	gga	acc	ggc	gcc	acc	gaa	att	499
Gln	Leu	Gln	Ala	Gly	Thr	Gly	Gln	Met	Gly	Thr	Gly	Ala	Thr	Glu	Ile	
		120				125						130				
gcc	gac	ggc	gtc	caa	aac	gca	gtc	gaa	caa	ctt	ggc	ggc	ctt	gtc	gtt	547
Ala	Asp	Gly	Val	Gln	Asn	Ala	Val	Glu	Gln	Leu	Gly	Gly	Leu	Val	Val	
		135				140					145					
gta	cag	cag	caa	ctc	tta	ggc	gcc	ctc	aac	gaa	gca	gac	aaa	caa	ctc	595
Val	Gln	Gln	Gln	Leu	Leu	Gly	Ala	Leu	Asn	Glu	Ala	Asp	Lys	Gln	Leu	
	150				155					160				165		
gcc	tcg	agc	aaa	atc	ccc	gaa	gcc	gaa	gac	ctg	cgc	aaa	caa	atc	acc	643
Ala	Ser	Ser	Lys	Ile	Pro	Glu	Ala	Glu	Asp	Leu	Arg	Lys	Gln	Ile	Thr	
			170					175						180		
gaa	gtc	cga	gga	cac	ctc	gaa	aac	ttc	ggc	atc	tcc	gta	gaa	atg	acc	691
Glu	Val	Arg	Gly	His	Leu	Glu	Asn	Phe	Gly	Ile	Ser	Val	Glu	Met	Thr	
			185					190					195			
gac	caa	ctc	gat	caa	cta	cgt	tcc	ggc	acc	cgc	gac	ctg	gct	aac	caa	739
Asp	Gln	Leu	Asp	Gln	Leu	Arg	Ser	Gly	Thr	Arg	Asp	Leu	Ala	Asn	Gln	
		200				205						210				
ctc	gca	gtc	ccc	ggc	tac	gga	ttc	cac	gat	ggc	att	tac	agc	gcc	acc	787
Leu	Ala	Val	Pro	Gly	Tyr	Gly	Phe	His	Asp	Gly	Ile	Tyr	Ser	Ala	Thr	
		215				220						225				
aat	gga	gca	gcc	gaa	tta	tct	gca	ggc	ttg	caa	gag	cta	gaa	gca	ggc	835
Asn	Gly	Ala	Ala	Glu	Leu	Ser	Ala	Gly	Leu	Gln	Glu	Leu	Glu	Ala	Gly	
	230				235					240				245		
gtt	ggg	act	gcc	gtc	gaa	ggc	ttc	acc	gca	ctc	gat	gaa	ggc	gca	aac	883
Val	Gly	Thr	Ala	Val	Glu	Gly	Phe	Thr	Ala	Leu	Asp	Glu	Gly	Ala	Asn	
			250					255						260		
cga	tta	gac	tcc	atg	gcc	acc	ctc	aac	gaa	gaa	aaa	acc	tcc	gca	gtc	931
Arg	Leu	Asp	Ser	Met	Ala	Thr	Leu	Asn	Glu	Glu	Lys	Thr	Ser	Ala	Val	
			265					270					275			
caa	cga	gcc	ctc	ccg	gta	ccc	caa	gta	ccc	gcc	ggc	aca	atc	gaa	ggc	979
Gln	Arg	Ala	Leu	Pro	Val	Pro	Gln	Val	Pro	Ala	Gly	Thr	Ile	Glu	Gly	

280	285	290	
acc gca gac gaa gaa cgc	acc agc gca cta gcg ccc	atg tac gcc ttc	1027
Thr Ala Asp Glu Glu Arg	Thr Ser Ala Leu Ala Pro	Met Tyr Ala Phe	
295	300	305	
tta att tca gca ttg gtc	atg ctg gcc ggt gca gca	ctt gga tgg gca	1075
Leu Ile Ser Ala Leu Val Met	Leu Ala Gly Ala Leu Gly	Trp Ala	
310	315	320	325
aca cta aaa aac aag tgg	ctg atg gcc ttt gct gtc	att ggt gtc act	1123
Thr Leu Lys Asn Lys Trp	Leu Met Ala Phe Ala Val	Ile Gly Val Thr	
330	335	340	
gca atc ggt ggc att atc	ttg ttc acc gta gct ttg	ggc ata tcc att	1171
Ala Ile Gly Gly Ile Ile	Leu Phe Thr Val Ala Leu	Gly Ile Ser Ile	
345	350	355	
gga gct ttg ttt gga gcc	tta gga att ttg ctt ctt	gcc act gtt gtt	1219
Gly Ala Leu Phe Gly Ala Leu	Gly Ile Leu Leu Leu Ala	Thr Val Val	
360	365	370	
gcc ggt att ctc tcc cgg	att ttg ctt gac gtg ttg	gga act acc ggg	1267
Ala Gly Ile Leu Ser Arg	Ile Leu Leu Asp Val Leu	Gly Thr Thr Gly	
375	380	385	
gct att gtg gtt tct gtt	ctg gga tgg gta gcc	caa gct gca gta att	1315
Ala Ile Val Val Ser Val Leu	Gly Trp Val Ala Gln Ala	Ala Val Ile	
390	395	400	405
ggc cat gta tgg agt gtt	acc gct gta tcc gat	atc gca ctt gtt tgg	1363
Gly His Val Trp Ser Val Thr	Ala Val Ser Asp Ile Ala	Leu Val Trp	
410	415	420	
cga gtc gtc gca ggc atg	atg cca ctg cat tat	cca acc ttt gca gtg	1411
Arg Val Val Ala Gly Met	Met Pro Leu His Tyr Pro	Thr Phe Ala Val	
425	430	435	
acc tcc att ggt aat ggc	gga tca gct gca gct	atc tgg atg tct gtt	1459
Thr Ser Ile Gly Asn Gly Gly	Ser Ala Ala Ala Ile	Trp Met Ser Val	
440	445	450	
gct gtc ttg ttg gca atg	gga gcg atc gga gct	gtt gcg ctt cgg aag	1507
Ala Val Leu Leu Ala Met	Gly Ala Ile Gly Ala Val	Ala Leu Arg Lys	
455	460	465	
cca aag gcg gtt gcg gtt	gag gtt gaa gaa gct	gtt gat gct gat gca	1555
Pro Lys Ala Val Ala Val	Glu Val Glu Glu Val	Asp Ala Asp Ala	
470	475	480	485
gac caa gca gcc tgc gaa	tcc tgatgggtttt	gggtctgattc gac	1599
Asp Gln Ala Ala Ser Glu	Ser		
490			

<210> 1846

<211> 492

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1846

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Leu Leu Val Pro Leu Ile Ala Gly Thr Ile Tyr Ala Ser Ala Met Gly
          20          25          30

Leu Asp Val Ser Arg Ala Trp Ser Ser Ala Asp Glu Val Thr Gly Ala
          35          40          45

Pro Ala Ala Ser Val Ala Thr Asn Asn Gln Glu Leu Ile Glu Ala Arg
          50          55          60

Arg Ala Ala Gly Glu Ala Gly Ala Gln Ala Gly Phe Leu Thr Ser Gly
          65          70          75          80

Thr Glu Glu Leu Thr Ser Gly Thr Gln Glu Leu Ile Asp Gly Ala Ala
          85          90          95

Pro Leu Glu Glu Gly Val Ser Ala Ala Ala Asp Gly Ala Ala Gln Leu
          100          105          110

His Asp Gly Leu Ile Gln Leu Gln Ala Gly Thr Gly Gln Met Gly Thr
          115          120          125

Gly Ala Thr Glu Ile Ala Asp Gly Val Gln Asn Ala Val Glu Gln Leu
          130          135          140

Gly Gly Leu Val Val Val Gln Gln Gln Leu Leu Gly Ala Leu Asn Glu
          145          150          155          160

Ala Asp Lys Gln Leu Ala Ser Ser Lys Ile Pro Glu Ala Glu Asp Leu
          165          170          175

Arg Lys Gln Ile Thr Glu Val Arg Gly His Leu Glu Asn Phe Gly Ile
          180          185          190

Ser Val Glu Met Thr Asp Gln Leu Asp Gln Leu Arg Ser Gly Thr Arg
          195          200          205

Asp Leu Ala Asn Gln Leu Ala Val Pro Gly Tyr Gly Phe His Asp Gly
          210          215          220

Ile Tyr Ser Ala Thr Asn Gly Ala Ala Glu Leu Ser Ala Gly Leu Gln
          225          230          235          240

Glu Leu Glu Ala Gly Val Gly Thr Ala Val Glu Gly Phe Thr Ala Leu
          245          250          255

Asp Glu Gly Ala Asn Arg Leu Asp Ser Met Ala Thr Leu Asn Glu Glu
          260          265          270

Lys Thr Ser Ala Val Gln Arg Ala Leu Pro Val Pro Gln Val Pro Ala
          275          280          285

Gly Thr Ile Glu Gly Thr Ala Asp Glu Glu Arg Thr Ser Ala Leu Ala
          290          295          300

Pro Met Tyr Ala Phe Leu Ile Ser Ala Leu Val Met Leu Ala Gly Ala
          305          310          315          320

Ala Leu Gly Trp Ala Thr Leu Lys Asn Lys Trp Leu Met Ala Phe Ala

```

11

gtg att gct cgt gag att aag aag cgt cgc gag tcc gct gag gtg tac 307
Val Ile Ala Arg Glu Ile Lys Lys Arg Arg Glu Ser Ala Glu Val Tyr
55 60 65

acc gaa aat ggt cgt cag gaa ttg gct gac gtt gag ctt aaa gag gct 355
Thr Glu Asn Gly Arg Gln Glu Leu Ala Asp Val Glu Leu Lys Glu Ala
70 75 80 85

gcc att ttg gag ggc tac cag cct gag cag ctt gat gat gat cag ctg 403
Ala Ile Leu Glu Gly Tyr Gln Pro Glu Gln Leu Asp Asp Asp Gln Leu
90 95 100

aac gcg ctg atc gat gag gct atc gct gaa gtc ggc ggc gag gcc gat 451
Asn Ala Leu Ile Asp Glu Ala Ile Ala Glu Val Gly Gly Glu Ala Asp
105 110 115

atg aag aag atg ggc cag atc atg aag gct gct acc gct aag gct gct 499
Met Lys Lys Met Gly Gln Ile Met Lys Ala Ala Thr Ala Lys Ala Ala
120 125 130

ggc cgt gca gat gga aaa cga ctc tcc acc gca gtg aag agc cgt ttg 547
Gly Arg Ala Asp Gly Lys Arg Leu Ser Thr Ala Val Lys Ser Arg Leu
135 140 145

agc aac taggtatttc tagcggaaga act 576
Ser Asn
150

<210> 1848

<211> 151

<212> PRT

<213> Corynebacterium glutamicum

<400> 1848

Met Ser Glu Leu Lys Asp Lys Ile Arg Ala Asp Leu Thr Thr Ala Met
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Lys Ala Arg Asp Lys Asp Thr Thr Gly Thr Leu Arg Met Leu Ser
20 25 30

Ala Leu Thr Gln Glu Glu Thr Ser Gly Thr Lys His Glu Leu Asn Asp
35 40 45

Glu Glu Val Leu Lys Val Ile Ala Arg Glu Ile Lys Lys Arg Arg Glu
50 55 60

Ser Ala Glu Val Tyr Thr Glu Asn Gly Arg Gln Glu Leu Ala Asp Val
65 70 75 80

Glu Leu Lys Glu Ala Ala Ile Leu Glu Gly Tyr Gln Pro Glu Gln Leu
85 90 95

Asp Asp Asp Gln Leu Asn Ala Leu Ile Asp Glu Ala Ile Ala Glu Val
100 105 110

Gly Gly Glu Ala Asp Met Lys Lys Met Gly Gln Ile Met Lys Ala Ala
115 120 125

Thr Ala Lys Ala Ala Gly Arg Ala Asp Gly Lys Arg Leu Ser Thr Ala

130

135

140

Val Lys Ser Arg Leu Ser Asn
145 150

<210> 1849

<211> 1038

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1015)

<223> RXA00614

<400> 1849

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ttagttcact catgtttgcc cagagtactc cccaggtagg gtg aat aag gtg tca 115
Val Asn Lys Val Ser
1 5

act atc gct aaa aca ctc act ttt tca agt gca gcc cta ctc gga gct 163
Thr Ile Ala Lys Thr Leu Thr Phe Ser Ser Ala Ala Leu Leu Gly Ala
10 15 20

ggg atc gcc acc gct gca tgg gga tac tca gag ctc aaa aaa ttc gag 211
Gly Ile Ala Thr Ala Ala Trp Gly Tyr Ser Glu Leu Lys Lys Phe Glu
25 30 35

ctc aaa aca gta gaa ctg cca att ttg aag cct gga acg ctc cgt gga 259
Leu Lys Thr Val Glu Leu Pro Ile Leu Lys Pro Gly Thr Leu Arg Gly
40 45 50

aag aag gaa ttc cgc ctt ctc cac atc tct gat ctc cac atg atc cca 307
Lys Lys Glu Phe Arg Leu Leu His Ile Ser Asp Leu His Met Ile Pro
55 60 65

ggc caa gaa acc aaa aaa gca tgg gtc tcc gca ctc gat tca cta agc 355
Gly Gln Glu Thr Lys Lys Ala Trp Val Ser Ala Leu Asp Ser Leu Ser
70 75 80 85

ccc gat ttg gtg atc aac acc ggt gac aac ctt agc gat gaa aaa gca 403
Pro Asp Leu Val Ile Asn Thr Gly Asp Asn Leu Ser Asp Glu Lys Ala
90 95 100

gtc ccc gac gtc ctc cgc gca ctc ggc cca ctg atg aac cgc ccc ggc 451
Val Pro Asp Val Leu Arg Ala Leu Gly Pro Leu Met Asn Arg Pro Gly
105 110 115

gcg ttc gtc ttc gga acc aac gat tac tgg gca ccc cgc ccc gtc aat 499
Ala Phe Val Phe Gly Thr Asn Asp Tyr Trp Ala Pro Arg Pro Val Asn
120 125 130

cct ttc ggc tac ctc ttc ggt aaa aaa cgc gaa gtg agc cac atc gac 547
Pro Phe Gly Tyr Leu Phe Gly Lys Lys Arg Glu Val Ser His Ile Asp
135 140 145

ctc ccc tgg cga gcc atg cga gct gct ttc atc gaa cac gga tgg caa 595
Leu Pro Trp Arg Ala Met Arg Ala Ala Phe Ile Glu His Gly Trp Gln

150	155	160	165	
gac gcc aac caa aag cga ctc gaa ttc caa gta ggt tcc gtc cgc ctc				643
Asp Ala Asn Gln Lys Arg Leu Glu Phe Gln Val Gly Ser Val Arg Leu				
170		175	180	
gcc atc tca ggt gtt gat gac ccc cac cat gac ctc gac gac tac aca				691
Ala Ile Ser Gly Val Asp Asp Pro His His Asp Leu Asp Asp Tyr Thr				
185	190		195	
gag atc gca ggg gca cca aac gtg gac gct gat ctg tcc ata cgc ttg				739
Glu Ile Ala Gly Ala Pro Asn Val Asp Ala Asp Leu Ser Ile Ala Leu				
200	205		210	
ctt cac gca cca gaa cct cga gtc ctc gct cag ttc gaa gcc gac ggc				787
Leu His Ala Pro Glu Pro Arg Val Leu Ala Gln Phe Glu Ala Asp Gly				
215	220		225	
tac cag ctt tcc ctc tcc ggc cac acc cac ggc ggt cag ctt tgt ctt				835
Tyr Gln Leu Ser Leu Ser Gly His Thr His Gly Gly Gln Leu Cys Leu				
230	235	240	245	
ccg ggc agc aag cca att gtc acc aac tgt gga atc gac cgc aaa cgc				883
Pro Gly Ser Lys Pro Ile Val Thr Asn Cys Gly Ile Asp Arg Lys Arg				
250	255		260	
gcc acc ggc ctc aac aaa ttt ggc gac atg tgg atg cac gtt tcc aac				931
Ala Thr Gly Leu Asn Lys Phe Gly Asp Met Trp Met His Val Ser Asn				
265	270		275	
ggc ctc ggc acc tca aaa ttc gtc cca ttc cgc atc ttc tgc cga ccc				979
Gly Leu Gly Thr Ser Lys Phe Val Pro Phe Arg Ile Phe Cys Arg Pro				
280	285		290	
agc gcc acc cta ata aag atc act gaa cag gca ctt tgacctgaaa				1025
Ser Ala Thr Leu Ile Lys Ile Thr Glu Gln Ala Leu				
295	300		305	
aaccacagg act				1038
 <210> 1850				
<211> 305				
<212> PRT				
<213> Corynebacterium glutamicum				
 <400> 1850				
Val Asn Lys Val Ser Thr Ile Ala Lys Thr Leu Thr Phe Ser Ser Ala				
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Ala Leu Leu Gly Ala Gly Ile Ala Thr Ala Ala Trp Gly Tyr Ser Glu				
20	25		30	
Leu Lys Lys Phe Glu Leu Lys Thr Val Glu Leu Pro Ile Leu Lys Pro				
35	40		45	
Gly Thr Leu Arg Gly Lys Lys Glu Phe Arg Leu Leu His Ile Ser Asp				
50	55	60		
Leu His Met Ile Pro Gly Gln Glu Thr Lys Lys Ala Trp Val Ser Ala				
65	70	75	80	


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Leu Asp Ser Leu Ser Pro Asp Leu Val Ile Asn Thr Gly Asp Asn Leu
      85                      90
Ser Asp Glu Lys Ala Val Pro Asp Val Leu Arg Ala Leu Gly Pro Leu
      100                    105
Met Asn Arg Pro Gly Ala Phe Val Phe Gly Thr Asn Asp Tyr Trp Ala
      115                    120
Pro Arg Pro Val Asn Pro Phe Gly Tyr Leu Phe Gly Lys Lys Arg Glu
      130                    140
Val Ser His Ile Asp Leu Pro Trp Arg Ala Met Arg Ala Ala Phe Ile
      145                    150
Glu His Gly Trp Gln Asp Ala Asn Gln Lys Arg Leu Glu Phe Gln Val
      165                    170
Gly Ser Val Arg Leu Ala Ile Ser Gly Val Asp Asp Pro His His Asp
      180                    185
Leu Asp Asp Tyr Thr Glu Ile Ala Gly Ala Pro Asn Val Asp Ala Asp
      195                    200
Leu Ser Ile Ala Leu Leu His Ala Pro Glu Pro Arg Val Leu Ala Gln
      210                    215
Phe Glu Ala Asp Gly Tyr Gln Leu Ser Leu Ser Gly His Thr His Gly
      225                    230
Gly Gln Leu Cys Leu Pro Gly Ser Lys Pro Ile Val Thr Asn Cys Gly
      245                    250
Ile Asp Arg Lys Arg Ala Thr Gly Leu Asn Lys Phe Gly Asp Met Trp
      260                    265
Met His Val Ser Asn Gly Leu Gly Thr Ser Lys Phe Val Pro Phe Arg
      275                    280
Ile Phe Cys Arg Pro Ser Ala Thr Leu Ile Lys Ile Thr Glu Gln Ala
      290                    300

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Leu
305

<210> 1851
 <211> 1183
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1183)
 <223> RXA00617

<400> 1851
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230	235	240	245	
gat gat gcc ggc cac gag ctg cgc acc ccg atc aca gtg gtg cgt ggc				883
Asp Asp Ala Gly His Glu Leu Arg Thr Pro Ile Thr Val Val Arg Gly				
	250	255	260	
cag tta gag ctt ctc gcc acc acc ccg ccg gag gaa caa cgc cgg tcg				931
Gln Leu Glu Leu Leu Ala Thr Thr Pro Pro Glu Glu Gln Ala Arg Ser				
	265	270	275	
att gag ctg gcc acc act gag ttg gat cga atg tcg cga atg gtc aat				979
Ile Glu Leu Ala Thr Thr Glu Leu Asp Arg Met Ser Arg Met Val Asn				
	280	285	290	
gat ctg ctc acc ctc gca gtc gcc gat tct ggc acc ttc atc cac gcc				1027
Asp Leu Leu Thr Leu Ala Val Ala Asp Ser Gly Thr Phe Ile His Ala				
	295	300	305	
cac ccc acg gat gtc acg gat tta aca atc gat atc gaa gac aaa gcc				1075
His Pro Thr Asp Val Thr Asp Leu Thr Ile Asp Ile Glu Asp Lys Ala				
	310	315	320	325
cgc acc atc agc gac cga att ttg ctt gtc gac gcc gcc gag ggc ctc				1123
Arg Thr Ile Ser Asp Arg Ile Leu Leu Val Asp Ala Ala Glu Gly Leu				
	330	335	340	
gtc agc ctc gac gag cag cgg gtc acc gag gca gtg ctg gag ttg ttc				1171
Val Ser Leu Asp Glu Gln Arg Val Thr Glu Ala Val Leu Glu Leu Phe				
	345	350	355	
ggc aat gcg ttg				1183
Gly Asn Ala Leu				
	360			
<210> 1852				
<211> 361				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 1852				
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1 5 10 15				
Arg Ser Val Leu Leu Ser Glu Val Thr Asn Thr Ala Asn Ser Ala Val				
20 25 30				
Glu Gln Glu Ile Glu Glu Phe Arg Arg Phe Ala Ala Glu Gly Ile Asp				
35 40 45				
Pro Thr Thr Ala Gln Pro Phe Glu Ser Gly His Arg Leu Met Glu Val				
50 55 60				
Tyr Leu Ser Arg Gln Ile Pro Asp Glu Asn Glu Ala Ile Val Gly Ile				
65 70 75 80				
Phe Pro Gly Glu Leu Ile Gln Val Asp Tyr Ser Gln Leu Ser Gly Ala				
85 90 95				
His Pro Leu Pro Leu Glu His Ser Asp Pro Leu Ile Ser Glu Ile Arg				
100 105 110				

Gln Thr Thr Leu Asn Ser Gly Val Phe Ser Asp Leu Glu Arg Gly Thr
 115 120 125
 Thr His Trp Gly Lys Val Asn Phe Gln Thr Ala Ser Gly Glu Ala Asp
 130 135 140
 Gly Glu Phe Val Val Ala Phe Phe Ala Asp Asn Leu Lys Asp Gln Val
 145 150 155 160
 Asn Gly Gln Ile Gln Ile Leu Ile Leu Ile Gly Thr Gly Gly Leu Ile
 165 170 175
 Ala Ser Ile Leu Ile Ala Trp Leu Ile Ala Gly Gln Ile Ile Ala Pro
 180 185 190
 Ile Arg Lys Leu Ser Ser Val Ser Ala Lys Ile Ser Asn Ser Asp Leu
 195 200 205
 Thr Trp Arg Val Pro Val Glu Gly Arg Asp Glu Ile Ala Gln Leu Ala
 210 215 220
 Arg Thr Phe Asn Ala Met Leu Asp Arg Ile Glu Ile Ala Tyr Asn Asp
 225 230 235 240
 Gln Arg Gln Phe Val Asp Asp Ala Gly His Glu Leu Arg Thr Pro Ile
 245 250 255
 Thr Val Val Arg Gly Gln Leu Glu Leu Leu Ala Thr Thr Pro Glu
 260 265 270
 Glu Gln Ala Arg Ser Ile Glu Leu Ala Thr Thr Glu Leu Asp Arg Met
 275 280 285
 Ser Arg Met Val Asn Asp Leu Leu Thr Leu Ala Val Ala Asp Ser Gly
 290 295 300
 Thr Phe Ile His Ala His Pro Thr Asp Val Thr Asp Leu Thr Ile Asp
 305 310 315 320
 Ile Glu Asp Lys Ala Arg Thr Ile Ser Asp Arg Ile Leu Leu Val Asp
 325 330 335
 Ala Ala Glu Gly Leu Val Ser Leu Asp Glu Gln Arg Val Thr Glu Ala
 340 345 350
 Val Leu Glu Leu Phe Gly Asn Ala Leu
 355 360

<210> 1853

<211> 531

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(508)

<223> RXA00628

<400> 1853

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aacctcaatt tggttgcacg ccaagtagta gtctgtgcat atg gct tct gta ttc 115
Met Ala Ser Val Phe
1 5
acg aaa att att aat ggc gag ctc ccc ggc cga ttt gtg tat cgt tcc 163
Thr Lys Ile Ile Asn Gly Glu Leu Pro Gly Arg Phe Val Tyr Arg Ser
10 15 20
gag aat gtc gtg gct ttt cta tcc atc gaa ccc ctc acc tac ggc cac 211
Glu Asn Val Val Ala Phe Leu Ser Ile Glu Pro Leu Thr Tyr Gly His
25 30 35
acc cta gtc gta ccc gtt gca gaa gtt gac cgc tgg acc gac ctt cct 259
Thr Leu Val Val Pro Val Ala Glu Val Asp Arg Trp Thr Asp Leu Pro
40 45 50
cag aac atc tgg agc gaa gta aac gag gcc tcc cag ctc atc gga aat 307
Gln Asn Ile Trp Ser Glu Val Asn Glu Ala Ser Gln Leu Ile Gly Asn
55 60 65
gca atc cgc aca gca ttc gac gcc cct cga tgt ggt tac atc atc gca 355
Ala Ile Arg Thr Ala Phe Asp Ala Pro Arg Cys Gly Tyr Ile Ile Ala
70 75 80 85
gga ttc gat gtt ccc cac act cac atc cac ctc ttc ccc acc gac aaa 403
Gly Phe Asp Val Pro His Thr His Ile Leu Phe Pro Thr Asp Lys
90 95 100
atg gcc gat tac gat ttc cgc aac gcc atg gcc gca gac gcc acc gac 451
Met Ala Asp Tyr Asp Phe Arg Asn Ala Met Ala Ala Asp Ala Thr Asp
105 110 115
cct gca aaa atg gat gaa gct gca gag aag atc cgc gaa gcg ctg gac 499
Pro Ala Lys Met Asp Glu Ala Ala Glu Lys Ile Arg Glu Ala Leu Asp
120 125 130
ggt ctg gtc tagttcttgt agttctaatt gct 531
Gly Leu Val
135

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<210> 1854

<211> 136

<212> PRT

<213> Corynebacterium glutamicum

<400> 1854

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Met Ala Ser Val Phe Thr Lys Ile Ile Asn Gly Glu Leu Pro Gly Arg
1 5 10 15

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Phe Val Tyr Arg Ser Glu Asn Val Val Ala Phe Leu Ser Ile Glu Pro
20 25 30

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```

Leu Thr Tyr Gly His Thr Leu Val Val Pro Val Ala Glu Val Asp Arg
35 40 45

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Trp Thr Asp Leu Pro Gln Asn Ile Trp Ser Glu Val Asn Glu Ala Ser
50 55 60

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Gln Leu Ile Gly Asn Ala Ile Arg Thr Ala Phe Asp Ala Pro Arg Cys
65 70 75 80

Gly Tyr Ile Ile Ala Gly Phe Asp Val Pro His Thr His Ile His Leu
85 90 95

Phe Pro Thr Asp Lys Met Ala Asp Tyr Asp Phe Arg Asn Ala Met Ala
100 105 110

Ala Asp Ala Thr Asp Pro Ala Lys Met Asp Glu Ala Ala Glu Lys Ile
115 120 125

Arg Glu Ala Leu Asp Gly Leu Val
130 135

<210> 1855

<211> 1578

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1555)

<223> RXA00631

<400> 1855

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ttggatatgt tctgcgccacc ccacgtagct aaattctcct atg gaa aat cct tat 115
Met Glu Asn Pro Tyr
1 5

gtt gct gcg ctc gat gac gaa aac caa gaa gtc ggc gta aaa aaa gaa 163
Val Ala Ala Leu Asp Asp Glu Asn Gln Glu Val Gly Val Lys Lys Glu
10 15 20

gca gaa aaa gaa cct gaa ata ggt ccc atc aga gct gcc gga cga gcc 211
Ala Glu Lys Glu Pro Glu Ile Gly Pro Ile Arg Ala Ala Gly Arg Ala
25 30 35

ata ccg ctg cgc acc cgc atc att ttg atc gtg gtg ggt atc gcc ggg 259
Ile Pro Leu Arg Thr Arg Ile Ile Leu Ile Val Val Gly Ile Ala Gly
40 45 50

ctt ggt ttg ctg gtc aac gcg att gct gtc tcc agc ctc atg cgt gaa 307
Leu Gly Leu Leu Val Asn Ala Ile Ala Val Ser Ser Leu Met Arg Glu
55 60 65

gtt tcc tat acc cgc atg gat caa gag cta gag acc tcg atg ggg acg 355
Val Ser Tyr Thr Arg Met Asp Gln Glu Leu Glu Thr Ser Met Gly Thr
70 75 80 85

tgg gcg cat aac gtt gag ctg ttt aat ttc gat ggc gtc cgc caa ggg 403
Trp Ala His Asn Val Glu Leu Phe Asn Phe Asp Gly Val Arg Gln Gly
90 95 100

cca ccc agc gat tat tat gtg gcc aag gtt ttt cct gat gga tcc agc 451
Pro Pro Ser Asp Tyr Tyr Val Ala Lys Val Phe Pro Asp Gly Ser Ser
105 110 115

atc atc ttc aac gat gca caa tcg gca ccc gat cta gct gaa acc acc 499
 Ile Ile Phe Asn Asp Ala Gln Ser Ala Pro Asp Leu Ala Glu Thr Thr
 120 125 130

atc ggt act ggt cca cac act gtg gat gct gct agc ggt tct gcc tcc 547
 Ile Gly Thr Gly Pro His Thr Val Asp Ala Ala Ser Gly Ser Ala Ser
 135 140 145

aac act ccg tgg cgt gtg atg gcg gaa aag aac ggt gac att atc acc 595
 Asn Thr Pro Trp Arg Val Met Ala Glu Lys Asn Gly Asp Ile Ile Thr
 150 155 160 165

gtg gtg ggt aaa agc atg ggg cgt gaa aca aac ctg ctg tac cga ttg 643
 Val Val Gly Lys Ser Met Gly Arg Glu Thr Asn Leu Leu Tyr Arg Leu
 170 175 180

gtg atg gtg cag atg atc atc ggc gcg ctg att ctg gtt gct att ttg 691
 Val Met Val Gln Met Ile Ile Gly Ala Leu Ile Leu Val Ala Ile Leu
 185 190 195

att act tca ctc ttc cta gtc aga cgc tcg ttg cgg ccg ttg aga gaa 739
 Ile Thr Ser Leu Phe Leu Val Arg Arg Ser Leu Arg Pro Leu Arg Glu
 200 205 210

gtt gaa gag acc gcc acc agg att gcg ggc ggt gat ttg gat cga cgt 787
 Val Glu Glu Thr Ala Thr Arg Ile Ala Gly Gly Asp Leu Asp Arg Arg
 215 220 225

gtc ccg cag tgg cca atg acc aca gaa gtc gga cag ctg tcg aat gcc 835
 Val Pro Gln Trp Pro Met Thr Thr Glu Val Gly Gln Leu Ser Asn Ala
 230 235 240 245

ctc aat atc atg ttg gag cag ctc caa gcc tca att ctg acc gcc cag 883
 Leu Asn Ile Met Leu Glu Gln Leu Gln Ala Ser Ile Leu Thr Ala Gln
 250 255 260

caa aaa gaa gct cag atg cgc cga ttc gtt ggc gat gcc tcc cac gag 931
 Gln Lys Glu Ala Gln Met Arg Arg Phe Val Gly Asp Ala Ser His Glu
 265 270 275

ctc cgc aca cca ctg acc tct gtg aag ggc ttc acc gag ctg tat tca 979
 Leu Arg Thr Pro Leu Thr Ser Val Lys Gly Phe Thr Glu Leu Tyr Ser
 280 285 290

tca ggt gca aca gat gat gcc aac tgg gtc atg tcc aag atc ggt ggc 1027
 Ser Gly Ala Thr Asp Asp Ala Asn Trp Val Met Ser Lys Ile Gly Gly
 295 300 305

gaa gcc caa cgc atg agt gtg ctt gtg gaa gac ctc ctg tca ctg acg 1075
 Glu Ala Gln Arg Met Ser Val Leu Val Glu Asp Leu Leu Ser Leu Thr
 310 315 320 325

cgt gcc gaa ggc cag caa atg gag aag cac cgc gtt gac gtg ctg gaa 1123
 Arg Ala Glu Gly Gln Gln Met Glu Lys His Arg Val Asp Val Leu Glu
 330 335 340

ctc gcc ttg gca gta cgc gga tcc atg cga gca gcc tgg cca gat cgc 1171
 Leu Ala Leu Ala Val Arg Gly Ser Met Arg Ala Ala Trp Pro Asp Arg
 345 350 355

aca gtc aat gta tcc aac aaa gct gag tcc att ccg gtt gtc aaa ggc 1219

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Thr Val Asn Val Ser Asn Lys Ala Glu Ser Ile Pro Val Val Lys Gly
      360                      365                      370

gac cca act cgc ctc cac caa gtg ctt acc aac ctg gtt gcc aac gga 1267
Asp Pro Thr Arg Leu His Gln Val Leu Thr Asn Leu Val Ala Asn Gly
      375                      380                      385

cta aac cac ggc gga ccg gac gcg gaa gtc agc att gag atc aac acc 1315
Leu Asn His Gly Gly Pro Asp Ala Glu Val Ser Ile Glu Ile Asn Thr
      390                      395                      400                      405

gat gga caa aac gtg agg att ctc gtg gca gac aac ggt gtc gga atg 1363
Asp Gly Gln Asn Val Arg Ile Leu Val Ala Asp Asn Gly Val Gly Met
      410                      415

tct gaa gaa gat gct cag cat atc ttc gag cgt ttc tac cgc gcc gat 1411
Ser Glu Glu Asp Ala Gln His Ile Phe Glu Arg Phe Tyr Arg Ala Asp
      425                      430                      435

tcc tcc cgc tca cgc gca tcc ggc gga tcg ggc ctc ggc ctt gcg atc 1459
Ser Ser Arg Ser Arg Ala Ser Gly Gly Ser Gly Leu Gly Leu Ala Ile
      440                      445                      450

acg aaa tcc ctg gtc gaa ggc cac ggc ggc aca gtc acc gtc gac agc 1507
Thr Lys Ser Leu Val Glu Gly His Gly Gly Thr Val Thr Val Asp Ser
      455                      460                      465

gtg caa ggc gaa ggc acg gtg ttc acg atc acc ttg ccg gcg gtt tct 1555
Val Gln Gly Glu Gly Thr Val Phe Thr Ile Thr Leu Pro Ala Val Ser
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taaaggccatc aagggccgga aaa 1578

<210> 1856
<211> 485
<212> PRT
<213> Corynebacterium glutamicum

<400> 1856
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Gly Val Lys Lys Glu Ala Glu Lys Glu Pro Glu Ile Gly Pro Ile Arg
      20                      25                      30

Ala Ala Gly Arg Ala Ile Pro Leu Arg Thr Arg Ile Ile Leu Ile Val
      35                      40                      45

Val Gly Ile Ala Gly Leu Gly Leu Leu Val Asn Ala Ile Ala Val Ser
      50                      55                      60

Ser Leu Met Arg Glu Val Ser Tyr Thr Arg Met Asp Gln Glu Leu Glu
      65                      70                      75                      80

Thr Ser Met Gly Thr Trp Ala His Asn Val Glu Leu Phe Asn Phe Asp
      85                      90                      95

Gly Val Arg Gln Gly Pro Pro Ser Asp Tyr Tyr Val Ala Lys Val Phe
      100                      105                      110

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Pro Asp Gly Ser Ser Ile Ile Phe Asn Asp Ala Gln Ser Ala Pro Asp
 115 120 125
 Leu Ala Glu Thr Thr Ile Gly Thr Gly Pro His Thr Val Asp Ala Ala
 130 135 140
 Ser Gly Ser Ala Ser Asn Thr Pro Trp Arg Val Met Ala Glu Lys Asn
 145 150 155 160
 Gly Asp Ile Ile Thr Val Val Gly Lys Ser Met Gly Arg Glu Thr Asn
 165 170 175
 Leu Leu Tyr Arg Leu Val Met Val Gln Met Ile Ile Gly Ala Leu Ile
 180 185 190
 Leu Val Ala Ile Leu Ile Thr Ser Leu Phe Leu Val Arg Arg Ser Leu
 195 200 205
 Arg Pro Leu Arg Glu Val Glu Glu Thr Ala Thr Arg Ile Ala Gly Gly
 210 215 220
 Asp Leu Asp Arg Arg Val Pro Gln Trp Pro Met Thr Thr Glu Val Gly
 225 230 235 240
 Gln Leu Ser Asn Ala Leu Asn Ile Met Leu Glu Gln Leu Gln Ala Ser
 245 250 255
 Ile Leu Thr Ala Gln Gln Lys Glu Ala Gln Met Arg Arg Phe Val Gly
 260 265 270
 Asp Ala Ser His Glu Leu Arg Thr Pro Leu Thr Ser Val Lys Gly Phe
 275 280 285
 Thr Glu Leu Tyr Ser Ser Gly Ala Thr Asp Asp Ala Asn Trp Val Met
 290 295 300
 Ser Lys Ile Gly Gly Glu Ala Gln Arg Met Ser Val Leu Val Glu Asp
 305 310 315 320
 Leu Leu Ser Leu Thr Arg Ala Glu Gly Gln Met Glu Lys His Arg
 325 330 335
 Val Asp Val Leu Glu Leu Ala Leu Ala Val Arg Gly Ser Met Arg Ala
 340 345 350
 Ala Trp Pro Asp Arg Thr Val Asn Val Ser Asn Lys Ala Glu Ser Ile
 355 360 365
 Pro Val Val Lys Gly Asp Pro Thr Arg Leu His Gln Val Leu Thr Asn
 370 375 380
 Leu Val Ala Asn Gly Leu Asn His Gly Gly Pro Asp Ala Glu Val Ser
 385 390 395 400
 Ile Glu Ile Asn Thr Asp Gly Gln Asn Val Arg Ile Leu Val Ala Asp
 405 410 415
 Asn Gly Val Gly Met Ser Glu Glu Asp Ala Gln His Ile Phe Glu Arg
 420 425 430
 Phe Tyr Arg Ala Asp Ser Ser Arg Ser Arg Ala Ser Gly Gly Ser Gly

[illegible]

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tgg ggc gac acc ccg gag tgg aaa gaa tcc caa aag atc cag gag aag      547
Trp Gly Asp Thr Pro Glu Trp Lys Glu Ser Gln Lys Ile Gln Glu Lys
    135                      140                      145

atg acc aag gag gat ttt cag agg gcg aaa gat gaa cat gag ggg ttc      595
Met Thr Lys Glu Asp Phe Gln Arg Ala Lys Asp Glu His Glu Gly Phe
    150                      155                      160                      165

gtc gaa aag ctt atc gac gcc tcc ctg cgc ggc atc gcg ccc ggc tct      643
Val Glu Lys Leu Ile Asp Ala Ser Leu Arg Gly Ile Ala Pro Gly Ser
    170                      175                      180

gca gag ggc aat gag cta gcg ctt gcg cac gcg gca agc atc ggt cag      691
Ala Glu Gly Asn Glu Leu Ala Leu Ala His Arg Ala Ser Ile Gly Gln
    185                      190                      195

tgg tac acc gtg agt gca aac aag caa gta att ttg gct cgg atg tac      739
Trp Tyr Thr Val Ser Ala Asn Lys Gln Val Ile Leu Ala Arg Met Tyr
    200                      205                      210

gtg gaa gac gag cgt ttt aac gaa act tac aaa gga cac gcc tca tat      787
Val Glu Asp Glu Arg Phe Asn Glu Thr Tyr Lys Gly His Ala Ser Tyr
    215                      220                      225

ctt tta aca ctt att gaa gca ttg gcg cag gta gaa ggc gtg gac ttg      835
Leu Leu Thr Leu Ile Glu Ala Leu Ala Gln Val Glu Gly Val Asp Leu
    230                      235                      240                      245

gag aat gtg gag tgg gaa taatcccaat ttcaactcct tca                      876
Glu Asn Val Glu Trp Glu
    250

<210> 1858
<211> 251
<212> PRT
<213> Corynebacterium glutamicum

<400> 1858
Met Thr Asp Arg Thr Ile Gly Glu Ala Ala Glu Leu Leu Gly Val Thr
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Thr Arg Thr Leu Arg His Trp Asp Ser Ile Gly Leu Leu Gln Pro Ser
    20           25           30

Trp Arg Thr Thr Thr Asp Tyr Arg Leu Tyr Thr Glu Asp Asp Val Glu
    35           40           45

Arg Ala Leu Gln Ile Leu Ile Tyr Arg Ala Ala Gly Ile Gly Leu Lys
    50           55           60

Asp Ile Ala Glu Val Leu Asp Gln Pro Asp Ser Ala Asn Gln His Leu
    65           70           75           80

Arg Arg Gln Arg Glu Leu Leu Val Glu Gln Ile Gly Gln Leu His Arg
    85           90           95

Met Val Arg Ala Val Asp Glu Ile Leu Gly Lys Asp Ala Ile Ser Val
    100          105          110

Lys Glu Lys Ile Glu Ile Phe Gly Glu Asp Leu Pro Lys Tyr Gln Glu

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[illegible]

Ala Trp Glu Val Gln Val Asp Val Leu Val Arg Asn Pro Asp Gly Ser	
70 75 80 85	
tac atg ccc gtg atg gtg agc aat cac cgt gtc gcc cgt ccg gat ccg	403
Tyr Met Pro Val Met Val Ser Asn His Arg Val Ala Arg Pro Asp Pro	
90 95 100	
cac aaa act atg cag ggc att gcc gtc acc cgc ctc ggt ttg ggt cag	451
His Lys Thr Met Gln Gly Ile Ala Val Thr Arg Leu Gly Leu Gly Gln	
105 110 115	
ccg cta gag ctc aag gca acg ctg cgc cac cac acg atc gat ggc tat	499
Pro Leu Glu Leu Lys Ala Thr Leu Arg His His Thr Ile Asp Gly Tyr	
120 125 130	
cgc ctc acc ctc gcg ttg atg ggt ttg gag gaa gct gga gca	541
Arg Leu Thr Leu Ala Leu Met Gly Leu Glu Ala Gly Ala	
135 140 145	

<210> 1860

<211> 147

<212> PRT

<213> Corynebacterium glutamicum

<400> 1860

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20 25 30	
Ala Asp Leu Asp Asn Asp Ala Glu Leu Ala Glu Phe Glu Thr Leu Glu	
35 40 45	
Ala Ile Ala Ala Gly Asp Thr Leu Ile Thr Gly Ala Val Phe Thr Gly	
50 55 60	
Thr Leu Glu Gly Val Ala Trp Glu Val Gln Val Asp Val Leu Val Arg	
65 70 75 80	
Asn Pro Asp Gly Ser Tyr Met Pro Val Met Val Ser Asn His Arg Val	
85 90 95	
Ala Arg Pro Asp Pro His Lys Thr Met Gln Gly Ile Ala Val Thr Arg	
100 105 110	
Leu Gly Leu Gly Gln Pro Leu Glu Leu Lys Ala Thr Leu Arg His His	
115 120 125	
Thr Ile Asp Gly Tyr Arg Leu Thr Leu Ala Leu Met Gly Leu Glu Glu	
130 135 140	
Ala Gly Ala	
145	

<210> 1861

<211> 579

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(556)

<223> RXA00649

<400> 1861

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cattttgtgc	aagatgcaat	agctggcaaa	ctggagagcc	atg	agc	acc	gac	ccc	115
				Met	Ser	Thr	Asp	Pro	
				1				5	

atc	gcg	gcc	ttg	gaa	tac	gaa	tcc	acc	atc	ttc	gcc	cgt	cac	cg	aat	163
Ile	Ala	Ala	Leu	Glu	Tyr	Glu	Ser	Thr	Ile	Phe	Ala	Arg	His	Arg	Asn	
			10						15					20		

caa	tac	acc	ggc	caa	gca	ggt	acg	aat	gct	ggc	gtc	ctc	gat	tcc	agc	211
Gln	Tyr	Thr	Gly	Gln	Ala	Gly	Thr	Asn	Ala	Gly	Val	Leu	Asp	Ser	Ser	
			25					30					35			

ggc	tac	aac	cta	ctc	acg	ctg	ctc	cag	tta	cgt	ggc	ccc	tcc	acc	atc	259
Gly	Tyr	Asn	Leu	Leu	Thr	Leu	Gln	Leu	Arg	Gly	Pro	Ser	Thr	Ile		
		40				45						50				

ggc	gaa	ctc	agc	gcc	atc	acc	ggc	cta	gac	gca	tct	acc	ctt	aac	cgt	307
Gly	Glu	Leu	Ser	Ala	Ile	Thr	Gly	Leu	Asp	Ala	Ser	Thr	Leu	Asn	Arg	
	55					60					65					

cag	aca	aaa	gcc	cta	cta	acc	aaa	gga	ttt	gtc	gaa	cgc	atc	cca	gat	355
Gln	Thr	Lys	Ala	Leu	Leu	Thr	Lys	Gly	Phe	Val	Glu	Arg	Ile	Pro	Asp	
	70					75				80				85		

ccc	gac	ggt	gga	atc	gct	cgg	aaa	ttc	cac	ccc	acc	gac	ctc	ggc	aat	403
Pro	Asp	Gly	Gly	Ile	Ala	Arg	Lys	Phe	His	Pro	Thr	Asp	Leu	Gly	Asn	
			90					95					100			

gaa	ctg	ctc	aac	gag	gaa	cgc	aca	tcc	agc	caa	gaa	aaa	tat	gcc	gag	451
Glu	Leu	Leu	Asn	Glu	Glu	Arg	Thr	Ser	Ser	Gln	Glu	Lys	Tyr	Ala	Glu	
			105					110					115			

tta	ctt	tca	gac	tgg	ccc	gaa	gag	gat	cta	cgc	acc	ttc	gtc	aaa	ctt	499
Leu	Leu	Ser	Asp	Trp	Pro	Glu	Glu	Asp	Leu	Arg	Thr	Phe	Val	Lys	Leu	
			120				125						130			

ctt	gaa	aaa	cta	aat	aaa	gcc	gtg	gag	aca	cgc	gtc	gga	aag	cat	tgg	547
Leu	Glu	Lys	Leu	Asn	Lys	Ala	Val	Glu	Thr	Arg	Val	Gly	Lys	His	Trp	
		135				140					145					

ccg	cgc	ccc	tgactcagcc	caagccagag	ccc	579
Pro	Arg	Pro				
150						

<210> 1862

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 1862

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 20 25 30
 Val Leu Asp Ser Ser Gly Tyr Asn Leu Leu Thr Leu Leu Gln Leu Arg
 35 40 45
 Gly Pro Ser Thr Ile Gly Glu Leu Ser Ala Ile Thr Gly Leu Asp Ala
 50 55 60
 Ser Thr Leu Asn Arg Gln Thr Lys Ala Leu Leu Thr Lys Gly Phe Val
 65 70 75 80
 Glu Arg Ile Pro Asp Pro Asp Gly Gly Ile Ala Arg Lys Phe His Pro
 85 90 95
 Thr Asp Leu Gly Asn Glu Leu Leu Asn Glu Glu Arg Thr Ser Ser Gln
 100 105 110
 Glu Lys Tyr Ala Glu Leu Leu Ser Asp Trp Pro Glu Glu Asp Leu Arg
 115 120 125
 Thr Phe Val Lys Leu Leu Glu Lys Leu Asn Lys Ala Val Glu Thr Arg
 130 135 140
 Val Gly Lys His Trp Pro Arg Pro
 145 150

 <210> 1863
 <211> 672
 <212> DNA
 <213> *Corynebacterium glutamicum*

 <220>
 <221> CDS
 <222> (101)..(649)
 <223> RXA00652

 <400> 1863
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 attgcggtccg gtttccgaca cagcatctag gcttgactgc atg cgt cgt aca tta 115
 Met Arg Arg Thr Leu
 1 5
 cct act atc ctc gct gct tcc atc atg ctc acc gct tgt acc ccg gcg 163
 Pro Thr Ile Leu Ala Ala Ser Ile Met Leu Thr Ala Cys Thr Pro Ala
 10 15 20
 gaa cct gaa gca acc cca gag acc acc acc gag gca gcc ccg gaa gta 211
 Glu Pro Glu Ala Thr Pro Glu Thr Thr Thr Glu Ala Ala Pro Glu Val
 25 30 35
 att act gac ggc ctt ccc atc gac gcg atg ccc gcg gtc gaa cgc acc 259
 Ile Thr Asp Gly Leu Pro Ile Asp Ala Met Pro Ala Val Glu Arg Thr
 40 45 50
 gca caa acc gca tgc ccc tac ctg ggc acc gac tgg gtc gcc gat acc 307
 Ala Gln Thr Ala Cys Pro Tyr Leu Gly Thr Asp Trp Val Ala Asp Thr

55	60	65	
aac ggc cag cgc gtc acg ggt tac ggc aca gac gaa cgc ttt tcg acg			355
Asn Gly Gln Arg Val Thr Gly Tyr Gly Thr Asp Glu Arg Phe Ser Thr			
70	75	80	85
ccc tcc tgc gtt ttt tac tcc tac ccc gaa gaa cca caa ctc acg gtg			403
Pro Ser Cys Val Phe Tyr Ser Tyr Pro Glu Glu Pro Gln Leu Thr Val			
	90	95	100
att gtc cgc gat atg gcc acc acg gat gac gct atc gcg gta gtg gat			451
Ile Val Arg Asp Met Ala Thr Thr Asp Asp Ala Ile Ala Val Val Asp			
	105	110	115
tgg gca gcc ccc atc gat tcc act gag ccc gct gag gaa ccc gca ggg			499
Trp Ala Ala Pro Ile Asp Ser Thr Glu Pro Ala Glu Glu Pro Ala Gly			
	120	125	130
tgg tcc ggt ggc cgc cga ggt gga aac gat act tca ggc gca ctc tac			547
Trp Ser Gly Gly Arg Arg Gly Gly Asn Asp Thr Ser Gly Ala Leu Tyr			
	135	140	145
gcg gtt caa aac ggc ccc acc gcg gtc atc gtg ttc acc aat cag gat			595
Ala Val Gln Asn Gly Pro Thr Ala Val Ile Val Phe Thr Asn Gln Asp			
	150	155	160
caa tcc ctc aaa gcg cag tta atc gct gag gaa gta atc cag aat ctt			643
Gln Ser Leu Lys Ala Gln Leu Ile Ala Glu Glu Val Ile Gln Asn Leu			
	170	175	180
ggt ctc taactattag aaggccacat cgt			672
Gly Leu			
<210> 1864			
<211> 183			
<212> PRT			
<213> <i>Corynebacterium glutamicum</i>			
<400> 1864			
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Ala Cys Thr Pro Ala Glu Pro Glu Ala Thr Pro Glu Thr Thr Glu			
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Ala Ala Pro Glu Val Ile Thr Asp Gly Leu Pro Ile Asp Ala Met Pro			
	35	40	45
Ala Val Glu Arg Thr Ala Gln Thr Ala Cys Pro Tyr Leu Gly Thr Asp			
	50	55	60
Trp Val Ala Asp Thr Asn Gly Gln Arg Val Thr Gly Tyr Gly Thr Asp			
	65	70	75
Glu Arg Phe Ser Thr Pro Ser Cys Val Phe Tyr Ser Tyr Pro Glu Glu			
	85	90	95
Pro Gln Leu Thr Val Ile Val Arg Asp Met Ala Thr Thr Asp Ala			
	100	105	110


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Ile Ala Val Val Asp Trp Ala Ala Pro Ile Asp Ser Thr Glu Pro Ala
   115                      120                      125

Glu Glu Pro Ala Gly Trp Ser Gly Gly Arg Arg Gly Gly Asn Asp Thr
   130                      135                      140

Ser Gly Ala Leu Tyr Ala Val Gln Asn Gly Pro Thr Ala Val Ile Val
   145                      150                      155                      160

Phe Thr Asn Gln Asp Gln Ser Leu Lys Ala Gln Leu Ile Ala Glu Glu
   165                      170                      175

Val Ile Gln Asn Leu Gly Leu
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<210> 1865

<211> 1389

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1366)

<223> RXA00654

<400> 1865

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tgctgtgaag tgccacctgt ttggaaaggc gaacacgata gtg ctc gat att ttg 115
                                   Val Leu Asp Ile Leu
                                   1                      5

att tac cgc gtg tct gga gtg atg aag ctg tgg cac ctg ctt ctt cac 163
Ile Tyr Pro Val Ser Gly Val Met Lys Leu Trp His Leu Leu Leu His
   10                      15                      20

aac gtt cgc ggt ttg gac gat tca ctg cgc tgg ttc ttt tcc ctt ttc 211
Asn Val Ala Gly Leu Asp Asp Ser Leu Ala Trp Phe Phe Ser Leu Phe
   25                      30                      35

ggc ctt gtc atc acg atc cgt gca att atc gcg cct ttc acc tgg cag 259
Gly Leu Val Ile Thr Ile Arg Ala Ile Ile Ala Pro Phe Thr Trp Gln
   40                      45                      50

atg tat aag tcg ggc cgc act gcc gca cat att cgt cct cac cgc gct 307
Met Tyr Lys Ser Gly Arg Thr Ala Ala His Ile Arg Pro His Arg Ala
   55                      60                      65

gcg ctc cgg gaa gaa tac aag gga aag tac gat gaa cgc tcc att cgg 355
Ala Leu Arg Glu Glu Tyr Lys Gly Lys Tyr Asp Glu Ala Ser Ile Arg
   70                      75                      80                      85

gag ttg cag aag cgc cag aat gat ttg aat aag gaa tac ggc att aac 403
Glu Leu Gln Lys Arg Gln Asn Asp Leu Asn Lys Glu Tyr Gly Ile Asn
   90                      95                      100

ccg ctg gca ggt tgt gtg cct ggg ctg atc cag ata ccg att gtc ctt 451
Pro Leu Ala Gly Cys Val Pro Gly Leu Ile Gln Ile Pro Ile Val Leu
  105                      110                      115

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ggt ctt tac tgg gca ctt ctc cgc atg gct cgc cct gaa ggt ggt ttg	499
Gly Leu Tyr Trp Ala Leu Leu Arg Met Ala Arg Pro Glu Gly Gly Leu	
120 125 130	
gaa aat ccc gtc ttc cag tgc atc ggc ttc cta act cct gag gaa gtg	547
Glu Asn Pro Val Phe Gln Ser Ile Gly Phe Leu Thr Pro Glu Glu Val	
135 140 145	
gaa tct ttc ctc gct ggt cgc gtg agc aat gtg cct ctg ccc gct tat	595
Glu Ser Phe Leu Ala Gly Arg Val Ser Asn Val Pro Leu Pro Ala Tyr	
150 155 160 165	
gtt tgc atg ccc act gag cag cta aaa tat ttg agc acc acg cag gcg	643
Val Ser Met Pro Thr Glu Gln Leu Lys Tyr Leu Ser Thr Thr Gln Ala	
170 175 180	
gaa gtt ctt agt ttc gtt ttg cca ctg ttc atc aca gcc gca atc ctc	691
Glu Val Leu Ser Phe Val Leu Pro Leu Phe Ile Thr Ala Ala Ile Leu	
185 190 195	
acc gca atc aac atg gcg atg tcc atg tac cgc agc ttc caa acc aac	739
Thr Ala Ile Asn Met Ala Met Ser Met Tyr Arg Ser Phe Gln Thr Asn	
200 205 210	
gat tac gca tcc gga ttc tct aac ggc atg ctg aag ttc atg atc gtg	787
Asp Tyr Ala Ser Gly Phe Ser Asn Gly Met Leu Lys Phe Met Ile Val	
215 220 225	
atg tgc atc ctc gcg ccg atc ttc cca ctg tcc ctt ggc ctc aca gga	835
Met Ser Ile Leu Ala Pro Ile Phe Pro Leu Ser Leu Gly Leu Thr Gly	
230 235 240 245	
cca ttc ccc aca gca atc gca ctc tat tgg gtc agc aac aac ctg tgg	883
Pro Phe Pro Thr Ala Ile Ala Leu Tyr Trp Val Ser Asn Asn Leu Trp	
250 255 260	
acg ctc ctc caa aca atc atc atg atg gtc att ttg gaa cgc aaa tac	931
Thr Leu Leu Gln Thr Ile Ile Met Met Val Ile Leu Glu Arg Lys Tyr	
265 270 275	
cca ctt acc gac gat ttc aaa gtg cac cac cta gag cag cgc gac atc	979
Pro Leu Thr Asp Asp Phe Lys Val His His Leu Glu Gln Arg Asp Ile	
280 285 290	
tac cgc gca aaa caa aaa gaa aag cgc atc ttc ctg tgg aca cga cgc	1027
Tyr Arg Ala Lys Gln Lys Glu Lys Arg Ile Phe Leu Trp Thr Arg Arg	
295 300 305	
aaa aac cgc gcc ctg atg att ctc acc cca tgg aac gcc tca acg ctt	1075
Lys Asn Arg Ala Leu Met Ile Leu Thr Pro Trp Asn Ala Ser Thr Leu	
310 315 320 325	
cac gca aca aac gtg gaa ctc acc aaa acc cgt act gcc gaa atc aac	1123
His Ala Thr Asn Val Glu Leu Thr Lys Thr Arg Thr Ala Glu Ile Asn	
330 335 340	
gaa gca aaa cag gcc cgc aaa gaa atc gcg aac aag agg cgc gaa acg	1171
Glu Ala Lys Gln Ala Arg Lys Glu Ile Ala Asn Lys Arg Arg Glu Thr	
345 350 355	

caa cgt gaa atg aac cgc gcc gcc atg cag cgc tta aag cag cgt cgc 1219
 Gln Arg Glu Met Asn Arg Ala Ala Met Gln Arg Leu Lys Gln Arg Arg
 360 365 370

gct gag gtt aaa gct aaa aag aag ggg ctt atc gac gcc tcc ccc aac 1267
 Ala Glu Val Lys Ala Lys Lys Lys Gly Leu Ile Asp Ala Ser Pro Asn
 375 380 385

gaa gat acc cct tcg gaa aat gaa gaa act aaa ttg agt agt ccg cag 1315
 Glu Asp Thr Pro Ser Glu Asn Glu Glu Thr Lys Leu Ser Ser Pro Gln
 390 395 400 405

gtg gag ccg aca aca act gcc gag cca aat cgc gag ccg tct caa gag 1363
 Val Glu Pro Thr Thr Thr Ala Glu Pro Asn Arg Glu Pro Ser Gln Glu
 410 415 420

gac tgatgttgatg gaccaatcga gat 1389
 Asp

<210> 1866

<211> 422

<212> PRT

<213> Corynebacterium glutamicum

<400> 1866

Val Leu Asp Ile Leu Ile Tyr Pro Val Ser Gly Val Met Lys Leu Trp
 1 5 10 15

His Leu Leu Leu His Asn Val Ala Gly Leu Asp Asp Ser Leu Ala Trp
 20 25 30

Phe Phe Ser Leu Phe Gly Leu Val Ile Thr Ile Arg Ala Ile Ile Ala
 35 40 45

Pro Phe Thr Trp Gln Met Tyr Lys Ser Gly Arg Thr Ala Ala His Ile
 50 55 60

Arg Pro His Arg Ala Ala Leu Arg Glu Glu Tyr Lys Gly Lys Tyr Asp
 65 70 75 80

Glu Ala Ser Ile Arg Glu Leu Gln Lys Arg Gln Asn Asp Leu Asn Lys
 85 90 95

Glu Tyr Gly Ile Asn Pro Leu Ala Gly Cys Val Pro Gly Leu Ile Gln
 100 105 110

Ile Pro Ile Val Leu Gly Leu Tyr Trp Ala Leu Leu Arg Met Ala Arg
 115 120 125

Pro Glu Gly Gly Leu Glu Asn Pro Val Phe Gln Ser Ile Gly Phe Leu
 130 135 140

Thr Pro Glu Glu Val Glu Ser Phe Leu Ala Gly Arg Val Ser Asn Val
 145 150 155 160

Pro Leu Pro Ala Tyr Val Ser Met Pro Thr Glu Gln Leu Lys Tyr Leu
 165 170 175

Ser Thr Thr Gln Ala Glu Val Leu Ser Phe Val Leu Pro Leu Phe Ile

180										185										190										
Thr	Ala	Ala	Ile	Leu	Thr	Ala	Ile	Asn	Met	Ala	Met	Ser	Met	Tyr	Arg															
	195						200					205																		
Ser	Phe	Gln	Thr	Asn	Asp	Tyr	Ala	Ser	Gly	Phe	Ser	Asn	Gly	Met	Leu															
	210					215						220																		
Lys	Phe	Met	Ile	Val	Met	Ser	Ile	Leu	Ala	Pro	Ile	Phe	Pro	Leu	Ser															
	225					230				235					240															
Leu	Gly	Leu	Thr	Gly	Pro	Phe	Pro	Thr	Ala	Ile	Ala	Leu	Tyr	Trp	Val															
				245					250					255																
Ser	Asn	Asn	Leu	Trp	Thr	Leu	Leu	Gln	Thr	Ile	Ile	Met	Met	Val	Ile															
			260					265					270																	
Leu	Glu	Arg	Lys	Tyr	Pro	Leu	Thr	Asp	Asp	Phe	Lys	Val	His	His	Leu															
			275				280					285																		
Glu	Gln	Arg	Asp	Ile	Tyr	Arg	Ala	Lys	Gln	Lys	Glu	Lys	Arg	Ile	Phe															
			290			295					300																			
Leu	Trp	Thr	Arg	Arg	Lys	Asn	Arg	Ala	Leu	Met	Ile	Leu	Thr	Pro	Trp															
	305				310					315				320																
Asn	Ala	Ser	Thr	Leu	His	Ala	Thr	Asn	Val	Glu	Leu	Thr	Lys	Thr	Arg															
				325					330					335																
Thr	Ala	Glu	Ile	Asn	Glu	Ala	Lys	Gln	Ala	Arg	Lys	Glu	Ile	Ala	Asn															
			340					345					350																	
Lys	Arg	Arg	Glu	Thr	Gln	Arg	Glu	Met	Asn	Arg	Ala	Ala	Met	Gln	Arg															
		355					360					365																		
Leu	Lys	Gln	Arg	Arg	Ala	Glu	Val	Lys	Ala	Lys	Lys	Lys	Gly	Leu	Ile															
		370				375					380																			
Asp	Ala	Ser	Pro	Asn	Glu	Asp	Thr	Pro	Ser	Glu	Asn	Glu	Glu	Thr	Lys															
					390					395				400																
Leu	Ser	Ser	Pro	Gln	Val	Glu	Pro	Thr	Thr	Thr	Ala	Glu	Pro	Asn	Arg															
				405				410						415																
Glu	Pro	Ser	Gln	Glu	Asp																									
				420																										

<210> 1867

<211> 384

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(361)

<223> RXA00656

<400> 1867

cctttaata acaatacaat gaataattgg aataggtcga cacctttgga gcggagccgg 60

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ttaaatttg cagcattcac cgaagaaaa ggagaaccac atg ctt gcc cta ggt 115
                               Met Leu Ala Leu Gly
                               1                               5

tgg att aca tgg atc att att ggt ggt cta gct ggt tgg att gcc tcc 163
Trp Ile Thr Trp Ile Ile Ile Gly Gly Leu Ala Gly Trp Ile Ala Ser
                               10                               15                               20

aag att aaa ggc act gat gct cag caa gga att ttg ctg aac ata gtc 211
Lys Ile Lys Gly Thr Asp Ala Gln Gln Gly Ile Leu Leu Asn Ile Val
                               25                               30                               35

gtc ggt att atc ggt ggt ttg tta ggc ggc tgg ctg ctt gga atc ttc 259
Val Gly Ile Ile Gly Gly Leu Leu Gly Gly Trp Leu Leu Gly Ile Phe
                               40                               45                               50

gga gtg gat gtt gcc ggt ggc ggc ttg atc ttc agc ttc atc aca tgt 307
Gly Val Asp Val Ala Gly Gly Gly Leu Ile Phe Ser Phe Ile Thr Cys
                               55                               60                               65

ctg att ggt gct gtc att ttg ctg acg atc gtg cag ttc ttc act cgg 355
Leu Ile Gly Ala Val Ile Leu Leu Thr Ile Val Gln Phe Phe Thr Arg
                               70                               75                               80                               85

aag aag taatctgctt taaatccgta ggg 384
Lys Lys

<210> 1868
<211> 87
<212> PRT
<213> Corynebacterium glutamicum

<400> 1868
Met Leu Ala Leu Gly Trp Ile Thr Trp Ile Ile Ile Gly Gly Leu Ala
 1                               5                               10                               15

Gly Trp Ile Ala Ser Lys Ile Lys Gly Thr Asp Ala Gln Gln Gly Ile
 20                               25                               30

Leu Leu Asn Ile Val Val Gly Ile Ile Gly Gly Leu Leu Gly Gly Trp
 35                               40                               45

Leu Leu Gly Ile Phe Gly Val Asp Val Ala Gly Gly Gly Leu Ile Phe
 50                               55                               60

Ser Phe Ile Thr Cys Leu Ile Gly Ala Val Ile Leu Leu Thr Ile Val
 65                               70                               75                               80

Gln Phe Phe Thr Arg Lys Lys
 85

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<210> 1869
<211> 986
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS

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<222> (61)..(963)

<223> RXA00657

<400> 1869

gatcatgagt ttccacgaac tgtaacgcag gattcaccaa tcaatgaaag gtcgaccgac 60

atg	agc	act	gaa	gac	att	gtc	gtc	gta	gca	gta	gat	ggc	tcg	gac	gcc	108
Met	Ser	Thr	Glu	Asp	Ile	Val	Val	Val	Ala	Val	Asp	Gly	Ser	Asp	Ala	

1

5

10

15

tca	aaa	caa	gct	gtt	cgg	tggt	gct	gca	aat	acc	gcc	aac	aaa	cgt	ggc	156
Ser	Lys	Gln	Ala	Val	Arg	Trp	Ala	Asn	Thr	Ala	Asn	Lys	Arg	Gly		

20

25

30

att	cca	ctt	cgc	ttg	gct	tcc	agc	tac	acc	atg	cct	cag	ttc	ctc	tac	204
Ile	Pro	Leu	Arg	Leu	Ala	Ser	Ser	Tyr	Thr	Met	Pro	Gln	Phe	Leu	Tyr	

35

40

45

gca	gag	gga	atg	gtt	cca	cca	caa	gag	ctt	ttc	gat	gac	ctc	cag	gcc	252
Ala	Glu	Gly	Met	Val	Pro	Pro	Gln	Glu	Leu	Phe	Asp	Asp	Leu	Gln	Ala	

50

55

60

gaa	gcc	ctg	gaa	aag	att	aac	gaa	gcc	cgt	gac	atc	gcc	cat	gag	gta	300
Glu	Ala	Leu	Glu	Lys	Ile	Asn	Glu	Ala	Arg	Asp	Ile	Ala	His	Glu	Val	

65

70

75

80

gcg	cca	gaa	atc	aag	atc	ggg	cac	acc	atc	gct	gaa	ggc	agt	ccc	atc	348
Ala	Pro	Glu	Ile	Lys	Ile	Gly	His	Thr	Ile	Ala	Glu	Gly	Ser	Pro	Ile	

85

90

95

gac	atg	ctg	ttg	gaa	atg	tct	ccc	gat	gcc	aca	atg	atc	gtc	atg	ggg	396
Asp	Met	Leu	Glu	Met	Ser	Pro	Asp	Ala	Thr	Met	Ile	Val	Met	Gly		

100

105

110

tcc	cgc	gga	ctc	ggc	gga	ctc	tcc	gga	atg	gtc	atg	ggc	tcc	gtc	tcc	444
Ser	Arg	Gly	Leu	Gly	Gly	Leu	Ser	Gly	Met	Val	Met	Gly	Ser	Val	Ser	

115

120

125

ggt	gca	gtg	gtc	agc	cac	gca	aag	tgt	cca	gtc	gtt	gtt	gtc	cgt	gaa	492
Gly	Ala	Val	Val	Ser	His	Ala	Lys	Cys	Pro	Val	Val	Val	Val	Arg	Glu	

130

135

140

gac	agc	gca	gtc	aac	gaa	gac	agc	aag	tac	ggc	cca	gtc	gtc	gtc	ggg	540
Asp	Ser	Ala	Val	Asn	Glu	Asp	Ser	Lys	Tyr	Gly	Pro	Val	Val	Val	Gly	

145

150

155

160

gtg	gat	ggc	tcc	gaa	gtc	tcc	caa	cag	gca	acc	gaa	tac	gca	ttt	gcg	588
Val	Asp	Gly	Ser	Glu	Val	Ser	Gln	Gln	Ala	Thr	Ala	Tyr	Ala	Phe	Ala	

165

170

175

gaa	gct	gaa	gct	cgt	ggc	gcc	gaa	ctc	gtt	gca	gtt	cac	acc	tggt	atg	636
Glu	Ala	Glu	Ala	Arg	Gly	Ala	Glu	Leu	Val	Ala	Val	His	Thr	Trp	Met	

180

185

190

gac	atg	cag	gta	cag	gca	tca	ctt	gca	ggt	ctt	gca	gct	gct	caa	cag	684
Asp	Met	Gln	Val	Gln	Ala	Ser	Leu	Ala	Gly	Leu	Ala	Ala	Ala	Gln	Gln	

195

200

205

cag	tggt	gat	gaa	gtg	gaa	cgt	cag	caa	acc	gac	atg	ctg	atc	gaa	cgc	732
Gln	Trp	Asp	Glu	Val	Glu	Arg	Gln	Gln	Thr	Asp	Met	Leu	Ile	Glu	Arg	

210

215

220

ctc gca cca ctg gtg gaa aag tac cca agt gta acc gtc aag aag atc 780
 Leu Ala Pro Leu Val Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile
 225 230 235 240

atc acc cgt gac cgc cca gtt cgc gca ctt gca gaa gca tct gaa aac 828
 Ile Thr Arg Asp Arg Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn
 245 250 255

gcg cag ctc cta gtc gtt ggt tcc cat ggt cgt ggc gga ttt aag ggc 876
 Ala Gln Leu Leu Val Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly
 260 265 270

atg ctc ctt ggc tcc acc tcc cgc gca ctg ctg caa tcc gca cgg tgc 924
 Met Leu Leu Gly Ser Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys
 275 280 285

cca atg atg gtg gtt cgc cca cct gag aag att aag aag tagttttttt 973
 Pro Met Met Val Val Arg Pro Pro Glu Lys Ile Lys Lys
 290 295 300

taagtttcga tgc 986

<210> 1870

<211> 301

<212> PRT

<213> Corynebacterium glutamicum

<400> 1870

Met Ser Thr Glu Asp Ile Val Val Val Ala Val Asp Gly Ser Asp Ala
 1 5 10 15

Ser Lys Gln Ala Val Arg Trp Ala Ala Asn Thr Ala Asn Lys Arg Gly
 20 25 30

Ile Pro Leu Arg Leu Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr
 35 40 45

Ala Glu Gly Met Val Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala
 50 55 60

Glu Ala Leu Glu Lys Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val
 65 70 75 80

Ala Pro Glu Ile Lys Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile
 85 90 95

Asp Met Leu Leu Glu Met Ser Pro Asp Ala Thr Met Ile Val Met Gly
 100 105 110

Ser Arg Gly Leu Gly Gly Leu Ser Gly Met Val Met Gly Ser Val Ser
 115 120 125

Gly Ala Val Val Ser His Ala Lys Cys Pro Val Val Val Val Arg Glu
 130 135 140

Asp Ser Ala Val Asn Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly
 145 150 155 160

Val Asp Gly Ser Glu Val Ser Gln Gln Ala Thr Glu Tyr Ala Phe Ala

[illegible]


```

Leu Asp Leu Tyr Gly Gln Ala Gly Arg Gln Ile Met Phe Ile Ile Val
 70          75          80          85

agt ggt tat ggc tgg tac caa tgg tgg gcc gca aaa cgt cgc gca ctc 403
Ser Gly Tyr Gly Trp Tyr Gln Trp Ser Ala Ala Lys Arg Arg Ala Leu
          90          95          100

acc cca gaa aat gca gta gca gtg gtt cct cgc tgg gca agc acc aaa 451
Thr Pro Glu Asn Ala Val Ala Val Val Pro Arg Trp Ala Ser Thr Lys
          105          110          115

gaa cgc gcc ggc att gtg att gcg gcg gtt gtg gga aca ctc agc ttt 499
Glu Arg Ala Gly Ile Val Ile Ala Ala Val Val Gly Thr Leu Ser Phe
          120          125          130

gcc tgg att ttc caa gca ctc ggc tcc tgg ggg cca tgg gcc gac gcg 547
Ala Trp Ile Phe Gln Ala Leu Gly Ser Trp Gly Pro Trp Ala Asp Ala
          135          140          145

tgg att ttc gtc gcc tca atc ctg gct acc tac gga atg gct cgc gga 595
Trp Ile Phe Val Gly Ser Ile Leu Ala Thr Tyr Gly Met Ala Arg Gly
          150          155          160          165

tgg aca gag ttc tgg ctg atc tgg atc gcc gtc gac ata gtt gcc gtt 643
Trp Thr Glu Phe Trp Leu Ile Trp Ile Ala Val Asp Ile Val Gly Val
          170          175          180

cct cta ctt ttg act gct gcc tac tac cca tcc gcg gtg ctt tac ctg 691
Pro Leu Leu Leu Thr Ala Gly Tyr Trp Pro Ser Ala Val Leu Tyr Leu
          185          190          195

gtg tac ggt gcg ttt gtc agc tgg gga ttt gtc gtg tgg ctg cgg gtg 739
Val Tyr Gly Ala Phe Val Ser Trp Gly Phe Val Val Trp Leu Arg Val
          200          205          210

caa aaa gca gac aag gct cgt gcg ctg gaa gct cag gag tct gtg aca 787
Gln Lys Ala Asp Lys Ala Arg Ala Leu Glu Ala Gln Glu Ser Val Thr
          215          220          225

gtc tgaaaagcgt ttactaaata gaa 813
Val
230

```

<210> 1872

<211> 230

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1872

```

Met Asn Pro Ile Thr Glu Leu Leu Asp Ala Thr Leu Trp Ile Gly Gly
 1          5          10          15

Val Pro Ile Leu Trp Arg Glu Ile Ile Gly Asn Val Phe Gly Leu Phe
          20          25          30

Ser Ala Trp Ala Gly Met Arg Arg Ile Val Trp Ala Trp Pro Ile Gly
          35          40          45

Ile Ile Gly Asn Ala Leu Leu Phe Thr Val Phe Met Gly Gly Leu Phe
          50          55          60

```

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His Thr Pro Gln Asn Leu Asp Leu Tyr Gly Gln Ala Gly Arg Gln Ile
 65          70          75          80
Met Phe Ile Ile Val Ser Gly Tyr Gly Trp Tyr Gln Trp Ser Ala Ala
          85          90          95
Lys Arg Arg Ala Leu Thr Pro Glu Asn Ala Val Ala Val Val Pro Arg
          100          105          110
Trp Ala Ser Thr Lys Glu Arg Ala Gly Ile Val Ile Ala Ala Val Val
          115          120          125
Gly Thr Leu Ser Phe Ala Trp Ile Phe Gln Ala Leu Gly Ser Trp Gly
          130          135          140
Pro Trp Ala Asp Ala Trp Ile Phe Val Gly Ser Ile Leu Ala Thr Tyr
          145          150          155          160
Gly Met Ala Arg Gly Trp Thr Glu Phe Trp Leu Ile Trp Ile Ala Val
          165          170          175
Asp Ile Val Gly Val Pro Leu Leu Leu Thr Ala Gly Tyr Tyr Pro Ser
          180          185          190
Ala Val Leu Tyr Leu Val Tyr Gly Ala Phe Val Ser Trp Gly Phe Val
          195          200          205
Val Trp Leu Arg Val Gln Lys Ala Asp Lys Ala Arg Ala Leu Glu Ala
          210          215          220
Gln Glu Ser Val Thr Val
          225          230

```

<210> 1873

<211> 685

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(685)

<223> RXA00667

<400> 1873

ggcatcagtg tttgaaggga aaagcaggtc aaacaaggtg cggctgattt gagcgatcac 60

```

agcaccgaga tctgtgctga agaattcaat gattgggttg atg att gcg ttg aag    115
                               Met Ile Ala Leu Lys
                               1          5

```

```

tcc atg tct aac agg gta gta caa aag cca aaa atg aaa gcg ccg cta    163
Ser Met Ser Asn Arg Val Val Gln Lys Pro Lys Met Lys Ala Pro Leu
          10          15          20

```

```

ccc atc cgc gac gcc ctc aac cct tcc cgt gtg cgc ttg ccg ctc gac    211
Pro Ile Arg Asp Gly Leu Asn Pro Ser Arg Val Arg Leu Pro Leu Asp
          25          30          35

```

gcg gcg ccg atc cgc gcc atc gat ttt gtt gaa tac ctc att tcc acg 259

Ala Ala Pro Ile Arg Ala Ile Asp Phe Val Glu Tyr Leu Ile Ser Thr
 40 45 50

cag cgc cac cgc aat ccg gcc gac aac gcc gaa cgc ctt caa cgc cgt 307
 Gln Arg His Arg Asn Pro Ala Asp Asn Ala Glu Ala Leu Gln Ala Arg
 55 60 65

ttc gac gcc gac ctt gtt gtc aac cac tac ggc gag ccc tac gcc ccc 355
 Phe Asp Ala Asp Leu Val Val Asn His Tyr Gly Glu Pro Tyr Ala Pro
 70 75 80 85

gac acc atg gtt cag ccc gac gac gac att tgg ttc tac cgc atg ccc 403
 Asp Thr Met Val Gln Pro Asp Asp Asp Ile Trp Phe Tyr Arg Met Pro
 90 95 100

gcc gcc gaa cgg ccg atc cct tac aaa att cat gtc att cac gaa gac 451
 Ala Ala Glu Arg Pro Ile Pro Tyr Lys Ile His Val Ile His Glu Asp
 105 110 115

gat gac atc ctc gtc att gac aag cca ccc tac cta gca acc atg cct 499
 Asp Asp Ile Leu Val Ile Asp Lys Pro Pro Tyr Leu Ala Thr Met Pro
 120 125 130

cgt gcc cgc cac atc acc gaa acc gct ctg gtg aaa atg cgt gtg ctg 547
 Arg Gly Arg His Ile Thr Glu Thr Ala Leu Val Lys Met Arg Val Leu
 135 140 145

act gga aac aac gat ctc acc cca gct cac cgc ctc gat cgc ctg act 595
 Thr Gly Asn Asn Asp Leu Thr Pro Ala His Arg Leu Asp Arg Leu Thr
 150 155 160 165

tcc ggt gtg tta gtc atg gtg aaa aaa cca gaa ctc cgt gcc gct tac 643
 Ser Gly Val Leu Val Met Val Lys Lys Pro Glu Leu Arg Gly Ala Tyr
 170 175 180

caa acc ttg ttt gcc cga cgt gag gcg tcc aaa acc tat gag 685
 Gln Thr Leu Phe Ala Arg Arg Glu Ala Ser Lys Thr Tyr Glu
 185 190 195

<210> 1874

<211> 195

<212> PRT

<213> Corynebacterium glutamicum

<400> 1874

Met Ile Ala Leu Lys Ser Met Ser Asn Arg Val Val Gln Lys Pro Lys
 1 5 10 15

Met Lys Ala Pro Leu Pro Ile Arg Asp Gly Leu Asn Pro Ser Arg Val
 20 25 30

Arg Leu Pro Leu Asp Ala Ala Pro Ile Arg Ala Ile Asp Phe Val Glu
 35 40 45

Tyr Leu Ile Ser Thr Gln Arg His Arg Asn Pro Ala Asp Asn Ala Glu
 50 55 60

Ala Leu Gln Ala Arg Phe Asp Ala Asp Leu Val Val Asn His Tyr Gly
 65 70 75 80

tcc att ggg cca gca gcc ctc cca gtc cgc gca gcg gta gac aat gcc 355
 Ser Ile Gly Pro Ala Ala Leu Pro Val Arg Ala Ala Val Asp Asn Ala
 70 75 80 85

```

atc aac ggc atg ttc cca gga ctt gtt gat gaa aag gtt gca gca gag 403
Ile Asn Gly Met Phe Pro Gly Leu Val Asp Glu Lys Val Ala Ala Glu
          90                      95          100

cag gaa gct gca cgc gca gaa gct gag cgc gaa gca gca gct gca cgt 451
Gln Glu Ala Ala Arg Ala Glu Ala Glu Arg Glu Ala Ala Ala Arg
          105          110          115

gaa gca gaa gca gcc cgc gta gcc gca gaa gaa gcc gca cgc ttt gac 499
Glu Ala Glu Ala Ala Arg Val Ala Ala Glu Glu Ala Ala Arg Phe Asp
          120          125          130

cgc ggc tct tgc cca gca atc gct gat gtc tgc gtg gac att gat ggt 547
Arg Gly Ser Cys Pro Ala Ile Ala Asp Val Cys Val Asp Ile Asp Gly
          135          140          145

gga cgt acc tgg ctg cag gaa aac ggt cag gtc acc tac ggt gca gtc 595
Gly Arg Thr Trp Leu Gln Glu Asn Gly Gln Val Thr Tyr Gly Ala Val
          150          155          160          165

cca gtt tcc tcc ggc gga gtt ggc cag gaa acc cct cgc gga acg ttc 643
Pro Val Ser Ser Gly Gly Val Gly Gln Glu Thr Pro Arg Gly Thr Phe
          170          175          180

tac atc aac cgc aag gtc aag gat gaa atc tct tac gag ttc ggt aac 691
Tyr Ile Asn Arg Lys Val Lys Asp Glu Ile Ser Tyr Glu Phe Gly Asn
          185          190          195

gcc cca atg ccg tac gcc atg tac ttc acc tac aac ggc cac gca ttc 739
Ala Pro Met Pro Tyr Ala Met Tyr Phe Thr Tyr Asn Gly His Ala Phe
          200          205          210

cac cag ggc aat gtt cgc act act tcc gct ggt tgt gtt cgc cta aac 787
His Gln Gly Asn Val Ala Thr Thr Ser Ala Gly Cys Val Arg Leu Asn
          215          220          225

act caa gat gcc atc tac tac ttc aac aac gtt ggc atc ggc gac atg 835
Thr Gln Asp Ala Ile Tyr Tyr Phe Asn Asn Val Gly Ile Gly Asp Met
          230          235          240          245

gtg tac atc tac taaaactcac cgttgctagc agg 870
Val Tyr Ile Tyr

```

<210> 1876

<211> 249

<212> PRT

<213> Corynebacterium glutamicum

<400> 1876

```

Met Ala Lys Asn Ser Arg Ile Arg Tyr Ser Ala Ser Ile Lys Arg Ala
 1          5          10          15

Ala Ala Ala Ile Leu Thr Ala Ala Ala Thr Ser Val Ala Leu Ile Ala
 20          25          30

Val Pro Ala Thr Ala Ser Ala Gln Asp Leu Ala Thr Gly Ser Ser Gln
 35          40          45

```

```

Ile Gln Thr Asp Ala Arg Glu Gly Ala Trp Ala Thr Arg Asn Thr Ile
  50                      55                      60

Gln Asp Gln Leu Ala Ser Ile Gly Pro Ala Ala Leu Pro Val Arg Ala
  65                      70                      75                      80

Ala Val Asp Asn Ala Ile Asn Gly Met Phe Pro Gly Leu Val Asp Glu
                      85                      90                      95

Lys Val Ala Ala Glu Gln Glu Ala Ala Arg Ala Glu Ala Glu Arg Glu
 100                      105                      110

Ala Ala Ala Ala Arg Glu Ala Glu Ala Ala Arg Val Ala Ala Glu Glu
 115                      120                      125

Ala Ala Arg Phe Asp Arg Gly Ser Cys Pro Ala Ile Ala Asp Val Cys
 130                      135                      140

Val Asp Ile Asp Gly Gly Arg Thr Trp Leu Gln Glu Asn Gly Gln Val
 145                      150                      155                      160

Thr Tyr Gly Ala Val Pro Val Ser Ser Gly Gly Val Gly Gln Glu Thr
 165                      170                      175

Pro Arg Gly Thr Phe Tyr Ile Asn Arg Lys Val Lys Asp Glu Ile Ser
 180                      185                      190

Tyr Glu Phe Gly Asn Ala Pro Met Pro Tyr Ala Met Tyr Phe Thr Tyr
 195                      200                      205

Asn Gly His Ala Phe His Gln Gly Asn Val Ala Thr Thr Ser Ala Gly
 210                      215                      220

Cys Val Arg Leu Asn Thr Gln Asp Ala Ile Tyr Tyr Phe Asn Asn Val
 225                      230                      235                      240

Gly Ile Gly Asp Met Val Tyr Ile Tyr
 245

```

<210> 1877

<211> 858

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(835)

<223> RXA00678

<400> 1877

tgcgagctgc actttccagg aacccaaata tcccgccga ccttgctgca gatatttcgc 60

```

agccgctgaa aaaactagcc gttgacctgg aggttacccg atg act cgc agt aat 115
                Met Thr Arg Ser Asn
                1                      5

```

```

tta ccc gct tgg gag caa gca gac ccc agc gtc cac gcc tct gat ccc 163
Leu Pro Ala Trp      Glu Gln Ala Asp Pro Ser Val His Ala Ser Asp Pro
                10                      15                      20

```

```

cgc gcc atc act ttt gcg gag gat ttt ggg att cgt ccc atc ccg gcc 211
Arg Ala Ile Thr Phe Ala Glu Asp Phe Gly Ile Arg Pro Ile Pro Ala
      25                      30                      35

gta ggt cca att gat acc acc gct atc tgt gca aca cct tca aat gga 259
Val Gly Pro Ile Asp Thr Thr Ala Ile Cys Ala Thr Pro Ser Asn Gly
      40                      45                      50

ttt gag caa tta tgg aaa gcc att gag ccg gaa acc cgc acc cgc gcc 307
Phe Glu Gln Leu Trp Lys Ala Ile Glu Pro Glu Thr Arg Thr Arg Ala
      55                      60                      65

aac gac att cat ctt ccc atc gtc gtg ccg tac gct gaa cgt ctc tgc 355
Asn Asp Ile His Leu Pro Ile Val Val Ala Tyr Ala Glu Arg Leu Cys
      70                      75                      80                      85

gac gct tac cca ctg gca gat aga gaa ttg gtt ctc gta gcc gca atc 403
Asp Ala Tyr Pro Leu Ala Asp Arg Glu Leu Val Leu Val Ala Ala Ile
      90                      95                      100

ctc cac gac acg ggc tgg gca cat gtc gat gag agc cga atc atc tcc 451
Leu His Asp Thr Gly Trp Ala His Val Asp Glu Ser Arg Ile Ile Ser
      105                      110                      115

gaa gga ttc tcc gga aac tgg cgc aaa gca gca atc cgc ttc gaa cac 499
Glu Gly Phe Ser Gly Asn Trp Arg Lys Ala Ala Ile Arg Phe Glu His
      120                      125                      130

gaa aca gaa ggc tgc act gtg gcc cgc cga gtg ctt cca tcc ctc gga 547
Glu Thr Glu Gly Cys Thr Val Ala Arg Arg Val Leu Pro Ser Leu Gly
      135                      140                      145

tat act gtc gat ttt gtc gag cat gtc tgc gac atc atc gac gga cac 595
Tyr Thr Val Asp Phe Val Glu His Val Cys Asp Ile Ile Asp Gly His
      150                      155                      160                      165

gac acc cgc caa gtg gcc tac tca cta gaa gac gct ctt gtt cgc gat 643
Asp Thr Arg Gln Val Ala Tyr Ser Leu Glu Asp Ala Leu Val Arg Asp
      170                      175                      180

tgc gac cga ctc tgg cgt ttc gac cgc gcc ggg atc acg gct tct agc 691
Cys Asp Arg Leu Trp Arg Phe Asp Arg Ala Gly Ile Thr Ala Ser Ser
      185                      190                      195

tca tgg ttc ggg atg cca gtc tca gat tat gtc gac cgc ctg cac agg 739
Ser Trp Phe Gly Met Pro Val Ser Asp Tyr Val Asp Arg Leu His Arg
      200                      205                      210

gaa atc ctc cca gaa tta atc acc gaa gct gca cac cag atg gct act 787
Glu Ile Leu Pro Glu Leu Ile Thr Glu Ala Ala His Gln Met Ala Thr
      215                      220                      225

gca gac ctc aat cgt gca aag gcc ctg tta aga acg gat ccg atc cga 835
Ala Asp Leu Asn Arg Ala Lys Ala Leu Leu Arg Thr Asp Ala Ile Arg
      230                      235                      240                      245

tgaatgctgc aaccaggcgt gct 858

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<210> 1878

<211> 245

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1878

Met	Thr	Arg	Ser	Asn	Leu	Pro	Ala	Trp	Glu	Gln	Ala	Asp	Pro	Ser	Val
1				5					10					15	

His	Ala	Ser	Asp	Pro	Arg	Ala	Ile	Thr	Phe	Ala	Glu	Asp	Phe	Gly	Ile
		20						25					30		

Arg	Pro	Ile	Pro	Ala	Val	Gly	Pro	Ile	Asp	Thr	Thr	Ala	Ile	Cys	Ala
	35					40						45			

Thr	Pro	Ser	Asn	Gly	Phe	Glu	Gln	Leu	Trp	Lys	Ala	Ile	Glu	Pro	Glu
	50					55					60				

Thr	Arg	Thr	Arg	Ala	Asn	Asp	Ile	His	Leu	Pro	Ile	Val	Val	Ala	Tyr
65					70					75					80

Ala	Glu	Arg	Leu	Cys	Asp	Ala	Tyr	Pro	Leu	Ala	Asp	Arg	Glu	Leu	Val
			85						90					95	

Leu	Val	Ala	Ala	Ile	Leu	His	Asp	Thr	Gly	Trp	Ala	His	Val	Asp	Glu
			100					105					110		

Ser	Arg	Ile	Ile	Ser	Glu	Gly	Phe	Ser	Gly	Asn	Trp	Arg	Lys	Ala	Ala
		115					120						125		

Ile	Arg	Phe	Glu	His	Glu	Thr	Glu	Gly	Cys	Thr	Val	Ala	Arg	Arg	Val
	130					135					140				

Leu	Pro	Ser	Leu	Gly	Tyr	Thr	Val	Asp	Phe	Val	Glu	His	Val	Cys	Asp
145					150					155				160	

Ile	Ile	Asp	Gly	His	Asp	Thr	Arg	Gln	Val	Ala	Tyr	Ser	Leu	Glu	Asp
			165						170					175	

Ala	Leu	Val	Arg	Asp	Cys	Asp	Arg	Leu	Trp	Arg	Phe	Asp	Arg	Ala	Gly
		180						185					190		

Ile	Thr	Ala	Ser	Ser	Ser	Trp	Phe	Gly	Met	Pro	Val	Ser	Asp	Tyr	Val
		195					200						205		

Asp	Arg	Leu	His	Arg	Glu	Ile	Leu	Pro	Glu	Leu	Ile	Thr	Glu	Ala	Ala
		210				215						220			

His	Gln	Met	Ala	Thr	Ala	Asp	Leu	Asn	Arg	Ala	Lys	Ala	Leu	Leu	Arg
225					230					235					240

Thr	Asp	Ala	Ile	Arg
				245

<210> 1879

<211> 1053

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1030)

<223> RXA00691

<400> 1879

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tgcagctgca gtcgcactat ggattgttct tgccatatcg ccatgggttc cttctgcgca 60
cgccttgacc acgccttctg aagacgacca agtgacagtg atg gtt gag ggc aac 115
Met Val Glu Gly Asn
1 5
acc atc ggc tgt gct gac gcc gcc gga aat ggc tat caa acg ctt ctt 163
Thr Ile Gly Cys Ala Asp Ala Gly Gly Asn Gly Tyr Gln Thr Leu Leu
10 15 20
gat gcc gga ttt gat gtg gaa acc acc gtt cag ttt cca gaa ttc ttg 211
Asp Ala Gly Phe Asp Val Glu Thr Thr Val Gln Phe Pro Glu Phe Leu
25 30 35
tgc cga atc aat gat ttc cca ggt cct gat gtg gac gat tgc atg acc 259
Cys Arg Ile Asn Asp Phe Pro Gly Pro Asp Val Asp Cys Met Thr
40 45 50
gca tca cct gct gaa gct tat tgg tct tat tgg cat gct ccc ctc ggc 307
Ala Ser Pro Ala Glu Ala Tyr Trp Ser Tyr Trp His Ala Pro Leu Gly
55 60 65
gga gat gaa tgg gaa tac agc aac ctt gga gct ttc ctc tac tac ccc 355
Gly Asp Glu Trp Glu Tyr Ser Asn Leu Gly Ala Phe Leu Tyr Tyr Pro
70 75 80 85
aaa ccc ggc act gtt gaa gcg tgg tat tgg gga gat act gat cgt ccc 403
Lys Pro Gly Thr Val Glu Ala Trp Tyr Trp Gly Asp Thr Asp Arg Pro
90 95 100
ggc gcg atc ccg gtg agt aaa tct cag gcg gag ttg ggg tta gac tcc 451
Gly Ala Ile Pro Val Ser Lys Ser Gln Ala Glu Leu Gly Leu Asp Ser
105 110 115
cgc gat ccg gat tac aaa att gat ttt gat cca aat gat ttc atc acc 499
Ala Asp Pro Asp Tyr Lys Ile Asp Phe Asp Pro Asn Asp Phe Ile Thr
120 125 130
aca acc cca acc tcc gag tcc cct atc gcc gat tta ggg ggt gac gaa 547
Thr Thr Pro Thr Ser Glu Ser Pro Ile Ala Asp Leu Gly Gly Asp Glu
135 140 145
gag ccc act gaa act act gaa gct cct atc gca ggg gct gga gct ggt 595
Glu Pro Thr Glu Thr Thr Glu Ala Pro Ile Ala Gly Ala Gly Ala Gly
150 155 160 165
tcg gca aga gga caa gca gct gaa ccc act gtt gag gta aac cct gag 643
Ser Ala Arg Gly Gln Ala Ala Glu Pro Thr Val Glu Val Asn Pro Glu
170 175 180
aac cct aat gag gta ttg gtg tat cag gat tct gaa gga aac tcg att 691
Asn Pro Asn Glu Val Leu Val Tyr Gln Asp Ser Glu Gly Asn Ser Ile
185 190 195
act aaa ggt cag tac gag aac ttg gtt gct gca gca gcc gct aag acc 739
Thr Lys Gly Gln Tyr Glu Asn Leu Val Ala Ala Ala Ala Lys Thr
200 205 210

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act gct gct gtc caa gcc cca gct ggg gct ggt gaa gca aat agc caa 787
 Thr Ala Ala Val Gln Ala Pro Ala Gly Ala Gly Glu Ala Asn Ser Gln
 215 220 225

ccg cag gca aca gcg gtg gca gaa gct cct gaa gtt gat ccg atg acc 835
 Pro Gln Ala Thr Ala Val Ala Glu Ala Pro Glu Val Asp Pro Met Thr
 230 235 240 245

acg cag gtt ctt atg gcg cct gcg ggc caa gat gga gac gtc atg gct 883
 Thr Gln Val Leu Met Ala Pro Ala Gly Gln Asp Gly Asp Val Met Ala
 250 255 260

gag ggt tcg acg cag cag acg tac gcc aca ggc acg gtg gat tct tct 931
 Glu Gly Ser Thr Gln Gln Thr Tyr Ala Thr Gly Thr Val Asp Ser Ser
 265 270 275

gct cag gga tgg atc att gga ctc aca ctg gct gtc att tcc ttg gtt 979
 Ala Gln Gly Trp Ile Ile Gly Leu Thr Leu Ala Val Ile Ser Leu Val
 280 285 290

tca gcg tct gct gtg gcg gcg tgg gcg att cgt cgt tca gag gtc cag 1027
 Ser Ala Ser Ala Val Ala Ala Trp Ala Ile Arg Arg Ser Glu Val Gln
 295 300 305

ggc taaagcttcg tgaaatggat tga 1053
 Gly
 310

<210> 1880

<211> 310

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1880

Met Val Glu Gly Asn Thr Ile Gly Cys Ala Asp Ala Gly Gly Asn Gly
 1 5 10 15

Tyr Gln Thr Leu Leu Asp Ala Gly Phe Asp Val Glu Thr Thr Val Gln
 20 25 30

Phe Pro Glu Phe Leu Cys Arg Ile Asn Asp Phe Pro Gly Pro Asp Val
 35 40 45

Asp Asp Cys Met Thr Ala Ser Pro Ala Glu Ala Tyr Trp Ser Tyr Trp
 50 55 60

His Ala Pro Leu Gly Gly Asp Glu Trp Glu Tyr Ser Asn Leu Gly Ala
 65 70 75 80

Phe Leu Tyr Tyr Pro Lys Pro Gly Thr Val Glu Ala Trp Tyr Trp Gly
 85 90 95

Asp Thr Asp Arg Pro Gly Ala Ile Pro Val Ser Lys Ser Gln Ala Glu
 100 105 110

Leu Gly Leu Asp Ser Ala Asp Pro Asp Tyr Lys Ile Asp Phe Asp Pro
 115 120 125

Asn Asp Phe Ile Thr Thr Thr Pro Thr Ser Glu Ser Pro Ile Ala Asp
 130 135 140

Leu Gly Gly Asp Glu Glu Pro Thr Glu Thr Thr Glu Ala Pro Ile Ala
145 150 155 160

Gly Ala Gly Ala Gly Ser Ala Arg Gly Gln Ala Ala Glu Pro Thr Val
165 170 175

Glu Val Asn Pro Glu Asn Pro Asn Glu Val Leu Val Tyr Gln Asp Ser
180 185 190

Glu Gly Asn Ser Ile Thr Lys Gly Gln Tyr Glu Asn Leu Val Ala Ala
195 200 205

Ala Ala Ala Lys Thr Thr Ala Ala Val Gln Ala Pro Ala Gly Ala Gly
210 215 220

Glu Ala Asn Ser Gln Pro Gln Ala Thr Ala Val Ala Glu Ala Pro Glu
225 230 235 240

Val Asp Pro Met Thr Thr Gln Val Leu Met Ala Pro Ala Gly Gln Asp
245 250 255

Gly Asp Val Met Ala Glu Gly Ser Thr Gln Gln Thr Tyr Ala Thr Gly
260 265 270

Thr Val Asp Ser Ser Ala Gln Gly Trp Ile Ile Gly Leu Thr Leu Ala
275 280 285

Val Ile Ser Leu Val Ser Ala Ser Ala Val Ala Ala Trp Ala Ile Arg
290 295 300

Arg Ser Glu Val Gln Gly
305 310

<210> 1881

<211> 1257

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1234)

<223> RXA00692

<400> 1881

ccttaagcgg gggtcagaac atttctccaa ttcatttttaa ggacatgttt tcatgggetca 60

tctactgtggg aagagaacca ttcgctggtc tgctgcaacc gtg gct tta gca acc 115
Val Ala Leu Ala Thr
1 5

ggc gtt tcc ctg ttg gct cca cag gtc gtt gct gca cag gat gca tca 163
Gly Val Ser Leu Leu Ala Pro Gln Val Val Ala Ala Gln Asp Ala Ser
10 15 20

tcg gat att caa tta gct acc caa ttc atc gaa aaa gaa ttt gca acg 211
Ser Asp Ile Gln Leu Ala Thr Gln Phe Ile Glu Lys Glu Phe Ala Thr
25 30 35

aat ggc etc atc cct ggg cct gta ggt act cca gat att ggg etc aat 259

Asn	Gly	Leu	Ile	Pro	Gly	Pro	Val	Gly	Thr	Pro	Asp	Ile	Gly	Leu	Asn	
		40					45					50				
cag	gat	ctg	ttg	ctg	tcc	cta	aat	gcg	ctt	gcc	cct	gat	tct	cca	gag	307
Gln	Asp	Leu	Leu	Leu	Ser	Leu	Asn	Ala	Leu	Ala	Pro	Asp	Ser	Pro	Glu	
		55				60					65					
atc	gac	gct	gca	tat	gct	gca	att	gct	ccg	gag	ctc	gag	ggc	tat	gtc	355
Ile	Asp	Ala	Ala	Tyr	Ala	Ala	Ile	Ala	Pro	Glu	Leu	Glu	Gly	Tyr	Val	
		70			75				80					85		
tca	gtt	tct	gac	tac	atc	ttc	agc	gat	cgt	cta	gcc	aag	acc	gta	gct	403
Ser	Val	Ser	Asp	Tyr	Ile	Phe	Ser	Asp	Arg	Leu	Ala	Lys	Thr	Val	Ala	
				90				95					100			
ttc	caa	gat	gcc	ctc	ggc	gtc	aga	gat	gct	gat	ttt	atc	gcg	caa	ctt	451
Phe	Gln	Asp	Ala	Leu	Gly	Val	Arg	Asp	Ala	Asp	Phe	Ile	Ala	Gln	Leu	
			105					110				115				
gtc	agc	gct	gtt	caa	gaa	aac	ggc	cag	atc	aaa	aac	tta	gat	aat	ggc	499
Val	Ser	Ala	Val	Gln	Glu	Asn	Gly	Gln	Ile	Lys	Asn	Leu	Asp	Asn	Gly	
		120				125						130				
gaa	gcc	aca	act	gca	att	aat	aac	ttc	agc	cag	gcc	tgg	ggc	gtt	cta	547
Glu	Ala	Thr	Thr	Ala	Ile	Asn	Asn	Phe	Ser	Gln	Ala	Trp	Gly	Val	Leu	
		135				140					145					
gct	ctg	cac	cgc	gtc	ggc	gaa	acc	gaa	gca	gcc	gag	cgc	gca	aca	gaa	595
Ala	Leu	His	Arg	Val	Gly	Glu	Thr	Glu	Ala	Ala	Glu	Arg	Ala	Thr	Glu	
		150			155				160					165		
ttc	ctt	aaa	act	caa	gtg	tgc	tcc	gac	ggc	ggc	gtc	caa	tta	gcc	tca	643
Phe	Leu	Lys	Thr	Gln	Val	Cys	Ser	Asp	Gly	Gly	Val	Gln	Leu	Ala	Ser	
			170					175					180			
gca	atc	gaa	cct	aca	tgc	aaa	acc	acg	gat	tcc	gat	gtc	act	gca	atg	691
Ala	Ile	Glu	Pro	Thr	Cys	Lys	Thr	Thr	Asp	Ser	Asp	Val	Thr	Ala	Met	
			185					190					195			
gct	gca	cag	gct	ttg	act	ctg	gca	aat	ggc	gcg	cag	gat	cca	acc	aca	739
Ala	Ala	Gln	Ala	Leu	Thr	Leu	Ala	Asn	Gly	Ala	Gln	Asp	Pro	Thr	Thr	
		200				205						210				
caa	gcc	act	ctc	gat	tac	ctc	gtc	acc	acg	atg	gat	gag	acc	ggc	ggc	787
Gln	Ala	Thr	Leu	Asp	Tyr	Leu	Val	Thr	Thr	Met	Asp	Glu	Thr	Gly	Gly	
		215				220					225					
gtc	aaa	aat	act	tgg	acc	ggc	gtg	aat	tcc	aac	tcc	acg	gga	att	gtc	835
Val	Lys	Asn	Thr	Trp	Thr	Gly	Val	Asn	Ser	Asn	Ser	Thr	Gly	Ile	Val	
		230			235					240				245		
gga	tcc	gct	ttt	gct	ctt	gcg	ggc	gat	gag	gaa	aac	tac	ctc	aag	gct	883
Gly	Ser	Ala	Phe	Ala	Leu	Ala	Gly	Asp	Glu	Glu	Asn	Tyr	Leu	Lys	Ala	
			250					255					260			
cgt	gaa	tac	ctg	gca	tct	gtt	caa	ttt	ggc	gaa	gat	gca	gac	cca	tcg	931
Arg	Glu	Tyr	Leu	Ala	Ser	Val	Gln	Phe	Gly	Glu	Asp	Ala	Asp	Pro	Ser	
			265					270					275			
att	cag	ggc	ggc	ttt	gct	ttc	acc	gtg	aag	gct	aag	gaa	acc	aac	act	979
Ile	Gln	Gly	Gly	Phe	Ala	Phe	Thr	Val	Lys	Ala	Lys	Glu	Thr	Asn	Thr	

280 285 290

gcg att agc gat cag att cga cgc gca act ggc caa gca gca tta ggt 1027
 Ala Ile Ser Asp Gln Ile Arg Arg Ala Thr Gly Gln Ala Ala Leu Gly
 295 300 305

ttt gca ggc ggt aac tac gcc aac gat aaa ctg atc acc att gcg aac 1075
 Phe Ala Gly Gly Asn Tyr Ala Asn Asp Lys Leu Ile Thr Ile Ala Asn
 310 315 320 325

cca gta gat cca act cca gat cca gaa att cca act ccc cca gct gat 1123
 Pro Val Asp Pro Thr Pro Asp Pro Glu Ile Pro Thr Pro Pro Ala Asp
 330 335 340

tca gag gga tcc acc ggt gga att ggc ggc gct gga att atc atc gcc 1171
 Ser Glu Gly Ser Thr Gly Gly Ile Gly Gly Ala Gly Ile Ile Ile Ala
 345 350 355

atc ttg gcc atc ctt gcc gcc atc gct ggt gtc atg gga cca atg atg 1219
 Ile Leu Ala Ile Leu Ala Ala Ile Ala Gly Val Met Gly Pro Met Met
 360 365 370

gct aac ctg cag ttt taacatctga gagaagtaca gtg 1257
 Ala Asn Leu Gln Phe
 375

<210> 1882
 <211> 378
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1882
 Val Ala Leu Ala Thr Gly Val Ser Leu Leu Ala Pro Gln Val Val Ala
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Ala Gln Asp Ala Ser Ser Asp Ile Gln Leu Ala Thr Gln Phe Ile Glu
 20 25 30

Lys Glu Phe Ala Thr Asn Gly Leu Ile Pro Gly Pro Val Gly Thr Pro
 35 40 45

Asp Ile Gly Leu Asn Gln Asp Leu Leu Leu Ser Leu Asn Ala Leu Ala
 50 55 60

Pro Asp Ser Pro Glu Ile Asp Ala Ala Tyr Ala Ala Ile Ala Pro Glu
 65 70 75 80

Leu Glu Gly Tyr Val Ser Val Ser Asp Tyr Ile Phe Ser Asp Arg Leu
 85 90 95

Ala Lys Thr Val Ala Phe Gln Asp Ala Leu Gly Val Arg Asp Ala Asp
 100 105 110

Phe Ile Ala Gln Leu Val Ser Ala Val Gln Glu Asn Gly Gln Ile Lys
 115 120 125

Asn Leu Asp Asn Gly Glu Ala Thr Thr Ala Ile Asn Asn Phe Ser Gln
 130 135 140

Ala Trp Gly Val Leu Ala Leu His Arg Val Gly Glu Thr Glu Ala Ala

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145              150              155              160
Glu Arg Ala Thr Glu Phe Leu Lys Thr Gln Val Cys Ser Asp Gly Gly
                165              170              175
Val Gln Leu Ala Ser Ala Ile Glu Pro Thr Cys Lys Thr Thr Asp Ser
                180              185              190
Asp Val Thr Ala Met Ala Ala Gln Ala Leu Thr Leu Ala Asn Gly Ala
                195              200              205
Gln Asp Pro Thr Thr Gln Ala Thr Leu Asp Tyr Leu Val Thr Thr Met
                210              215              220
Asp Glu Thr Gly Gly Val Lys Asn Thr Trp Thr Gly Val Asn Ser Asn
                225              230              235              240
Ser Thr Gly Ile Val Gly Ser Ala Phe Ala Leu Ala Gly Asp Glu Glu
                245              250              255
Asn Tyr Leu Lys Ala Arg Glu Tyr Leu Ala Ser Val Gln Phe Gly Glu
                260              265              270
Asp Ala Asp Pro Ser Ile Gln Gly Gly Phe Ala Phe Thr Val Lys Ala
                275              280              285
Lys Glu Thr Asn Thr Ala Ile Ser Asp Gln Ile Arg Arg Ala Thr Gly
                290              295              300
Gln Ala Ala Leu Gly Phe Ala Gly Gly Asn Tyr Ala Asn Asp Lys Leu
                305              310              315              320
Ile Thr Ile Ala Asn Pro Val Asp Pro Thr Pro Asp Pro Glu Ile Pro
                325              330              335
Thr Pro Pro Ala Asp Ser Glu Gly Ser Thr Gly Gly Ile Gly Gly Ala
                340              345              350
Gly Ile Ile Ile Ala Ile Leu Ala Ile Leu Ala Ala Ile Ala Gly Val
                355              360              365
Met Gly Pro Met Met Ala Asn Leu Gln Phe
                370              375

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<210> 1883

<211> 606

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(583)

<223> RXA00693

<400> 1883

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gatgtacaaa ttaatctcac cgcatttgtc aggccacgcc atg tgg aaa gag gct 115
 Met Trp Lys Glu Ala

1

5

ttg gaa gaa ttc gga tca ggc ccc atc cac ggc tgc ggt tat ttc gag 163
 Leu Glu Glu Phe Pro Gly Ser Gly Pro Ile His Gly Ser Gly Tyr Phe Glu
 10 15 20

aac tat ctt ccc atc gac tat tcc gaa gca gga ttt cac cac tac ctc 211
 Asn Tyr Leu Pro Ile Asp Tyr Ser Ser Glu Ala Gly Phe His His Tyr Leu
 25 30 35

aag gag cgc act gac gcg gcc gat cct tgc gtt cca cca ccg gaa ggt 259
 Lys Glu Arg Thr Asp Ala Ala Asp Pro Ser Val Pro Pro Pro Glu Gly
 40 45 50

ttt gtg cac tgc agc tat ttc tgg atc gtt gat gat gac gat gtt ctt 307
 Phe Val His Cys Ser Tyr Phe Trp Ile Val Asp Asp Asp Val Leu
 55 60 65

gtc gga ttc tta gct tta agg cac gag ctg aac caa cat ctc ctg gaa 355
 Val Gly Phe Leu Ala Leu Arg His Glu Leu Asn Gln His Leu Leu Glu
 70 75 80 85

gtc gcg ggc cac att ggt tac ggc gtg cgc ccg tct gcg cgt cga aaa 403
 Val Ala Gly His Ile Gly Tyr Gly Val Arg Pro Ser Ala Arg Arg Lys
 90 95 100

ggc gct gca acc gca gcg ctg aaa ctc ggt gtt cat gaa gct cag gcc 451
 Gly Ala Ala Thr Ala Ala Leu Lys Leu Gly Val His Glu Ala Gln Ala
 105 110 115

ttg ggc atc gac aag gtt ttg ctg tgc gtc gca gga gat aac gaa cgc 499
 Leu Gly Ile Asp Lys Val Leu Leu Cys Val Ala Gly Asp Asn Glu Ala
 120 125 130

tcc agg aac gtc atc gaa aag tgc ggt gga gtt tat gaa tcc acg atc 547
 Ser Arg Asn Val Ile Glu Lys Cys Gly Gly Val Tyr Glu Ser Thr Ile
 135 140 145

cgt gga atg cga cgc tat tgg ata gcc aca gat tct taaaaaatct 593
 Arg Gly Met Arg Arg Tyr Trp Ile Ala Thr Asp Ser
 150 155 160

tcgcaagaac tta 606

<210> 1884

<211> 161

<212> PRT

<213> Corynebacterium glutamicum

<400> 1884

Met Trp Lys Glu Ala Leu Glu Glu Phe Gly Ser Gly Pro Ile His Gly
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Ser Gly Tyr Phe Glu Asn Tyr Leu Pro Ile Asp Tyr Ser Glu Ala Gly
 20 25 30

Phe His His Tyr Leu Lys Glu Arg Thr Asp Ala Ala Asp Pro Ser Val
 35 40 45

Pro Pro Pro Glu Gly Phe Val His Cys Ser Tyr Phe Trp Ile Val Asp
 50 55 60

Asp Asp Asp Val Leu Val Gly Phe Leu Ala Leu Arg His Glu Leu Asn
 65 70 75 80
 Gln His Leu Leu Glu Val Ala Gly His Ile Gly Tyr Gly Val Arg Pro
 85 90 95
 Ser Ala Arg Arg Lys Gly Ala Ala Thr Ala Ala Leu Lys Leu Gly Val
 100 105 110
 His Glu Ala Gln Ala Leu Gly Ile Asp Lys Val Leu Leu Cys Val Ala
 115 120 125
 Gly Asp Asn Glu Ala Ser Arg Asn Val Ile Glu Lys Cys Gly Gly Val
 130 135 140
 Tyr Glu Ser Thr Ile Arg Gly Met Arg Arg Tyr Trp Ile Ala Thr Asp
 145 150 155 160
 Ser

<210> 1885
 <211> 498
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(475)
 <223> RXA00701

<400> 1885
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 gtaggccgcg gccgaagctg acccaggcgg ctgcgagcat ttg gta ggg gag cca 115
 Leu Val Gly Glu Pro
 1 5
 cgg tcc gat tcc tgc ggt gag cag cgc gga tgc gaa cag tcc ggt gtt 163
 Arg Ser Asp Ser Cys Gly Glu Gln Arg Gly Cys Glu Gln Ser Gly Val
 10 15 20
 gcc gag gat gaa tcc gaa gcc ggg tcc gaa ggc tgc tcc gcc gag gat 211
 Ala Glu Asp Glu Ser Glu Ala Gly Ser Glu Gly Ser Ser Ala Glu Asp
 25 30 35
 gag gac aaa gaa gac tgc ttc aaa gcc tgc tgc gcc ggc acc gaa tgg 259
 Glu Asp Lys Glu Asp Cys Phe Lys Ala Cys Cys Ala Gly Thr Glu Trp
 40 45 50
 tgc gac tac ggc aac cat ggc ggt gag gac gcc gag cat ggc tac ggc 307
 Ser Asp Tyr Gly Asn His Gly Gly Glu Asp Ala Gly His Gly Tyr Gly
 55 60 65
 ttt aac gtc gaa tcc gtt ttc act gat ttc ggc gat gac agc ggc cag 355
 Phe Asn Val Glu Ser Val Phe Thr Asp Phe Gly Asp Asp Ser Gly Gln
 70 75 80 85
 cac gag ggg aat gac gat cgc gat gta gag ggg cgc ttg ggc ttt gtc 403


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His Glu Gly Asn Asp Asp Arg Asp Val Glu Gly Arg Leu Gly Phe Val
      90                      95                      100

gga cag gaa gga ttc cgg gtt gac gat cag cgg cca gaa gaa aat cac 451
Gly Gln Glu Gly Phe Arg Val Asp Asp Gln Arg Pro Glu Glu Asn His
      105                      110                      115

gat gct caa aac cgc aag gaa gct taaggtgagg aaggttttgg gct 498
Asp Ala Gln Asn Arg Lys Glu Ala
      120                      125

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<210> 1886

<211> 125

<212> PRT

<213> Corynebacterium glutamicum

<400> 1886

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Leu Val Gly Glu Pro Arg Ser Asp Ser Cys Gly Glu Gln Arg Gly Cys
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Glu Gln Ser Gly Val Ala Glu Asp Glu Ser Glu Ala Gly Ser Glu Gly
      20                      25                      30

Ser Ser Ala Glu Asp Glu Asp Lys Glu Asp Cys Phe Lys Ala Cys Cys
      35                      40                      45

Ala Gly Thr Glu Trp Ser Asp Tyr Gly Asn His Gly Gly Glu Asp Ala
      50                      55                      60

Glu His Gly Tyr Gly Phe Asn Val Glu Ser Val Phe Thr Asp Phe Gly
      65                      70                      75                      80

Asp Asp Ser Gly Gln His Glu Gly Asn Asp Asp Arg Asp Val Glu Gly
      85                      90                      95

Arg Leu Gly Phe Val Gly Gln Glu Gly Phe Arg Val Asp Asp Gln Arg
      100                      105                      110

Pro Glu Glu Asn His Asp Ala Gln Asn Arg Lys Glu Ala
      115                      120                      125

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<210> 1887

<211> 1095

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1072)

<223> RXA00707

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<400> 1887
tagttaaaag cacttacctt aactggtagg tgcttttttc atgtctacgc agtgggtaac 60

tttcagagga aaattacca accaaaaacaa aggaactttc atg aac gtg caa cgc 115
Met Asn Val Gln Arg
      1                      5

aaa ctg ctg gcg atc gta ggg gct ttc atg gca ggg tct tta gcc ttg 163

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Lys	Leu	Leu	Ala	Ile	Val	Gly	Ala	Phe	Met	Ala	Gly	Ser	Leu	Ala	Leu		
				10					15					20			
gga	aca	cca	act	gca	cag	gcc	caa	agc	att	ggc	agc	agt	gcc	tca	cag	211	
Gly	Thr	Pro	Thr	Ala	Gln	Ala	Gln	Ser	Ile	Gly	Ser	Ser	Ala	Ser	Gln		
			25					30					35				
aga	act	gaa	gtc	tta	cgt	ggg	ctg	acc	tca	tct	gcc	gga	ata	cca	gat	259	
Arg	Thr	Glu	Val	Leu	Arg	Gly	Leu	Thr	Ser	Ser	Ala	Gly	Ile	Pro	Asp		
		40					45					50					
gcc	aca	gcg	ccg	gaa	ggc	ggg	gca	aaa	gtc	gtg	gtc	ttt	gga	gat	tca	307	
Ala	Thr	Ala	Pro	Glu	Gly	Gly	Ala	Lys	Val	Val	Val	Phe	Gly	Asp	Ser		
	55				60						65						
cat	gca	tca	gga	acc	aat	gca	cca	ttt	gat	gtg	gat	gaa	cgc	ggc	tgc	355	
His	Ala	Ser	Gly	Thr	Asn	Ala	Pro	Phe	Asp	Val	Asp	Glu	Arg	Gly	Cys		
	70				75				80					85			
ctc	aag	ggg	aac	caa	tcg	tgg	cct	gat	caa	ttg	caa	gca	caa	caa	gga	403	
Leu	Lys	Gly	Asn	Gln	Ser	Trp	Pro	Asp	Gln	Leu	Ala	Gln	Gln	Gly			
			90					95					100				
ttg	cag	cag	ggg	gag	ctc	att	gac	ctt	tcc	tgc	aac	ggc	gcc	tcc	atc	451	
Leu	Gln	Gln	Gly	Glu	Leu	Ile	Asp	Leu	Ser	Cys	Asn	Gly	Ala	Ser	Ile		
			105				110						115				
aac	tcg	acg	ggt	ttc	cac	ttt	tcc	gat	gaa	gtt	cgg	cat	gca	gaa	gca	499	
Asn	Ser	Thr	Gly	Phe	His	Phe	Ser	Asp	Glu	Val	Arg	His	Ala	Glu	Ala		
	120						125					130					
cta	ggg	gcc	att	gga	cca	aat	acc	gag	aac	atc	ttc	atc	caa	ttt	ggc	547	
Leu	Gly	Ala	Ile	Gly	Pro	Asn	Thr	Glu	Asn	Ile	Phe	Ile	Gln	Phe	Gly		
	135				140						145						
aag	aat	gat	cag	tgg	gga	cac	tca	cca	atc	aat	ttg	cgc	tat	tcc	gtg	595	
Lys	Asn	Asp	Gln	Trp	Gly	His	Ser	Pro	Ile	Asn	Leu	Arg	Tyr	Ser	Val		
	150				155					160				165			
atc	aac	tgc	ctt	ttt	gat	gcg	gcc	aac	gga	tgc	ggt	gag	aaa	gct	gta	643	
Ile	Asn	Cys	Leu	Phe	Asp	Ala	Ala	Asn	Gly	Cys	Gly	Glu	Lys	Ala	Val		
			170					175					180				
gcg	gct	gga	acc	atg	cag	gat	ccc	tcc	tcg	gtc	acc	ggc	gaa	aac	tat	691	
Ala	Ala	Gly	Thr	Met	Gln	Asp	Pro	Ser	Ser	Val	Thr	Gly	Glu	Asn	Tyr		
			185				190					195					
gct	cag	cgg	atg	aaa	cct	gtc	atc	gac	tac	ctc	aag	tac	tac	gct	cca	739	
Ala	Gln	Arg	Met	Lys	Pro	Val	Ile	Asp	Tyr	Leu	Lys	Tyr	Tyr	Ala	Pro		
		200					205					210					
aat	gcg	cag	atc	acg	ttg	ctg	gga	tac	cag	gaa	tac	acc	cca	cga	agc	787	
Asn	Ala	Gln	Ile	Thr	Leu	Leu	Gly	Tyr	Gln	Glu	Tyr	Thr	Pro	Arg	Ser		
	215				220						225						
gga	agc	gag	att	tgt	gtc	cgc	gtg	gga	ggt	acg	gaa	cta	agg	aaa	cca	835	
Gly	Ser	Glu	Ile	Cys	Val	Arg	Val	Gly	Gly	Thr	Glu	Leu	Arg	Lys	Pro		
	230				235				240					245			
gac	gcc	acc	aac	ctg	gtg	tcc	tat	atg	aac	aat	ctt	gag	tcg	gcc	att	883	
Asp	Ala	Thr	Asn	Leu	Val	Ser	Tyr	Met	Asn	Asn	Leu	Glu	Ser	Ala	Ile		

	250	255	260	
ttt gaa gcc tct gag att ctt gac gtc cag cat gcc aat ctc cgt gag				931
Phe Glu Ala Ser Glu Ile Leu Asp Val Gln His Ala Asn Leu Arg Glu				
	265	270	275	
gcc act gca gga cac agc agc tgc tca gct gaa ccg tgg gtc aac gga				979
Ala Thr Ala Gly His Ser Ser Cys Ser Ala Glu Pro Trp Val Asn Gly				
	280	285	290	
gtg ctg gat atg cgg gta aac gct gta gga gcc acc tgg cac cca tct				1027
Val Leu Asp Met Arg Val Asn Ala Val Gly Gly Thr Trp His Pro Ser				
	295	300	305	
cca aag gga gat gaa gtg acc gcg ggc ctc ctc gga acc ttg atg				1072
Pro Lys Gly Asp Glu Val Thr Ala Gly Leu Glu Gly Thr Leu Met				
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taactatcta gaattcttca tag				1095
<210> 1888				
<211> 324				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 1888				
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Gly Ser Leu Ala Leu Gly Thr Pro Thr Ala Gln Ala Gln Ser Ile Gly				
20 25 30				
Ser Ser Ala Ser Gln Arg Thr Glu Val Leu Arg Gly Leu Thr Ser Ser				
35 40 45				
Ala Gly Ile Pro Asp Ala Thr Ala Pro Glu Gly Gly Ala Lys Val Val				
50 55 60				
Val Phe Gly Asp Ser His Ala Ser Gly Thr Asn Ala Pro Phe Asp Val				
65 70 75 80				
Asp Glu Arg Gly Cys Leu Lys Gly Asn Gln Ser Trp Pro Asp Gln Leu				
85 90 95				
Gln Ala Gln Gln Gly Leu Gln Gln Gly Glu Leu Ile Asp Leu Ser Cys				
100 105 110				
Asn Gly Ala Ser Ile Asn Ser Thr Gly Phe His Phe Ser Asp Glu Val				
115 120 125				
Arg His Ala Glu Ala Leu Gly Ala Ile Gly Pro Asn Thr Glu Asn Ile				
130 135 140				
Phe Ile Gln Phe Gly Lys Asn Asp Gln Trp Gly His Ser Pro Ile Asn				
145 150 155 160				
Leu Arg Tyr Ser Val Ile Asn Cys Leu Phe Asp Ala Ala Asn Gly Cys				
165 170 175				
Gly Glu Lys Ala Val Ala Ala Gly Thr Met Gln Asp Pro Ser Ser Val				

$$\begin{aligned} \frac{1}{\Gamma(\alpha)} \int_0^t (t-\tau)^{\alpha-1} \frac{d}{d\tau} \left(\frac{1}{\Gamma(\beta)} \int_0^\tau (\tau-s)^{\beta-1} \frac{d}{ds} \left(\frac{1}{\Gamma(\gamma)} \int_0^s (s-u)^{\gamma-1} \frac{d}{du} \left(\frac{1}{\Gamma(\delta)} \int_0^u (u-v)^{\delta-1} \frac{d}{dv} f(v) dv \right) du \right) ds \right) d\tau \\ = \frac{1}{\Gamma(\alpha+\beta+\gamma+\delta)} \int_0^t (t-u)^{\alpha+\beta+\gamma+\delta-1} f(u) du \end{aligned}$$
[illegible]

234

65	70	75	
ctt ctc ctg cag ctg att acc aag aag aaa ctt gat gtc act gaa gtt Leu Leu Leu Gln Leu Ile Thr Lys Lys Lys Leu Asp Val Thr Glu Val			349
80	85	90	
gcc ttg gcc cag gtg acc gac gag ttt att gct tac acc cga aaa ctg Ala Leu Ala Gln Val Thr Asp Glu Phe Ile Ala Tyr Thr Arg Lys Leu			397
95	100	105	
ggc gaa acc agc gat ttg gat gag acc aca gag ttc tta gtg gtg gcc Gly Glu Thr Ser Asp Leu Asp Glu Thr Thr Glu Phe Leu Val Val Ala			445
110	115	120	125
gca acg ctg ttg gat ctt aaa aca gct cgc ctg ctc ccg cgt ggt gaa Ala Thr Leu Leu Asp Leu Lys Thr Ala Arg Leu Leu Pro Arg Gly Glu			493
130	135	140	
gtc gac gat gaa gat gat ctc gaa ttg ctc gaa ata aag gat ctc ctt Val Asp Asp Glu Asp Asp Leu Glu Leu Leu Glu Ile Lys Asp Leu Leu			541
145	150	155	
ttc gcc agg ttg ttg cag tat cgc gct tac aag caa gtt gcg gaa atg Phe Ala Arg Leu Leu Gln Tyr Arg Ala Tyr Lys Gln Val Ala Glu Met			589
160	165	170	
ttt gcg caa tgg cag cga gat gct cga cgc agg tac ccg cgc gct gtc Phe Ala Gln Trp Gln Arg Asp Ala Arg Arg Arg Tyr Pro Arg Ala Val			637
175	180	185	
tca tta gaa act cag ttt gcc aac ctc ttg ccg ccc gtt tcc ttg ggt Ser Leu Glu Thr Gln Phe Ala Asn Leu Leu Pro Pro Val Ser Leu Gly			685
190	195	200	205
cat tcc tta aaa agt ttc agc gag ttg gct gct gtg gtg ttt cgt ccg His Ser Leu Lys Ser Phe Ser Glu Leu Ala Ala Val Val Phe Arg Pro			733
210	215	220	
aaa ccc cca gag acg gtg aaa aca gat cac gtg cac caa gtt gcg gtg Lys Pro Pro Glu Thr Val Lys Thr Asp His Val His Gln Val Ala Val			781
225	230	235	
tca gtt cca gag caa gcg gcc agg att ctt aac acg ttg aaa ctt gcc Ser Val Pro Glu Gln Ala Gly Arg Ile Leu Asn Thr Leu Lys Leu Ala			829
240	245	250	
gga att gat cat tat ttg agc ttt cag ctg ctc aca cgt gat tgt acc Gly Ile Asp His Tyr Leu Ser Phe Gln Leu Leu Thr Arg Asp Cys Thr			877
255	260	265	
gcg tca atg gaa gtg att gcc cgc ttc ctt gcc ttg ctg gaa ttg tat Ala Ser Met Glu Val Ile Gly Arg Phe Leu Ala Leu Leu Glu Leu Tyr			925
270	275	280	285
aag gca cgc gct att gaa acc ttg caa gaa gag cca ctc gcc gag ctt Lys Ala Arg Ala Ile Glu Thr Leu Gln Glu Glu Pro Leu Gly Glu Leu			973
290	295	300	
aaa gtt tcg tgg act gcc att gat gtc gat cca gca gtc gtc gcg gcg Lys Val Ser Trp Thr Gly Ile Asp Val Asp Pro Ala Val Val Ala Ala			1021
305	310	315	

agt gac tgg gag taatcagttt ttcttaagga aac
 Ser Asp Trp Glu
 320

1056

<210> 1890

<211> 321

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1890

Met Thr Lys Val Ala Glu Leu Asp Gln Glu Trp Ser Glu Val Asp Asp
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Ala Glu Leu Asp Ala Gln Ser Ala Gly Thr Ser Asp Ser Ser Ser Thr
 20 25 30

Asp Asp Phe Ala Asp Ala Glu Asn Thr Ser Glu Asn Leu Gly Pro Ile
 35 40 45

Gly Pro Glu Pro Leu Pro Glu Pro Asp Gly Asp Val Pro Ala Ser Gly
 50 55 60

Phe Gln Val Gln Leu Asp Asn Phe Glu Gly Pro Phe Asp Leu Leu Leu
 65 70 75 80

Gln Leu Ile Thr Lys Lys Lys Leu Asp Val Thr Glu Val Ala Leu Ala
 85 90 95

Gln Val Thr Asp Glu Phe Ile Ala Tyr Thr Arg Lys Leu Gly Glu Thr
 100 105 110

Ser Asp Leu Asp Glu Thr Thr Glu Phe Leu Val Val Ala Ala Thr Leu
 115 120 125

Leu Asp Leu Lys Thr Ala Arg Leu Leu Pro Arg Gly Glu Val Asp Asp
 130 135 140

Glu Asp Asp Leu Glu Leu Leu Glu Ile Lys Asp Leu Leu Phe Ala Arg
 145 150 155 160

Leu Leu Gln Tyr Arg Ala Tyr Lys Gln Val Ala Glu Met Phe Ala Gln
 165 170 175

Trp Gln Arg Asp Ala Arg Arg Arg Tyr Pro Arg Ala Val Ser Leu Glu
 180 185 190

Thr Gln Phe Ala Asn Leu Leu Pro Pro Val Ser Leu Gly His Ser Leu
 195 200 205

Lys Ser Phe Ser Glu Leu Ala Ala Val Val Phe Arg Pro Lys Pro Pro
 210 215 220

Glu Thr Val Lys Thr Asp His Val His Gln Val Ala Val Ser Val Pro
 225 230 235 240

Glu Gln Ala Gly Arg Ile Leu Asn Thr Leu Lys Leu Ala Gly Ile Asp
 245 250 255

His Tyr Leu Ser Phe Gln Leu Leu Thr Arg Asp Cys Thr Ala Ser Met

260

265

270

Glu Val Ile Gly Arg Phe Leu Ala Leu Leu Glu Leu Tyr Lys Ala Arg
275 280 285

Ala Ile Glu Thr Leu Gln Glu Glu Pro Leu Gly Glu Leu Lys Val Ser
290 295 300

Trp Thr Gly Ile Asp Val Asp Pro Ala Val Val Ala Ala Ser Asp Trp
305 310 315 320

Glu

<210> 1891

<211> 684

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(661)

<223> RXA00714

<400> 1891

cggtcaatcaa gctgtcaaaa aaaatacaag ttagggtcaca aaatgatttc agtcgtgaga 60

accatcacat ataagacatc tcatgatcta acattttcttc atg gct acg att aca 115
Met Ala Thr Ile Thr
1 5

cgc acc gac aga ctg atc ctc gta ccg ctc act gtt gag ctc gaa gac 163
Arg Thr Asp Arg Leu Ile Leu Val Pro Leu Thr Val Glu Leu Glu Asp
10 15 20

gag gcc cac cag att tac tct gat tct cga atc tgg gaa cac cgc ccc 211
Glu Ala His Gln Ile Tyr Ser Asp Ser Arg Ile Trp Glu His Arg Pro
25 30 35

cag gcg cgt cac acc aac gtg cgt gtc acg cgc gac atc atc aag cgc 259
Gln Ala Arg His Thr Asn Val Arg Val Thr Arg Asp Ile Ile Lys Arg
40 45 50

acc aat gaa agc tgg ggc aag aaa gac ctt ggc ccc tgg ggt gtt tac 307
Thr Asn Glu Ser Trp Gly Lys Lys Asp Leu Gly Pro Trp Gly Val Tyr
55 60 65

ctc cgt gac cgc cca tcg gaa ttc gtt ggc gtt ggt ggc gtt gaa ctc 355
Leu Arg Asp Arg Pro Ser Glu Phe Val Gly Val Gly Gly Val Glu Leu
70 75 80 85

atc gac gga aaa gta tgg gac ctc aag tac cgc ctc cgc ccc gac cta 403
Ile Asp Gly Lys Val Trp Asp Leu Lys Tyr Arg Leu Arg Pro Asp Leu
90 95 100

tgg ggc aat gga tac gcc acg gaa atc tcc aac gcc gca aca ctg gcc 451
Trp Gly Asn Gly Tyr Ala Thr Glu Ile Ser Asn Ala Ala Thr Leu Ala
105 110 115

acc aag cgt atc gac gac agc ctc cca ctc acg gcc agg gtg act acc 499

```

Thr Lys Arg Ile Asp Asp Ser Leu Pro Leu Thr Ala Arg Val Thr Thr
    120                      125                      130
aac cac cct gcc tca ttc cgt att ttg gaa aaa ctg gga ctc acc ccc 547
Asn His Pro Ala Ser Phe Arg Ile Leu Glu Lys Leu Gly Leu Thr Pro
    135                      140                      145

gta tgg gaa ggc cga cga gtc gga acg gaa gat gac ccc aac gag cct 595
Val Trp Glu Gly Arg Arg Val Gly Thr Glu Asp Asp Pro Asn Glu Pro
    150                      155                      160

gat gtg aga att tat tct gac cgt ccg cta tcg gat gaa att ctt gaa 643
Asp Val Arg Ile Tyr Ser Asp Arg Pro Leu Ser Asp Glu Ile Leu Glu
    170                      175                      180

atg ctc aag caa cga cca tagaccagaa aatctcacc ctt 684
Met Leu Lys Gln Arg Pro
    185

```

<210> 1892

<211> 187

<212> PRT

<213> Corynebacterium glutamicum

<400> 1892

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Met Ala Thr Ile Thr Arg Thr Asp Arg Leu Ile Leu Val Pro Leu Thr
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Val Glu Leu Glu Asp Glu Ala His Gln Ile Tyr Ser Asp Ser Arg Ile
    20                      25                      30

Trp Glu His Arg Pro Gln Ala Arg His Thr Asn Val Arg Val Thr Arg
    35                      40                      45

Asp Ile Ile Lys Arg Thr Asn Glu Ser Trp Gly Lys Lys Asp Leu Gly
    50                      55                      60

Pro Trp Gly Val Tyr Leu Arg Asp Arg Pro Ser Glu Phe Val Gly Val
    65                      70                      75                      80

Gly Gly Val Glu Leu Ile Asp Gly Lys Val Trp Asp Leu Lys Tyr Arg
    85                      90                      95

Leu Arg Pro Asp Leu Trp Gly Asn Gly Tyr Ala Thr Glu Ile Ser Asn
    100                     105                     110

Ala Ala Thr Leu Ala Thr Lys Arg Ile Asp Asp Ser Leu Pro Leu Thr
    115                     120                     125

Ala Arg Val Thr Thr Asn His Pro Ala Ser Phe Arg Ile Leu Glu Lys
    130                     135                     140

Leu Gly Leu Thr Pro Val Trp Glu Gly Arg Arg Val Gly Thr Glu Asp
    145                     150                     155                     160

Asp Pro Asn Glu Pro Asp Val Arg Ile Tyr Ser Asp Arg Pro Leu Ser
    165                     170                     175

Asp Glu Ile Leu Glu Met Leu Lys Gln Arg Pro
    180                     185

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<210> 1893
 <211> 636
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(613)
 <223> RXA00716

<400> 1893
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 gatttccgcg atgagcctta tccctcagac gaggtctcgg atg gaa tca atc ttg 115
 Met Glu Ser Ile Leu
 1 5
 ttg gtg gtc gat acc cca gtt tca gca cgc acg ctg gct ggg gtg ttg 163
 Leu Val Val Asp Thr Pro Val Ser Ala Arg Thr Leu Ala Gly Val Leu
 10 15 20
 ggc att gac gtg cct gca aca gag gca att ttg aag gaa atg gcc ttt 211
 Gly Ile Asp Val Pro Ala Thr Glu Ala Ile Leu Lys Glu Met Ala Phe
 25 30 35
 gag ctt tct gaa cgg ggc agc ggc att gat ctg cgg gaa acg gca gaa 259
 Glu Leu Ser Glu Arg Gly Ser Gly Ile Asp Leu Arg Glu Thr Ala Glu
 40 45 50
 gga tgg cgc tat tac acc cgc ccg gaa aat gcg gac atc gtc gag caa 307
 Gly Trp Arg Tyr Tyr Thr Arg Pro Glu Asn Ala Asp Ile Val Glu Gln
 55 60 65
 ttc ctc ctc gat gga aac caa acc aga ctg tcc cgt gca gca ttg gaa 355
 Phe Leu Leu Asp Gly Asn Gln Thr Arg Leu Ser Arg Ala Ala Leu Glu
 70 75 80 85
 aca ctc gcg gtg gtg gca tat cgg cag ccg gtc aca cgc tcc cag att 403
 Thr Leu Ala Val Val Ala Tyr Arg Gln Pro Val Thr Arg Ser Gln Ile
 90 95 100
 tca gca gtg cgc gga gta aat gtc gac ggc gtc atg aga acc ttg cag 451
 Ser Ala Val Arg Gly Val Asn Val Asp Gly Val Met Arg Thr Leu Gln
 105 110 115
 ctt cga ggc cta gtc aaa gaa gtc gat gtg gac gaa tca acg ggc gca 499
 Leu Arg Gly Leu Val Lys Glu Val Asp Val Asp Glu Ser Thr Gly Ala
 120 125 130
 cac cgc tat ggc aca acg gaa ttg ctg ctt gag ctg ttg ggt att gat 547
 His Arg Tyr Gly Thr Thr Glu Leu Leu Leu Glu Leu Leu Gly Ile Asp
 135 140 145
 tct ttg gat aaa tta cca gat cta gca ccg ctt ttg ccg gat gtt gac 595
 Ser Leu Asp Lys Leu Pro Asp Leu Ala Pro Leu Leu Pro Asp Val Asp
 150 155 160 165
 tcc att gat gaa gac ttc taaagcatca gttaaagccc cga 636
 Ser Ile Asp Glu Asp Phe

170

<210> 1894

<211> 171

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1894

Met Glu Ser Ile Leu Leu Val Val Asp Thr Pro Val Ser Ala Arg Thr
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Leu Ala Gly Val Leu Gly Ile Asp Val Pro Ala Thr Glu Ala Ile Leu
 20 25 30

Lys Glu Met Ala Phe Glu Leu Ser Glu Arg Gly Ser Gly Ile Asp Leu
 35 40 45

Arg Glu Thr Ala Glu Gly Trp Arg Tyr Tyr Thr Arg Pro Glu Asn Ala
 50 55 60

Asp Ile Val Glu Gln Phe Leu Leu Asp Gly Asn Gln Thr Arg Leu Ser
 65 70 75 80

Arg Ala Ala Leu Glu Thr Leu Ala Val Val Ala Tyr Arg Gln Pro Val
 85 90 95

Thr Arg Ser Gln Ile Ser Ala Val Arg Gly Val Asn Val Asp Gly Val
 100 105 110

Met Arg Thr Leu Gln Leu Arg Gly Leu Val Lys Glu Val Asp Val Asp
 115 120 125

Glu Ser Thr Gly Ala His Arg Tyr Gly Thr Thr Glu Leu Leu Leu Glu
 130 135 140

Leu Leu Gly Ile Asp Ser Leu Asp Lys Leu Pro Asp Leu Ala Pro Leu
 145 150 155 160

Leu Pro Asp Val Asp Ser Ile Asp Glu Asp Phe
 165 170

<210> 1895

<211> 1752

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1729)

<223> RXA00719

<400> 1895

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tcattccacct agtggaagcc tccgctgaaa ggagcaacca gtg act gat aaa cac 115
 Val Thr Asp Lys His
 1 5

acc atg cct ggt gaa gag gac gac acc gta ttc gtc tac cac acc cac 163

Thr	Met	Pro	Gly	Glu	Glu	Asp	Asp	Thr	Val	Phe	Val	Tyr	His	Thr	His		
				10					15					20			
aaa	ggc	gaa	atg	gac	gtc	gaa	ggc	gcg	ttt	gct	gac	gaa	gaa	gaa	cta	211	
Lys	Gly	Glu	Met	Asp	Val	Glu	Gly	Ala	Phe	Ala	Asp	Glu	Glu	Glu	Leu		
			25					30					35				
gca	cca	cac	ggc	ggc	tgg	gct	tcc	gca	gat	ttc	gac	cca	gca	gaa	ttc	259	
Ala	Pro	His	Gly	Gly	Trp	Ala	Ser	Ala	Asp	Phe	Asp	Pro	Ala	Glu	Phe		
			40				45					50					
ggc	tac	gaa	gac	tct	gac	gat	gac	ttc	gat	gca	gag	gac	ttt	gac	gaa	307	
Gly	Tyr	Glu	Asp	Ser	Asp	Asp	Asp	Phe	Asp	Ala	Glu	Asp	Phe	Asp	Glu		
	55					60					65						
aca	gag	ttc	tcc	aac	cct	gat	ttc	ggc	gaa	gac	tac	tct	gat	gaa	gac	355	
Thr	Glu	Phe	Ser	Asn	Pro	Asp	Phe	Gly	Glu	Asp	Tyr	Ser	Asp	Glu	Asp		
	70					75					80				85		
tgg	gaa	gaa	atc	gag	acc	gca	ttc	gga	ttc	gac	cca	agc	cac	ctt	gaa	403	
Trp	Glu	Glu	Ile	Glu	Thr	Ala	Phe	Gly	Phe	Asp	Pro	Ser	His	Leu	Glu		
				90					95					100			
gaa	gct	ctc	tgc	acg	gtc	gct	atc	gtc	gga	cgc	cca	aat	gtt	ggc	aaa	451	
Glu	Ala	Leu	Cys	Thr	Val	Ala	Ile	Val	Gly	Arg	Pro	Asn	Val	Gly	Lys		
			105					110					115				
tca	acc	ttg	gtg	aac	cgc	ttt	att	gga	cgt	cga	gaa	gca	gtc	gtg	gaa	499	
Ser	Thr	Leu	Val	Asn	Arg	Phe	Ile	Gly	Arg	Arg	Glu	Ala	Val	Val	Glu		
		120					125					130					
gat	ttc	ccc	ggc	gta	acc	cgt	gac	cgc	atc	tcc	tac	atc	tct	gac	tgg	547	
Asp	Phe	Pro	Gly	Val	Thr	Arg	Asp	Arg	Ile	Ser	Tyr	Ile	Ser	Asp	Trp		
		135				140					145						
ggc	gga	cac	cgt	ttc	tgg	gtt	cag	gac	aca	ggc	gga	tgg	gat	cct	aac	595	
Gly	Gly	His	Arg	Phe	Trp	Val	Gln	Asp	Thr	Gly	Gly	Trp	Asp	Pro	Asn		
	150					155				160					165		
gtc	aag	ggc	atc	cac	gca	tcg	atc	gca	cag	caa	gca	gaa	gtt	gct	atg	643	
Val	Lys	Gly	Ile	His	Ala	Ser	Ile	Ala	Gln	Gln	Ala	Glu	Val	Ala	Met		
				170				175						180			
agc	act	gcc	gat	gtc	atc	gta	ttc	gtc	gtg	gac	acc	aag	gtg	ggc	atc	691	
Ser	Thr	Ala	Asp	Val	Ile	Val	Phe	Val	Val	Asp	Thr	Lys	Val	Gly	Ile		
			185					190					195				
acc	gaa	act	gac	tca	gtg	atg	gca	gca	aaa	ctg	ttg	cgc	tcg	gaa	gtg	739	
Thr	Glu	Thr	Asp	Ser	Val	Met	Ala	Ala	Lys	Leu	Leu	Arg	Ser	Glu	Val		
			200				205						210				
cca	gtg	atc	ttg	gtt	gcg	aac	aaa	ttc	gac	tcc	gac	agc	cag	tgg	gct	787	
Pro	Val	Ile	Leu	Val	Ala	Asn	Lys	Phe	Asp	Ser	Asp	Ser	Gln	Trp	Ala		
		215				220					225						
gac	atg	gct	gag	ttc	tac	agc	ctc	ggc	ctt	ggc	gat	cca	tac	cca	gtt	835	
Asp	Met	Ala	Glu	Phe	Tyr	Ser	Leu	Gly	Leu	Gly	Asp	Pro	Tyr	Pro	Val		
			230			235				240					245		
tca	gcc	cag	cat	gga	cgt	ggc	gct	gac	gtt	ttg	gac	aaa	gtc	ctt		883	
Ser	Ala	Gln	His	Gly	Arg	Gly	Gly	Ala	Asp	Val	Leu	Asp	Lys	Val	Leu		

	250	255	260	
	gaa ctc ttc cca gaa gag cct cgc tcc aag tcc atc gtg gaa ggc cct Glu Leu Phe Pro Glu Glu Pro Arg Ser Lys Ser Ile Val Glu Gly Pro 265	270	275	931
	cgt cgt gtc gcc ctt gtg ggt aag cca aac gtg ggt aag tct tca ctg Arg Arg Val Ala Leu Val Gly Lys Pro Asn Val Gly Lys Ser Ser Leu 280	285	290	979
	ctc aac aag ttt gct ggc gag acc cgc tct gtc gtg gac aat gtt gca Leu Asn Lys Phe Ala Gly Glu Thr Arg Ser Val Val Asp Asn Val Ala 295	300	305	1027
	gga acc acc gtt gac ccc gtt gac tcc ctg att cag ctg gat caa aaa Gly Thr Thr Val Asp Pro Val Asp Ser Leu Ile Gln Leu Asp Gln Lys 310	315	320	1075
	ctg tgg aaa ttc gtg gat act gct ggt ctt cgc aaa aag gtc aag act Leu Trp Lys Phe Val Asp Thr Ala Gly Leu Arg Lys Lys Val Lys Thr 330	335	340	1123
	gca tct ggc cac gag tac tac gca tca ctg cgt acc cac ggt gcc atc Ala Ser Gly His Glu Tyr Tyr Ala Ser Leu Arg Thr His Gly Ala Ile 345	350	355	1171
	gat gca gct gag ctg tgt gtt ttg ctt atc gat tcc tcc gaa ccc atc Asp Ala Ala Glu Leu Cys Val Leu Leu Ile Asp Ser Ser Glu Pro Ile 360	365	370	1219
	acc gag cag gat cag cgc gtg ctc gca atg atc acc gat gcc ggt aag Thr Glu Gln Asp Gln Arg Val Leu Ala Met Ile Thr Asp Ala Gly Lys 375	380	385	1267
	gca ctg gtt att cgc ttc aac aag tgg gat ctc atg gat gaa gat cgc Ala Leu Val Ile Ala Phe Asn Lys Trp Asp Leu Met Asp Glu Asp Arg 390	395	400	1315
	cgc atc gat ttg gat cgc gaa ctt gat ctc cag ttg gca cac gtg cct Arg Ile Asp Leu Asp Arg Glu Leu Asp Leu Gln Leu Ala His Val Pro 410	415	420	1363
	tgg gca aag cgc atc aac atc tcc gcc aaa acc ggt cgt gca ctg cag Trp Ala Lys Arg Ile Asn Ile Ser Ala Lys Thr Gly Arg Ala Leu Gln 425	430	435	1411
	cgc ctc gag cca gca atg ttg gaa cgc ctc gac aac tgg gat cgc cgt Arg Leu Glu Pro Ala Met Leu Glu Ala Leu Asp Asn Trp Asp Arg Arg 440	445	450	1459
	atc tcc act ggt cag ctg aac acc tgg ctg cgt gaa gca att gct cgc Ile Ser Thr Gly Gln Leu Asn Thr Trp Leu Arg Glu Ala Ile Ala Ala 455	460	465	1507
	aac cca cca cca atg cgt ggc gga cgt ttg cct cga gtg ctg ttt gcc Asn Pro Pro Pro Met Arg Gly Gly Arg Leu Pro Arg Val Leu Phe Ala 470	475	480	1555
	acc cag gca tct act cag cca cca gtg atc gta ctg ttc acc acc ggc Thr Gln Ala Ser Thr Gln Pro Pro Val Ile Val Leu Phe Thr Thr Gly 490	495	500	1603

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ttc ctc gaa gca ggt tac cga cga tac ctg gag cgc aag ttc cgt gaa 1651
Phe Leu Glu Ala Gly Tyr Arg Arg Tyr Leu Glu Arg Lys Phe Arg Glu
      505                        510                        515

cgt ttc ggc ttt gaa ggc act cca gtg cga atc gct gtg cgt gtt cgc 1699
Arg Phe Gly Phe Glu Gly Thr Pro Val Arg Ile Ala Val Arg Val Arg
      520                        525                        530

gag cgc cgc ggc aag ggc gga aac aag cag taaagcttga ttttcctaa 1749
Glu Arg Arg Gly Lys Gly Gly Asn Lys Gln
      535                        540

aag 1752

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<210> 1896

<211> 543

<212> PRT

<213> Corynebacterium glutamicum

<400> 1896

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Val Thr Asp Lys His Thr Met Pro Gly Glu Glu Asp Asp Thr Val Phe
 1          5          10          15

Val Tyr His Thr His Lys Gly Glu Met Asp Val Glu Gly Ala Phe Ala
      20          25          30

Asp Glu Glu Glu Leu Ala Pro His Gly Gly Trp Ala Ser Ala Asp Phe
      35          40          45

Asp Pro Ala Glu Phe Gly Tyr Glu Asp Ser Asp Asp Asp Phe Asp Ala
      50          55          60

Glu Asp Phe Asp Glu Thr Glu Phe Ser Asn Pro Asp Phe Gly Glu Asp
      65          70          75          80

Tyr Ser Asp Glu Asp Trp Glu Glu Ile Glu Thr Ala Phe Gly Phe Asp
      85          90          95

Pro Ser His Leu Glu Glu Ala Leu Cys Thr Val Ala Ile Val Gly Arg
      100         105         110

Pro Asn Val Gly Lys Ser Thr Leu Val Asn Arg Phe Ile Gly Arg Arg
      115         120         125

Glu Ala Val Val Glu Asp Phe Pro Gly Val Thr Arg Asp Arg Ile Ser
      130         135         140

Tyr Ile Ser Asp Trp Gly Gly His Arg Phe Trp Val Gln Asp Thr Gly
      145         150         155         160

Gly Trp Asp Pro Asn Val Lys Gly Ile His Ala Ser Ile Ala Gln Gln
      165         170         175

Ala Glu Val Ala Met Ser Thr Ala Asp Val Ile Val Phe Val Val Asp
      180         185         190

Thr Lys Val Gly Ile Thr Glu Thr Asp Ser Val Met Ala Ala Lys Leu
      195         200         205

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Leu Arg Ser Glu Val Pro Val Ile Leu Val Ala Asn Lys Phe Asp Ser
 210 215 220
 Asp Ser Gln Trp Ala Asp Met Ala Glu Phe Tyr Ser Leu Gly Leu Gly
 225 230 235 240
 Asp Pro Tyr Pro Val Ser Ala Gln His Gly Arg Gly Gly Ala Asp Val
 245 250 255
 Leu Asp Lys Val Leu Glu Leu Phe Pro Glu Glu Pro Arg Ser Lys Ser
 260 265 270
 Ile Val Glu Gly Pro Arg Arg Val Ala Leu Val Gly Lys Pro Asn Val
 275 280 285
 Gly Lys Ser Ser Leu Leu Asn Lys Phe Ala Gly Glu Thr Arg Ser Val
 290 295 300
 Val Asp Asn Val Ala Gly Thr Thr Val Asp Pro Val Asp Ser Leu Ile
 305 310 315 320
 Gln Leu Asp Gln Lys Leu Trp Lys Phe Val Asp Thr Ala Gly Leu Arg
 325 330 335
 Lys Lys Val Lys Thr Ala Ser Gly His Glu Tyr Tyr Ala Ser Leu Arg
 340 345 350
 Thr His Gly Ala Ile Asp Ala Ala Glu Leu Cys Val Leu Leu Ile Asp
 355 360 365
 Ser Ser Glu Pro Ile Thr Glu Gln Asp Gln Arg Val Leu Ala Met Ile
 370 375 380
 Thr Asp Ala Gly Lys Ala Leu Val Ile Ala Phe Asn Lys Trp Asp Leu
 385 390 395 400
 Met Asp Glu Asp Arg Arg Ile Asp Leu Asp Arg Glu Leu Asp Leu Gln
 405 410 415
 Leu Ala His Val Pro Trp Ala Lys Arg Ile Asn Ile Ser Ala Lys Thr
 420 425 430
 Gly Arg Ala Leu Gln Arg Leu Glu Pro Ala Met Leu Glu Ala Leu Asp
 435 440 445
 Asn Trp Asp Arg Arg Ile Ser Thr Gly Gln Leu Asn Thr Trp Leu Arg
 450 455 460
 Glu Ala Ile Ala Ala Asn Pro Pro Pro Met Arg Gly Gly Arg Leu Pro
 465 470 475 480
 Arg Val Leu Phe Ala Thr Gln Ala Ser Thr Gln Pro Pro Val Ile Val
 485 490 495
 Leu Phe Thr Thr Gly Phe Leu Glu Ala Gly Tyr Arg Arg Tyr Leu Glu
 500 505 510
 Arg Lys Phe Arg Glu Arg Phe Gly Phe Glu Gly Thr Pro Val Arg Ile
 515 520 525
 Ala Val Arg Val Arg Glu Arg Arg Gly Lys Gly Gly Asn Lys Gln

530

535

540

<210> 1897

<211> 671

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(648)

<223> RXA00724

<400> 1897

atc ggt gag gaa gtc ctc gcc gga cgc caa gcc tat gtg gtg tgt ccg 48

Ile Gly Glu Glu Val Leu Ala Gly Arg Gln Ala Tyr Val Val Cys Pro
1 5 10 15

cgc att gaa ggc gaa ggc gcc gtg ctg gaa atc cac gcc tat ctt tcc 96

Arg Ile Glu Gly Glu Gly Gly Val Leu Glu Ile His Ala Tyr Leu Ser
20 25 30

gaa cag gta tat cca gga ttg aat gtt gga atg ctg cac ggt cgc atg 144

Glu Gln Val Tyr Pro Gly Leu Asn Val Gly Met Leu His Gly Arg Met
35 40 45

gac acg gat ctc aaa gat tcg gtc atg cag gaa ttc gcc caa ggt gag 192

Asp Thr Asp Leu Lys Asp Ser Val Met Gln Glu Phe Ala Gln Gly Glu
50 55 60

atc gat att ttg gtc gcc acc acg gtc att gag gtc ggt att gac gtt 240

Ile Asp Ile Leu Val Ala Thr Thr Val Ile Glu Val Gly Ile Asp Val
65 70 75 80

gcc aac gcc acc gtc atg ctc atc cgc gag gcg gaa cgc ttc gcc gtt 288

Ala Asn Ala Thr Val Met Leu Ile Arg Glu Ala Glu Arg Phe Gly Val
85 90 95

tcc cag atc cac cag ctg cgc gcc cgt gtt gcc cgt ggg cag cac gat 336

Ser Gln Ile His Gln Leu Arg Gly Arg Val Gly Arg Gly Gln His Asp
100 105 110

tcc ctc tgc ctg ctg cac acc acc ttc gac gag gac tcc cca caa ggc 384

Ser Leu Cys Leu Leu His Thr Thr Phe Asp Glu Asp Ser Pro Gln Gly
115 120 125

caa cgc ctc gcc gca att tcc acc aca acc gac ggt ttt caa ctc tct 432

Gln Arg Leu Ala Ala Ile Ser Thr Thr Thr Asp Gly Phe Gln Leu Ser
130 135 140

gaa ctt gat ttg cag gta cgc caa gaa gcc gac gtg ttg gcc acc cgc 480

Glu Leu Asp Leu Gln Val Arg Gln Glu Gly Asp Val Leu Gly Thr Arg
145 150 155 160

cag tcc gcc agc gac acc aaa ctc cgt cac ctc tcg ttt atc agc gac 528

Gln Ser Gly Ser Asp Thr Lys Leu Arg His Leu Ser Phe Ile Ser Asp
165 170 175

caa aaa atc atc gag cgt gcg ctt atc gac gcc acc gag ctg gtt gcc 576

Gln Lys Ile Ile Glu Arg Ala Leu Ile Asp Ala Thr Glu Leu Val Ala
180 185 190

aac cag gaa tac ctg gaa aag agc tgatattgat agggtttaag tca 671
Asn Gln Glu Tyr Leu Glu Lys Ser
210 215

<213> Corynebacterium glutamicum

Ile Gly Glu Glu Val Leu Ala Gly Arg Gln Ala Tyr Val Val Cys Pro
1 5 10 15

Arg Ile Glu Gly Glu Gly Gly Val Leu Glu Ile His Ala Tyr Leu Ser
20 25 30

Glu Gln Val Tyr Pro Gly Leu Asn Val Gly Met Leu His Gly Arg Met
35 40 45

Asp Thr Asp Leu Lys Asp Ser Val Met Gln Glu Phe Ala Gln Gly Glu
50 55 60

Ile Asp Ile Leu Val Ala Thr Thr Val Ile Glu Val Gly Ile Asp Val
65 70 75 80

Ala Asn Ala Thr Val Met Leu Ile Arg Glu Ala Glu Arg Phe Gly Val
85 90 95

Ser Gln Ile His Gln Leu Arg Gly Arg Val Gly Arg Gly Gln His Asp
100 105 110

Ser Leu Cys Leu Leu His Thr Thr Phe Asp Glu Asp Ser Pro Gln Gly
115 120 125

Gln Arg Leu Ala Ala Ile Ser Thr Thr Thr Asp Gly Phe Gln Leu Ser
130 135 140

Glu Leu Asp Leu Gln Val Arg Gln Glu Gly Asp Val Leu Gly Thr Arg
145 150 155 160

Gln Ser Gly Ser Asp Thr Lys Leu Arg His Leu Ser Phe Ile Ser Asp
165 170 175

Gln Lys Ile Ile Glu Arg Ala Leu Ile Asp Ala Thr Glu Leu Val Ala
180 185 190

Ala Ser Arg Ser Arg Ala Leu Glu Leu Val Ser Asp Ile Ala Met Ile
195 200 205

Asn Gln Glu Tyr Leu Glu Lys Ser
210 215

<211> 164

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(141)

<223> RXA00726

<400> 1899

cac gaa atg ggc ttc gcc cac gaa gtc gcc gac cag gtc gtg ttc atg	48
His Glu Met Gly Phe Ala His Glu Val Ala Asp Gln Val Val Phe Met	
1 5 10 15	

gcc gat gga gtt gtc gtt gaa gcc gga acc ccc gaa caa gtt ctg gac	96
Ala Asp Gly Val Val Val Glu Ala Gly Thr Pro Glu Gln Val Leu Asp	
20 25 30	

aat cca aag gaa cag cgc acc aaa gac ttc ctg tct tct ctg ctc	141
Asn Pro Lys Glu Gln Arg Thr Lys Asp Phe Leu Ser Ser Leu Leu	
35 40 45	

taaccttttc ggggtcttaaa aaa	164
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<210> 1900

<211> 47

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1900

His Glu Met Gly Phe Ala His Glu Val Ala Asp Gln Val Val Phe Met
1 5 10 15

Ala Asp Gly Val Val Val Glu Ala Gly Thr Pro Glu Gln Val Leu Asp
20 25 30

Asn Pro Lys Glu Gln Arg Thr Lys Asp Phe Leu Ser Ser Leu Leu
35 40 45

<210> 1901

<211> 702

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(679)

<223> RXA00740

<400> 1901

gttataaata ttaaagtacg ctaaccatgg gtgcaggggg agacttctac agcagctcatg	60
gtccacacca cgactgtctg atatattaag gacgtaactc atg ttg aag aat aaa	115
Met Leu Lys Asn Lys	
1 5	

act ctt gcg ctg ctg gct gtc agt acg ctg atg ttt ggc tta tct gct	163
Thr Leu Ala Leu Leu Ala Val Ser Thr Leu Met Phe Gly Leu Ser Ala	
10 15 20	

$$\begin{aligned} \frac{1}{\Gamma(\frac{1}{2})} \int_0^1 \frac{1-t}{t} \ln \frac{1-t}{t} dt &= \frac{1}{\Gamma(\frac{1}{2})} \int_0^1 \frac{1-t}{t} \ln \frac{1-t}{t} dt \\ \frac{1}{\Gamma(\frac{1}{2})} \int_0^1 \frac{1-t}{t} \ln \frac{1-t}{t} dt &= \frac{1}{\Gamma(\frac{1}{2})} \int_0^1 \frac{1-t}{t} \ln \frac{1-t}{t} dt \\ \frac{1}{\Gamma(\frac{1}{2})} \int_0^1 \frac{1-t}{t} \ln \frac{1-t}{t} dt &= \frac{1}{\Gamma(\frac{1}{2})} \int_0^1 \frac{1-t}{t} \ln \frac{1-t}{t} dt \end{aligned}$$

<211> 19

213 Cor

Met Leu Lys Asn Lys Thr Leu Ala Leu Leu Ala Val Ser Thr Leu Met
1 5 10 15

Phe Gly Leu Ser Ala Cys Ser Ser Asp Ala Asp Gly Pro Asp Ser Ser
20 25 30

Gly Ala Ser Ser Ser Ser Thr Gly Ser Ser Ser Ala Ser Ala Asp Thr
35 40 45

Thr Asp Ser Ala Ala Val Asp Lys Asp Ala Gln Leu Asp Thr Phe Met
 50 55 60
 Arg Ser Ala Val Ala Asp Gly Ser Ser Ala Ala Val Ala Val Asp Asn
 65 70 75 80
 Ala Val Gly Lys Gly Phe Asp Lys Ala Asp Ala Gln Ala Ala Ala Glu
 85 90 95
 Arg Leu Gly Asp Gly Phe Gln Phe Ala Ala Asp Tyr Gln Ala Val Gly
 100 105 110
 Tyr Leu Glu Ser Trp Tyr Phe Gly Gly Ala Arg Ser Glu Lys Leu Asp
 115 120 125
 Glu Val Arg Ser Asp Val Ile Ala His Leu Ser Glu Leu Gly Phe Thr
 130 135 140
 Asp Leu Glu Ala Glu Ser Ser Ala Ser Arg Ile Thr Leu Gly Asp Tyr
 145 150 155 160
 Cys Asp Gly Val Pro Glu Tyr Cys Glu Leu Phe Phe Asp Gly Glu Ser
 165 170 175
 Pro Asp Leu Tyr Asp Met Gly Thr Glu Leu Asp Ser Tyr Lys Pro Thr
 180 185 190
 Glu

<210> 1903

<211> 1056

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1033)

<223> RXA00741

<400> 1903

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 ttgacaccga tcaaatgttt gatggattat gatatttagc atg act gat tct ctg 115
 Met Thr Asp Ser Leu
 1 5

 ctt gta tcc atc aga aaa ggc tta ata gaa gag cgt cca tta acg gag 163
 Leu Val Ser Ile Arg Lys Gly Leu Ile Glu Glu Arg Pro Leu Thr Glu
 10 15 20

 ctt ctt cgg gcg tgt atc ttc ctt gga agt gat act aac tcg gac tct 211
 Leu Leu Arg Ala Cys Ile Phe Leu Gly Ser Asp Thr Asn Ser Asp Ser
 25 30 35

 tta caa gag tgg gcg aaa aat gaa tta aat ggt tat ggc tcc att gat 259
 Leu Gln Glu Trp Ala Lys Asn Glu Leu Asn Gly Tyr Gly Ser Ile Asp
 40 45 50

ggt att ccg gaa tat cgc aaa ttg aaa gga cct cct gta ttc gcg aaa 307
 Gly Ile Pro Glu Tyr Arg Lys Leu Lys Gly Pro Pro Val Phe Ala Lys
 55 60 65

att caa gct ggt aat tca ata atg tct aat atg gta ctg ggg cca cat 355
 Ile Gln Ala Gly Asn Ser Ile Met Ser Asn Met Val Leu Gly Pro His
 70 75 80 85

aat gtt cct gaa aga gct cgt aag tat ttc cct gaa gag ctg cat ttt 403
 Asn Val Pro Glu Arg Ala Arg Lys Tyr Phe Pro Glu Glu Leu His Phe
 90 95 100

gat cag ccg att caa acg cta att gaa tgg tcg act agg cag gat ggg 451
 Asp Gln Pro Ile Gln Thr Leu Ile Glu Trp Ser Thr Arg Gln Asp Gly
 105 110 115

att aat tta tcg ccc ccg aat tta ctt cgg gtc cgc gat ctt cat aat 499
 Ile Asn Leu Ser Pro Pro Asn Leu Leu Arg Val Arg Asp Leu His Asn
 120 125 130

gat cag tac gcg cca tta aat caa att ttg aat tta aat gtt tac tta 547
 Asp Gln Tyr Ala Pro Leu Asn Gln Ile Leu Asn Leu Asn Val Tyr Leu
 135 140 145

gat aac tct tat ttt tcg gga att gtg gac cgc atc cga act cta atg 595
 Asp Asn Ser Tyr Phe Ser Gly Ile Val Asp Arg Ile Arg Thr Leu Met
 150 155 160 165

act tcc atg att gcc gac ctc aca cac gca act cct ctg gat gaa cta 643
 Thr Ser Met Ile Ala Asp Leu Thr His Ala Thr Pro Leu Asp Glu Leu
 170 175 180

cca agc agc gaa aag gtt aat gcc acg gtc atg aag cac att gaa aat 691
 Pro Ser Ser Glu Lys Val Asn Ala Thr Val Met Lys His Ile Glu Asn
 185 190 195

aac tac gaa act aca atc act caa gcc aat gga gct gta gcc att ggt 739
 Asn Tyr Glu Thr Thr Ile Thr Gln Ala Asn Gly Ala Val Ala Ile Gly
 200 205 210

aac agc gct aaa gct gtg cag aag gga ttg tcc gtg gat gac cta ctg 787
 Asn Ser Ala Lys Ala Val Gln Lys Gly Leu Ser Val Asp Asp Leu Leu
 215 220 225

aag att atg cag acc att aat cct gaa aag ttc gac tta ggg gaa gct 835
 Lys Ile Met Gln Thr Ile Asn Pro Glu Lys Phe Asp Leu Gly Glu Ala
 230 235 240 245

aga gct gaa gcc gaa gaa agc att caa tcc atc gcg gat gag ttg aag 883
 Arg Ala Glu Ala Glu Ser Ile Gln Ser Ile Ala Asp Glu Leu Lys
 250 255 260

aag gag tct ccg aat aaa ggt ttt atc cag aat gct ttt gaa aag ttg 931
 Lys Glu Ser Pro Asn Lys Gly Phe Ile Gln Asn Ala Phe Thr Lys Leu
 265 270 275

aag gaa ctc agc ata aaa gcc ggc gat aaa gcc ttc act aca atg tta 979
 Lys Glu Leu Ser Ile Lys Ala Gly Asp Lys Ala Phe Thr Thr Met Leu
 280 285 290

aat ctt gta ggt aaa cag ata atc gaa aac atc cca caa ctg gtt tca 1027

Asn Leu Val Gly Lys Gln Ile Ile Glu Asn Ile Pro Gln Leu Val Ser
 295 300 305

ggt ggc tagagaaatt caaggccgtc agc
 Gly Gly
 310

1056

<210> 1904

<211> 311

<212> PRT

<213> Corynebacterium glutamicum

<400> 1904

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Arg Pro Leu Thr Glu Leu Leu Arg Ala Cys Ile Phe Leu Gly Ser Asp
 20 25 30

Thr Asn Ser Asp Ser Leu Gln Glu Trp Ala Lys Asn Glu Leu Asn Gly
 35 40 45

Tyr Gly Ser Ile Asp Gly Ile Pro Glu Tyr Arg Lys Leu Lys Gly Pro
 50 55 60

Pro Val Phe Ala Lys Ile Gln Ala Gly Asn Ser Ile Met Ser Asn Met
 65 70 75 80

Val Leu Gly Pro His Asn Val Pro Glu Arg Ala Arg Lys Tyr Phe Pro
 85 90 95

Glu Glu Leu His Phe Asp Gln Pro Ile Gln Thr Leu Ile Glu Trp Ser
 100 105 110

Thr Arg Gln Asp Gly Ile Asn Leu Ser Pro Pro Asn Leu Arg Val
 115 120 125

Arg Asp Leu His Asn Asp Gln Tyr Ala Pro Leu Asn Gln Ile Leu Asn
 130 135 140

Leu Asn Val Tyr Leu Asp Asn Ser Tyr Phe Ser Gly Ile Val Asp Arg
 145 150 155 160

Ile Arg Thr Leu Met Thr Ser Met Ile Ala Asp Leu Thr His Ala Thr
 165 170 175

Pro Leu Asp Glu Leu Pro Ser Ser Glu Lys Val Asn Ala Thr Val Met
 180 185 190

Lys His Ile Glu Asn Asn Tyr Glu Thr Thr Ile Thr Gln Ala Asn Gly
 195 200 205

Ala Val Ala Ile Gly Asn Ser Ala Lys Ala Val Gln Lys Gly Leu Ser
 210 215 220

Val Asp Asp Leu Leu Lys Ile Met Gln Thr Ile Asn Pro Glu Lys Phe
 225 230 235 240

Asp Leu Gly Glu Ala Arg Ala Glu Ala Glu Ser Ile Gln Ser Ile
 245 250 255

Ala Asp Glu Leu Lys Lys Glu Ser Pro Asn Lys Gly Phe Ile Gln Asn
 260 265 270

Ala Phe Glu Lys Leu Lys Glu Leu Ser Ile Lys Ala Gly Asp Lys Ala
 275 280 285

Phe Thr Thr Met Leu Asn Leu Val Gly Lys Gln Ile Ile Glu Asn Ile
 290 295 300

Pro Gln Leu Val Ser Gly Gly
 305 310

<210> 1905
 <211> 1773
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1750)
 <223> RXA00742

<400> 1905
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taatgatgct tctggagcta agcgtagcgtt tgggggtcgg gtg aat gtt cag att 115
 Val Asn Val Gln Ile
 1 5

aaa ggg cga aag gtt aat gcc aag gct gcc gac tta aat agc tat ccg 163
 Lys Gly Arg Lys Val Asn Ala Lys Ala Ala Asp Leu Asn Ser Tyr Pro
 10 15 20

gtc tca gta gtt gat cta cga ggc ttc gtg aca ctg gct ggt ctc tta 211
 Val Ser Val Val Asp Leu Arg Gly Phe Val Thr Leu Ala Gly Leu Leu
 25 30 35

ttt ttt gtg gtt gat att gat aag aaa tca aat aag aaa tat cca aag 259
 Phe Phe Val Val Asp Ile Asp Lys Lys Ser Asn Lys Lys Tyr Pro Lys
 40 45 50

tat gtt ctt ttg aaa ccg ttt tat att cat gat cta ctg agt aaa gcg 307
 Tyr Val Leu Leu Lys Pro Phe Tyr Ile His Asp Leu Leu Ser Lys Ala
 55 60 65

aag ccg ggc caa aag aca att agc gtc cgc tta aaa ccg tta cca tct 355
 Lys Pro Gly Gln Lys Thr Ile Ser Val Arg Leu Lys Arg Leu Pro Ser
 70 75 80 85

gat gaa gat cga atg gaa gcc ata atc gca tta gcg ctc gca tcg agg 403
 Asp Glu Asp Arg Met Glu Ala Ile Ile Ala Leu Ala Leu Ala Ser Arg
 90 95 100

caa gaa aag ata gtc gag aac ccc agt aac tat ctc tat gaa aat atg 451
 Gln Glu Lys Ile Val Glu Asn Pro Ser Asn Tyr Leu Tyr Glu Asn Met
 105 110 115

gaa tca att act gtt aaa tcg gct gaa ccc ctt aat agg gat aag ctg 499
 Glu Ser Ile Thr Val Lys Ser Ala Glu Pro Leu Asn Arg Asp Lys Leu

120	125	130	
gct gta tat gat ggt agt tgc cca gac cat tgc atc att att cgt act			547
Ala Val Tyr Asp Gly Ser Ser Pro Asp His Ser Ile Ile Ile Arg Thr			
135	140	145	
ggg gat gga att gaa cag ttc gtc aat gcc acc gta gaa ata ata ccc			595
Gly Asp Gly Ile Glu Gln Phe Val Asn Ala Thr Val Glu Ile Ile Pro			
150	155	160	165
ccg aat atg cag ttt cat caa gcc aat tat aat gtt tgc tgt aat ggg			643
Pro Asn Met Gln Phe His Gln Ala Asn Tyr Asn Val Ser Cys Asn Gly			
170	175	180	
gtc gtc tat gac aat gtt ttg cat cga aac att gat gat gag cac att			691
Val Val Tyr Asp Asn Val Leu His Arg Asn Ile Asp Asp Glu His Ile			
185	190	195	
gaa ttg aaa atc gga aag ggg att act ctc cgc cta caa aag ctc gcc			739
Glu Leu Lys Ile Gly Lys Gly Ile Thr Leu Arg Leu Gln Lys Leu Ala			
200	205	210	
att gat gct ccg ggg agc gtt acg gtt gag ttt caa gat agt ctt cct			787
Ile Asp Ala Pro Gly Ser Val Thr Val Glu Phe Gln Asp Ser Leu Pro			
215	220	225	
gaa cgg tta aaa gac att gag ttc ttc cta gga gtg ctt cag gcg aat			835
Glu Arg Leu Lys Asp Ile Glu Phe Phe Leu Gly Val Leu Gln Ala Asn			
230	235	240	245
acg ttt ttt att aat gaa gaa cct gtt gtg ttg aag att aac tgc aac			883
Thr Phe Phe Ile Asn Glu Glu Pro Val Val Leu Lys Ile Asn Ser Asn			
250	255	260	
cgg act gtg gct gac ctt aag gat gaa gcg ggt gtt ctt cgt cag ttg			931
Arg Thr Val Ala Asp Leu Lys Asp Glu Ala Gly Val Leu Arg Gln Leu			
265	270	275	
gta gaa ata gct aac cat ttc aat att gat ccg tcc ctt att cga att			979
Val Glu Ile Ala Asn His Phe Asn Ile Asp Pro Ser Leu Ile Arg Ile			
280	285	290	
ggg gag att aca gaa aaa cag ttc tgg cag ttg gat att gtg tat cga			1027
Gly Glu Ile Thr Glu Lys Gln Phe Trp Gln Leu Asp Ile Val Tyr Arg			
295	300	305	
aca gcc gtt aag gga gaa tac gta aag aat tta gag gtt aaa gat gag			1075
Thr Ala Val Lys Gly Glu Tyr Val Lys Asn Leu Glu Val Lys Asp Glu			
310	315	320	325
act aga ctt ata ttg cag cct ttt ggt cgt tgg aat ctt cgc ttg ata			1123
Thr Arg Leu Ile Leu Gln Pro Phe Gly Arg Trp Asn Leu Ala Leu Ile			
330	335	340	
gct cac cct ggt gat gtt gca ggg gag tgg act tat cat gaa gta att			1171
Ala His Pro Gly Asp Val Ala Gly Glu Trp Thr Tyr His Glu Val Ile			
345	350	355	
tcc aag cgt cat cat ttt gct atg aca cct tca acg gat cgg agc gac			1219
Ser Lys Arg His His Phe Ala Met Thr Pro Ser Thr Asp Arg Ser Asp			
360	365	370	

tcc tca atc gag cga gtg acg ccg tac gag ctc att gat aat cga tgg 1267
 Ser Ser Ile Glu Arg Val Thr Pro Tyr Glu Leu Ile Asp Asn Arg Trp
 375 380 385

 ctt cca tca gta ttg aat ctg cat ttg gat aag ctt gtt gat ttc tat 1315
 Leu Pro Ser Val Leu Asn Leu His Leu Asp Lys Leu Val Asp Phe Tyr
 390 395 400 405

 tca gcg ctt gaa gaa act gtt gat gtt gat aat ctc gcc aca tgg atg 1363
 Ser Ala Leu Glu Glu Thr Val Asp Val Asp Asn Leu Ala Thr Trp Met
 410 415 420

 gtg ctt cgc cta att aag gca gct gat tct gag cag agc agg aaa act 1411
 Val Leu Arg Leu Ile Lys Ala Ala Asp Ser Glu Gln Ser Arg Lys Thr
 425 430 435

 gca ttt ctt ata gca gct caa gct ctc aat gat tgg ctc gtg gaa cga 1459
 Ala Phe Leu Ile Ala Ala Gln Ala Leu Asn Asp Trp Leu Val Glu Arg
 440 445 450

 gat cga gaa gag tcg cca att tac agg ctt aat ggt tgg caa att ttg 1507
 Asp Arg Glu Glu Ser Pro Ile Tyr Arg Leu Asn Gly Trp Gln Ile Leu
 455 460 465

 tat cgc caa act gga tta ctg gat tca caa aga aca gaa att cga tct 1555
 Tyr Arg Gln Thr Gly Leu Leu Asp Ser Gln Arg Thr Glu Ile Arg Ser
 470 475 480 485

 ttt agg cat aat ctt gat caa aca atg cac cca gac aac tat agc gag 1603
 Phe Arg His Asn Leu Asp Gln Thr Met His Pro Asp Asn Tyr Ser Glu
 490 495 500

 att atg att ggt tgc gct ttg ctt ctt gac gat aga gaa gag gcg aat 1651
 Ile Met Ile Gly Cys Ala Leu Leu Leu Asp Asp Arg Glu Glu Ala Asn
 505 510 515

 ttt ttg ctt act cag ctt tcg gtt gat cga cgc gca gtt ttt aat gaa 1699
 Phe Leu Leu Thr Gln Leu Ser Val Asp Arg Arg Ala Val Phe Asn Glu
 520 525 530

 tgg ccg ata gct caa ttg atg acg ggt gcc cta aaa gaa gag att gaa 1747
 Trp Pro Ile Ala Gln Leu Met Thr Gly Ala Leu Lys Glu Glu Ile Glu
 535 540 545

 aaa tgagttctga gatcttgatt taa 1773
 Lys
 550

<210> 1906

<211> 550

<212> PRT

<213> Corynebacterium glutamicum

<400> 1906

 Val Asn Val Gln Ile Lys Gly Arg Lys Val Asn Ala Lys Ala Ala Asp
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 20 25 30

Leu Ala Gly Leu Leu Phe Phe Val Val Asp Ile Asp Lys Lys Ser Asn
 35 40 45
 Lys Lys Tyr Pro Lys Tyr Val Leu Leu Lys Pro Phe Tyr Ile His Asp
 50 55 60
 Leu Leu Ser Lys Ala Lys Pro Gly Gln Lys Thr Ile Ser Val Arg Leu
 65 70 75 80
 Lys Arg Leu Pro Ser Asp Glu Asp Arg Met Glu Ala Ile Ile Ala Leu
 85 90 95
 Ala Leu Ala Ser Arg Gln Glu Lys Ile Val Glu Asn Pro Ser Asn Tyr
 100 105 110
 Leu Tyr Glu Asn Met Glu Ser Ile Thr Val Lys Ser Ala Glu Pro Leu
 115 120 125
 Asn Arg Asp Lys Leu Ala Val Tyr Asp Gly Ser Ser Pro Asp His Ser
 130 135 140
 Ile Ile Ile Arg Thr Gly Asp Gly Ile Glu Gln Phe Val Asn Ala Thr
 145 150 155 160
 Val Glu Ile Ile Pro Pro Asn Met Gln Phe His Gln Ala Asn Tyr Asn
 165 170 175
 Val Ser Cys Asn Gly Val Val Tyr Asp Asn Val Leu His Arg Asn Ile
 180 185 190
 Asp Asp Glu His Ile Glu Leu Lys Ile Gly Lys Gly Ile Thr Leu Arg
 195 200 205
 Leu Gln Lys Leu Ala Ile Asp Ala Pro Gly Ser Val Thr Val Glu Phe
 210 215 220
 Gln Asp Ser Leu Pro Glu Arg Leu Lys Asp Ile Glu Phe Phe Leu Gly
 225 230 235 240
 Val Leu Gln Ala Asn Thr Phe Phe Ile Asn Glu Glu Pro Val Val Leu
 245 250 255
 Lys Ile Asn Ser Asn Arg Thr Val Ala Asp Leu Lys Asp Glu Ala Gly
 260 265 270
 Val Leu Arg Gln Leu Val Glu Ile Ala Asn His Phe Asn Ile Asp Pro
 275 280 285
 Ser Leu Ile Arg Ile Gly Glu Ile Thr Glu Lys Gln Phe Trp Gln Leu
 290 295 300
 Asp Ile Val Tyr Arg Thr Ala Val Lys Gly Glu Tyr Val Lys Asn Leu
 305 310 315 320
 Glu Val Lys Asp Glu Thr Arg Leu Ile Leu Gln Pro Phe Gly Arg Trp
 325 330 335
 Asn Leu Ala Leu Ile Ala His Pro Gly Asp Val Ala Gly Glu Trp Thr
 340 345 350

Tyr His Glu Val Ile Ser Lys Arg His His Phe Ala Met Thr Pro Ser
 355 360 365
 Thr Asp Arg Ser Asp Ser Ser Ile Glu Arg Val Thr Pro Tyr Glu Leu
 370 375 380
 Ile Asp Asn Arg Trp Leu Pro Ser Val Leu Asn Leu His Leu Asp Lys
 385 390 395 400
 Leu Val Asp Phe Tyr Ser Ala Leu Glu Glu Thr Val Asp Val Asp Asn
 405 410 415
 Leu Ala Thr Trp Met Val Leu Arg Leu Ile Lys Ala Ala Asp Ser Glu
 420 425 430
 Gln Ser Arg Lys Thr Ala Phe Leu Ile Ala Ala Gln Ala Leu Asn Asp
 435 440 445
 Trp Leu Val Glu Arg Asp Arg Glu Glu Ser Pro Ile Tyr Arg Leu Asn
 450 455 460
 Gly Trp Gln Ile Leu Tyr Arg Gln Thr Gly Leu Leu Asp Ser Gln Arg
 465 470 475 480
 Thr Glu Ile Arg Ser Phe Arg His Asn Leu Asp Gln Thr Met His Pro
 485 490 495
 Asp Asn Tyr Ser Glu Ile Met Ile Gly Cys Ala Leu Leu Leu Asp Asp
 500 505 510
 Arg Glu Glu Ala Asn Phe Leu Leu Thr Gln Leu Ser Val Asp Arg Arg
 515 520 525
 Ala Val Phe Asn Glu Trp Pro Ile Ala Gln Leu Met Thr Gly Ala Leu
 530 535 540
 Lys Glu Glu Ile Glu Lys
 545 550

<210> 1907

<211> 546

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(523)

<223> RXA00743

<400> 1907

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catcatgtca gcgcatctac cttctcatca tgatgagtta gtg cag cac tta gtt 115
 Val Gln His Leu Val
 1 5

ctt gcg gat gta aag tat cgg gag ctc agt gcg tta tcg gtc aaa att 163
 Leu Ala Asp Val Lys Tyr Arg Glu Leu Ser Ala Leu Ser Val Lys Ile
 10 15 20

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gag gaa cca tca gat cgt cct gag ttt aaa ctt gga gtt act gtt aac 211
Glu Glu Pro Ser Asp Arg Pro Glu Phe Lys Leu Gly Val Thr Val Asn
      25                      30                      35

gac aag agt aaa gac gaa ggt gtg ccg cga atc att gag gtt tca 259
Asp Lys Ser Ser Asp Glu Glu Gly Val Pro Arg Ile Ile Glu Val Ser
      40                      45                      50

ttg agg gtg tcc atc gag gtt ccc gac gga aag ata acg gta gag cct 307
Leu Arg Val Ser Ile Glu Val Pro Asp Gly Lys Ile Thr Val Glu Pro
      55                      60                      65

gaa gca atc tat ttg att cct gag aat aag gtt tat tta acg gaa tct 355
Glu Ala Ile Tyr Leu Ile Pro Glu Asn Lys Val Tyr Leu Thr Glu Ser
      70                      75                      80                      85

gat gca atg gtg gat tat ttt aac aac cat gcg att ttt act ctg gtg 403
Asp Ala Met Val Asp Tyr Phe Asn Asn His Ala Ile Phe Thr Leu Val
      90                      95                      100

cca tat gca cga cag gcc gtg tct gat tta ggg cag cgt gca ttc cac 451
Pro Tyr Ala Arg Gln Ala Val Ser Asp Leu Gly Gln Arg Ala Phe His
      105                      110                      115

acg cag atc ctc atg cct gcg tta ggt cct ggt gat ttg gtt ttt agt 499
Thr Gln Ile Leu Met Pro Ala Leu Gly Pro Gly Asp Leu Val Phe Ser
      120                      125                      130

aaa tcg acg gcc tca cga gaa tgg tagagaatta cctgatagtt gca 546
Lys Ser Thr Ala Ser Arg Glu Trp
      135                      140

<210> 1908
<211> 141
<212> PRT
<213> Corynebacterium glutamicum

<400> 1908
Val Gln His Leu Val Leu Ala Asp Val Lys Tyr Arg Glu Leu Ser Ala
  1                      5                      10                      15

Leu Ser Val Lys Ile Glu Glu Pro Ser Asp Arg Pro Glu Phe Lys Leu
      20                      25                      30

Gly Val Thr Val Asn Asp Lys Ser Lys Asp Glu Glu Gly Val Pro Arg
      35                      40                      45

Ile Ile Glu Val Ser Leu Arg Val Ser Ile Glu Val Pro Asp Gly Lys
      50                      55                      60

Ile Thr Val Glu Pro Glu Ala Ile Tyr Leu Ile Pro Glu Asn Lys Val
      65                      70                      75                      80

Tyr Leu Thr Glu Ser Asp Ala Met Val Asp Tyr Phe Asn Asn His Ala
      85                      90                      95

Ile Phe Thr Leu Val Pro Tyr Ala Arg Gln Ala Val Ser Asp Leu Gly
      100                      105                      110

Gln Arg Ala Phe His Thr Gln Ile Leu Met Pro Ala Leu Gly Pro Gly

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	115	120	125	
Asp Leu Val Phe Ser Lys Ser Thr Ala Ser Arg Glu Trp				
	130	135	140	
<210> 1909				
<211> 657				
<212> DNA				
<213> <i>Corynebacterium glutamicum</i>				
<220>				
<221> CDS				
<222> (101)..(634)				
<223> RXA00745				
<400> 1909				
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gttcagcatt gttttccgca tcagataacg cgggtgggcga	gtg gct tat ctg tac	115		
	Val Ala Tyr Leu Tyr			
	1 5			
gga tct gcc gat ggg atg ctt aat aca gat ggt ttt aat atg ttt ccg	163			
Gly Ser Ala Asp Gly Met Leu Asn Thr Asp Gly Phe Asn Met Phe Pro				
	10 15 20			
cgt gcg tcg tac acc att ctt ggc cct atg gat gct gac gcg gtc ggt	211			
Arg Ala Ser Tyr Thr Ile Leu Gly Pro Met Asp Ala Asp Ala Val Gly				
	25 30 35			
gtg tac caa cag cta ctg aac agc acg att ccc atg gat ttg gca cgt	259			
Val Tyr Gln Gln Leu Leu Asn Ser Thr Ile Pro Met Asp Leu Ala Arg				
	40 45 50			
ctt gta acc acg cat aat tcc ggt gca agt tat ctt cgc cgc ggt gct	307			
Leu Val Thr Thr His Asn Ser Gly Ala Ser Tyr Leu Arg Arg Gly Ala				
	55 60 65			
acc aac gta gtt ttt gaa acg aat ctt gcc ctc ggt gtg aat ccg tat	355			
Thr Asn Val Val Phe Glu Thr Asn Leu Ala Leu Gly Val Asn Pro Tyr				
	70 75 80 85			
atg aag aaa cgc cga gca aca gaa gca caa cgt ggt aag aag cgt ttt	403			
Met Lys Lys Arg Arg Ala Thr Glu Ala Gln Arg Gly Lys Lys Arg Phe				
	90 95 100			
aaa cga gac agt cat tac ggc ggt ggc act gtg acc aca ggt act gct	451			
Lys Arg Asp Ser His Tyr Gly Gly Thr Val Thr Thr Gly Thr Ala				
	105 110 115			
gat ttg gat gtg gtg gcg atg cag gcg cgg gca gag cac cgg gaa gaa	499			
Asp Leu Asp Val Val Ala Met Gln Ala Arg Ala Glu His Arg Glu Glu				
	120 125 130			
agg ttg gga gaa aaa tct acc cgc aag aaa gag gag ctt gct gca gta	547			
Arg Leu Gly Glu Lys Ser Thr Arg Lys Lys Glu Leu Ala Ala Val				
	135 140 145			
gag gcg aaa gag tta gct gcg aag aag ggt ccg cag act gtg gaa gaa	595			
Glu Ala Lys Glu Leu Ala Ala Lys Lys Gly Pro Gln Thr Val Glu Glu				

150 155 160 165

ggt ctt gct gcg gtg gag aag aaa cac ctg gcg aag cgg taggcgacgt 644
Gly Leu Ala Ala Val Glu Lys Lys His Leu Ala Lys Arg
 170 175

gattggcggt ggg 657

<210> 1910

<211> 178

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1910

Val Ala Tyr Leu Tyr Gly Ser Ala Asp Gly Met Leu Asn Thr Asp Gly
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Phe Asn Met Phe Pro Arg Ala Ser Tyr Thr Ile Leu Gly Pro Met Asp
20 25 30

Ala Asp Ala Val Gly Val Tyr Gln Gln Leu Leu Asn Ser Thr Ile Pro
35 40 45

Met Asp Leu Ala Arg Leu Val Thr Thr His Asn Ser Gly Ala Ser Tyr
50 55 60

Leu Arg Arg Gly Ala Thr Asn Val Val Phe Glu Thr Asn Leu Ala Leu
65 70 75 80

Gly Val Asn Pro Tyr Met Lys Lys Arg Arg Ala Thr Glu Ala Gln Arg
85 90 95

Gly Lys Lys Arg Phe Lys Arg Asp Ser His Tyr Gly Gly Gly Thr Val
100 105 110

Thr Thr Gly Thr Ala Asp Leu Asp Val Val Ala Met Gln Ala Arg Ala
115 120 125

Glu His Arg Glu Glu Arg Leu Gly Glu Lys Ser Thr Arg Lys Lys Glu
130 135 140

Glu Leu Ala Ala Val Glu Ala Lys Glu Leu Ala Ala Lys Lys Gly Pro
145 150 155 160

Gln Thr Val Glu Glu Gly Leu Ala Ala Val Glu Lys Lys His Leu Ala
165 170 175

Lys Arg

<210> 1911

<211> 1314

<212> DNA

<213> Corynebacterium glutamicum

 $\langle 220 \rangle$

<221> CDS

<222> (101) .. (1291)

<223> RXA00746

<400> 1911

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gacgtgccaa atccatggga atcgtgctgt tcagtagctg ttg gta cac acc gac 115
                                Leu Val His Thr Asp
                                1                    5

cgc gtc agc atc cat agg gcc aag aat ggt gta cga cgc acg cgg aaa 163
Arg Val Ser Ile His Arg Ala Lys Asn Gly Val Arg Arg Thr Arg Lys
                        10                        15                        20

cat att aaa acc atc tgt att aag cat ccc atc gcc aga tcc gta cag 211
His Ile Lys Thr Ile Cys Ile Lys His Pro Ile Gly Arg Ser Val Gln
                        25                        30                        35

ata agc cac tcg ccc acc gcg tta tct gat gcg gaa aac aat gct gaa 259
Ile Ser His Ser Pro Thr Ala Leu Ser Asp Ala Glu Asn Asn Ala Glu
                        40                        45                        50

ctc acc act gca cag att ctg cac att gac ccc gtc acc ggt gtg gcc 307
Leu Thr Thr Ala Gln Ile Leu His Ile Asp Pro Val Thr Gly Val Ala
                        55                        60                        65

atc cca cgt caa aac att ctg ctg ggt gag gat ttt cag act atg gcc 355
Ile Pro Arg Gln Asn Ile Leu Leu Gly Glu Asp Phe Gln Thr Met Ala
                        70                        75                        80                        85

agc tct ttt agt caa atc cgc cat gga tgg ggt atc acc cag ctc atc 403
Ser Ser Phe Ser Gln Ile Arg His Gly Trp Gly Ile Thr Gln Leu Ile
                        90                        95                        100

gga caa gac ccc aac aga aac caa cca atc cgc tct gct gat acg tgg 451
Gly Gln Asp Pro Asn Arg Asn Gln Pro Ile Arg Ser Ala Asp Thr Trp
                        105                        110                        115

aca gtg act gga tcg act gga ctc acc gcc ttt aat act gct acg cat 499
Thr Val Thr Gly Ser Thr Gly Leu Thr Gly Phe Asn Thr Ala Thr His
                        120                        125                        130

aat aca gat gac aca gac gcc act gcc gca tat acc atg ccg gca agc 547
Asn Thr Asp Asp Thr Asp Ala Thr Ala Ala Tyr Thr Met Pro Ala Ser
                        135                        140                        145

gat cct gcc gta gga cta tgc gca ctg gaa tcc aac aaa gac gca ccg 595
Asp Pro Ala Val Gly Leu Cys Ala Leu Glu Ser Asn Lys Asp Ala Pro
                        150                        155                        160                        165

gtg gat gaa ttt cgc gat ctc agc ctc agt gct tta cgt acc gct acg 643
Val Asp Glu Phe Arg Asp Leu Ser Leu Ser Ala Leu Arg Thr Ala Thr
                        170                        175                        180

gtc atg tca agc tct gcc tcc gcc gtg att act atg cat gat cct atg 691
Val Met Ser Ser Ser Gly Ser Ala Val Ile Thr Met His Asp Pro Met
                        185                        190                        195

gtc atg agc acc act gcc gca ttg gaa gca cgt gca tac gtt gac gcc 739
Val Met Ser Thr Thr Gly Ala Leu Glu Ala Arg Ala Tyr Val Asp Gly
                        200                        205                        210

gaa gtc atc aac cag cac gat ctt gac tca ctg cgt gac cag cta ggt 787

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Glu Val Ile Asn Gln His Asp Leu Asp Ser Leu Arg Asp Gln Leu Gly
 215 220 225
 att act aca gac agc gca gat acc acc cct gcc cta cct gct gat ccc 835
 Ile Thr Thr Asp Ser Ala Asp Thr Thr Pro Ala Leu Pro Ala Asp Pro 245
 230 235 240
 ttg gca gca ttg ggc ttg agc aca cca act aca tca gct ctt gtc cca 883
 Leu Ala Ala Leu Gly Leu Ser Thr Pro Thr Ser Ala Leu Val Pro 260
 250 255
 ggt ctt gcc gag ctg gac tgc ctc aac act gat caa gct cgc acc tgg 931
 Gly Leu Ala Glu Leu Asp Cys Leu Asn Thr Asp Gln Ala Arg Thr Trp 275
 265 270
 cat gac cgt gac aac agc att ggc act ggt aaa cca gct att ctt gcc 979
 His Asp Arg Asp Asn Ser Ile Gly Thr Gly Lys Pro Ala Ile Leu Ala 290
 280 285
 gtg att aac gcc gag ctc gct gat gat tac acc ctg cag atc ctc aaa 1027
 Val Ile Asn Ala Glu Leu Ala Asp Asp Tyr Thr Leu Gln Ile Leu Lys 305
 295 300
 aat agc act gcg acc ccc acc gac tcc acc gac tcc agc gat act gct 1075
 Asn Ser Thr Ala Thr Pro Thr Asp Ser Thr Asp Ser Ser Asp Thr Ala 325
 310 315 320
 gaa cgc ttc gta gcg cag cta cct gcg gaa aca gcc ttt gtg ctt att 1123
 Glu Arg Phe Val Ala Gln Leu Pro Ala Glu Thr Ala Phe Val Leu Ile 340
 330 335
 gat ccg gac atc ggc gct gtg acc gat ctg ttc ttt atc aac agc ata 1171
 Asp Pro Asp Ile Gly Ala Val Thr Asp Leu Phe Phe Ile Asn Ser Ile 355
 345 350
 aat cag gat ctc ccc gca ccg aca acc cag atc aac tca gta gcg gta 1219
 Asn Gln Asp Leu Pro Ala Pro Thr Thr Gln Ile Asn Ser Val Ala Val 370
 360 365
 gat caa cgt gac ccc aac atc atc tac gcg acc ttt gcc aat gat gac 1267
 Asp Gln Arg Asp Pro Asn Ile Ile Tyr Ala Thr Phe Ala Asn Asp Asp 385
 375 380
 cgc gtg tac cag ctc atg ctg ggt taaccgcgac ccgtttttat ctg 1314
 Arg Val Tyr Gln Leu Met Leu Gly 395
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<210> 1912

<211> 397

<212> PRT

<213> Corynebacterium glutamicum

<400> 1912

Leu Val His Thr Asp Arg Val Ser Ile His Arg Ala Lys Asn Gly Val
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 20 25 30

Gly Arg Ser Val Gln Ile Ser His Ser Pro Thr Ala Leu Ser Asp Ala

35										40										45										
Glu	Asn	Asn	Ala	Glu	Leu	Thr	Thr	Ala	Gln	Ile	Leu	His	Ile	Asp	Pro															
50						55					60																			
Val	Thr	Gly	Val	Ala	Ile	Pro	Arg	Gln	Asn	Ile	Leu	Leu	Gly	Glu	Asp															
65					70					75					80															
Phe	Gln	Thr	Met	Ala	Ser	Ser	Phe	Ser	Gln	Ile	Arg	His	Gly	Trp	Gly															
				85					90					95																
Ile	Thr	Gln	Leu	Ile	Gly	Gln	Asp	Pro	Asn	Arg	Asn	Gln	Pro	Ile	Arg															
			100					105					110																	
Ser	Ala	Asp	Thr	Trp	Thr	Val	Thr	Gly	Ser	Thr	Gly	Leu	Thr	Gly	Phe															
		115					120					125																		
Asn	Thr	Ala	Thr	His	Asn	Thr	Asp	Asp	Thr	Asp	Ala	Thr	Ala	Ala	Tyr															
		130				135					140																			
Thr	Met	Pro	Ala	Ser	Asp	Pro	Ala	Val	Gly	Leu	Cys	Ala	Leu	Glu	Ser															
145					150					155				160																
Asn	Lys	Asp	Ala	Pro	Val	Asp	Glu	Phe	Arg	Asp	Leu	Ser	Leu	Ser	Ala															
			165					170					175																	
Leu	Arg	Thr	Ala	Thr	Val	Met	Ser	Ser	Gly	Ser	Ala	Val	Ile	Thr																
			180				185						190																	
Met	His	Asp	Pro	Met	Val	Met	Ser	Thr	Thr	Gly	Ala	Leu	Glu	Ala	Arg															
		195					200					205																		
Ala	Tyr	Val	Asp	Gly	Glu	Val	Ile	Asn	Gln	His	Asp	Leu	Asp	Ser	Leu															
		210				215					220																			
Arg	Asp	Gln	Leu	Gly	Ile	Thr	Thr	Asp	Ser	Ala	Asp	Thr	Thr	Pro	Ala															
225					230				235					240																
Leu	Pro	Ala	Asp	Pro	Leu	Ala	Ala	Leu	Gly	Leu	Ser	Thr	Pro	Thr	Thr															
			245					250					255																	
Ser	Ala	Leu	Val	Pro	Gly	Leu	Ala	Glu	Leu	Asp	Cys	Leu	Asn	Thr	Asp															
			260					265					270																	
Gln	Ala	Arg	Thr	Trp	His	Asp	Arg	Asp	Asn	Ser	Ile	Gly	Thr	Gly	Lys															
		275				280						285																		
Pro	Ala	Ile	Leu	Ala	Val	Ile	Asn	Ala	Glu	Leu	Ala	Asp	Asp	Tyr	Thr															
		290				295					300																			
Leu	Gln	Ile	Leu	Lys	Asn	Ser	Thr	Ala	Thr	Pro	Thr	Asp	Ser	Thr	Asp															
305				310					315					320																
Ser	Ser	Asp	Thr	Ala	Glu	Arg	Phe	Val	Ala	Gln	Leu	Pro	Ala	Glu	Thr															
			325				330						335																	
Ala	Phe	Val	Leu	Ile	Asp	Pro	Asp	Ile	Gly	Ala	Val	Thr	Asp	Leu	Phe															
			340				345					350																		
Phe	Ile	Asn	Ser	Ile	Asn	Gln	Asp	Leu	Pro	Ala	Pro	Thr	Thr	Gln	Ile															
		355				360					365																			

Asn Ser Val Ala Val Asp Gln Arg Asp Pro Asn Ile Ile Tyr Ala Thr
 370 375 380

Phe Ala Asn Asp Asp Arg Val Tyr Gln Leu Met Leu Gly
 385 390 395

<210> 1913

<211> 711

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(688)

<223> RXA00747

<400> 1913

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 Met Thr Phe Leu His
 1 5

cgt tcc gcc agt ttc cac cct cgt acc cac gat cac ctg agc gag ctg 163
 Arg Ser Ala Ser Phe His Pro Arg Thr His Asp His Leu Ser Glu Leu
 10 15 20

ggt ctt gat cct tat aag ctg tct caa gac atc ccc act gtt att tat 211
 Gly Leu Asp Pro Tyr Lys Leu Ser Gln Asp Ile Pro Thr Val Ile Tyr
 25 30 35

gaa gtc cag ccg cac agt gtg ttc att tta aaa ttc aac act gcc gat 259
 Glu Val Gln Pro His Ser Val Phe Ile Leu Lys Phe Asn Thr Ala Asp
 40 45 50

gtt cgg gtc tat cag gaa cac tcc gat ctg ttt gtg cga cat gct gtg 307
 Val Arg Val Tyr Gln Glu His Ser Asp Leu Phe Val Arg His Ala Val
 55 60 65

ctt gtt gat cca gaa cag cgt aaa cat gag cat gac cag ctg ctt aaa 355
 Leu Val Asp Pro Glu Gln Arg Lys His Glu His Asp Gln Leu Leu Lys
 70 75 80 85

gag att ctg gac ctg gat gcc cct cgt gtc aac gat gat att agt ggt 403
 Glu Ile Leu Asp Leu Asp Ala Pro Arg Val Asn Asp Asp Ile Ser Gly
 90 95 100

cgc acg aca gtg ttt ctg cac gat aaa aca gtt gtt acg cac agt ggt 451
 Arg Thr Thr Val Phe Leu His Asp Lys Thr Val Val Thr His Ser Gly
 105 110 115

ggc ccc att gcg att att ccg cac aat ccc gat gtc gcc agc gcc gct 499
 Gly Pro Ile Ala Ile Ile Pro His Asn Pro Asp Val Ala Ser Ala Ala
 120 125 130

gcg tca gct aat aaa cac aaa caa tct gtg atg aca aca tcc agg cat 547
 Ala Ser Ala Asn Lys His Lys Gln Ser Val Met Thr Thr Ser Arg His
 135 140 145

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cct tat gcg cag atg tct ctc agc gac atg ctg aaa caa ggc ttc acg      595
Pro Tyr Ala Gln Met Ser Leu Ser Asp Met Leu Lys Gln Gly Phe Thr
150                               155                               160                               165

ctc aca cct cta gag ttc ccc tac tgc gct gtt gat gac ccc gac agc      643
Leu Thr Pro Leu Glu Phe Pro Tyr Cys Ala Val Asp Asp Pro Asp Ser
                               170                               175                               180

tca cgc cac aca atg cac gtc atc aac gtt cga gat cat aca gtg      688
Ser Arg His Thr Met His Val Ile Asn Val Arg Asp His Thr Val
                               185                               190                               195

tgaactaccg cgccgctaga gat      711

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<210> 1914

<211> 196

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1914

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Met Thr Phe Leu His Arg Ser Ala Ser Phe His Pro Arg Thr His Asp
 1           5           10           15

His Leu Ser Glu Leu Gly Leu Asp Pro Tyr Lys Leu Ser Gln Asp Ile
          20           25           30

Pro Thr Val Ile Tyr Glu Val Gln Pro His Ser Val Phe Ile Leu Lys
          35           40           45

Phe Asn Thr Ala Asp Val Arg Val Tyr Gln Glu His Ser Asp Leu Phe
          50           55           60

Val Arg His Ala Val Leu Val Asp Pro Glu Gln Arg Lys His Glu His
          65           70           75           80

Asp Gln Leu Leu Lys Glu Ile Leu Asp Leu Asp Ala Pro Arg Val Asn
          85           90           95

Asp Asp Ile Ser Gly Arg Thr Thr Val Phe Leu His Asp Lys Thr Val
          100          105          110

Val Thr His Ser Gly Gly Pro Ile Ala Ile Ile Pro His Asn Pro Asp
          115          120          125

Val Ala Ser Ala Ala Ala Ser Ala Asn Lys His Lys Gln Ser Val Met
          130          135          140

Thr Thr Ser Arg His Pro Tyr Ala Gln Met Ser Leu Ser Asp Met Leu
          145          150          155          160

Lys Gln Gly Phe Thr Leu Thr Pro Leu Glu Phe Pro Tyr Cys Ala Val
          165          170          175

Asp Asp Pro Asp Ser Ser Arg His Thr Met His Val Ile Asn Val Arg
          180          185          190

Asp His Thr Val
          195

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<220>
<221> CDS
<222> (101) .. (544)
<223> RXA00748
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<210> 1916
<211> 148
<212> PRT
<213> Corynebacterium glutamicum
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<210> 1916
<211> 148
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 1916

Met Thr Tyr Phe Ala Leu Val Ala Arg Asn Tyr Ala Glu Thr Gly Val
 1 5 10 15

Ser Val Glu Phe His Glu Val Asp Asp Ala Asp Asn Ser Asn Gly
 20 25 30

Pro Asn Asn Thr Ser Asn Leu Pro Leu Lys Leu Leu Arg Asp His Ser
 35 40 45

Phe Asp Ala Thr Val Val Tyr Gly Asp Leu Val Leu His Thr Ser Ala
 50 55 60

His Leu Arg Asp Thr Ala Ile Ala Asn Ser Asp Asn Arg Pro Arg Val
 65 70 75 80

Val Thr Thr Ala Gln Lys Phe Phe Asp Tyr Ile Arg Leu Ala Thr Arg
 85 90 95

His Gly Ala Ile His Asp Met Ile Asn Asn Ala Pro Asp Thr Gly Thr
 100 105 110

Asp Ile Val Val Ile Thr Ala Thr Asn Asp Ala Leu Ile Ser Asp Glu
 115 120 125

Ser Glu Tyr Tyr Asp Glu Leu Phe His Ile Leu Glu Ser Ala Gln Gly
 130 135 140

Val Ile Leu Lys
 145

<210> 1917

<211> 822

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(799)

<223> RXA00749

<400> 1917

cggttcgatc atttgaaca ttcttattac aagactggaa ataaaggatga gtcaatcata 60

cagtcagatg tggatcatcg caaaacagaa aggaatcccg atg tta cga aaa aca 115
 Met Leu Arg Lys Thr
 1 5

gtt acc ggt gga att gtt gct ctt att gcg act gcc act ctc atg aat 163
 Val Thr Gly Gly Ile Val Ala Leu Ile Ala Thr Ala Thr Leu Met Asn
 10 15 20

tct gtc tct tct gct gaa gag gta tcc gga gat gtc tca gca gta gat 211
 Ser Val Ser Ser Ala Glu Glu Val Ser Gly Asp Val Ser Ala Val Asp
 25 30 35

ctc gca ttt gca gaa ttc gaa cgt aca act gca gag gac gtg gcc aat 259
 Leu Ala Phe Ala Glu Phe Glu Arg Thr Thr Ala Glu Asp Val Ala Asn
 40 45 50

gga gtg cca gag gct ata gct aat gca gaa aaa att tcc aat ttc act 307
 Gly Val Pro Glu Ala Ile Ala Asn Ala Glu Lys Ile Ser Asn Phe Thr
 55 60 65

ccg agc gaa cta gag ggc ttc aag agt ctt tta gct agt gat gca gtg 355
 Pro Ser Glu Leu Glu Gly Phe Lys Ser Leu Leu Ala Ser Asp Ala Val
 70 75 80 85

ctg agg tcg gtc tct gga gaa gaa att ctc cca gat aat gtt gaa gtg 403
 Leu Arg Ser Val Ser Gly Glu Glu Ile Leu Pro Asp Asn Val Glu Val
 90 95 100

gtt cag acg gac aac gta ggc gac gaa gat cca aat gtc att tct cca 451
 Val Gln Thr Trp Asn Val Gly Asp Glu Asp Pro Asn Val Ile Ser Pro
 105 110 115

gca gcc tgg cag ggt tct gat tat att gag ggg tgt tta acg aat act 499
 Ala Ala Trp Gln Gly Ser Asp Tyr Ile Glu Gly Cys Leu Thr Asn Thr
 120 125 130

ctc tac gga att gaa gtc cta aag gtt tgt act ggt gga acc tac tac 547
 Leu Tyr Gly Ile Glu Val Leu Lys Val Cys Thr Gly Gly Thr Tyr Tyr
 135 140 145

tcc aat gta gga atc gct act tct gtc agc aat cct cgc agt tac gta 595
 Ser Asn Val Gly Ile Ala Thr Ser Val Ser Asn Pro Arg Ser Tyr Val
 150 155 160 165

aag tat aac agt gct cca gga ttg gca gtg acg aca agc aat cca cgt 643
 Lys Tyr Asn Ser Ala Pro Gly Leu Ala Val Thr Thr Ser Asn Pro Arg
 170 175 180

gga ggt ata gag ggt ggt ctt gcg gcc ttc tat ggt gat gtt aac ctt 691
 Gly Gly Ile Glu Gly Gly Leu Ala Ala Phe Tyr Gly Asp Val Asn Leu
 185 190 195

gtt gct ttt cca aat att cca tgg gtg gga cca att agt tct tct gca 739
 Val Ala Phe Pro Asn Ile Pro Trp Val Gly Pro Ile Ser Ser Ser Ala
 200 205 210

gga act cac cgc gtt gtc gct aga tca ttt ccg aat tca gtg gtg ctt 787
 Gly Thr His Arg Val Val Ala Arg Ser Phe Pro Asn Ser Val Val Leu
 215 220 225

aac gtc tac tac taatcggttt tttagtttgaa aca 822
 Asn Val Tyr Tyr
 230

<210> 1918
 <211> 233
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 1918
 Met Leu Arg Lys Thr Val Thr Gly Gly Ile Val Ala Leu Ile Ala Thr
 1 5 10 15
 Ala Thr Leu Met Asn Ser Val Ser Ser Ala Glu Glu Val Ser Gly Asp
 20 25 30

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Val Ser Ala Val Asp Leu Ala Phe Ala Glu Phe Glu Arg Thr Thr Ala
    35                      40                      45

Glu Asp Val Ala Asn Gly Val Pro Glu Ala Ile Ala Asn Ala Glu Lys
    50                      55                      60

Ile Ser Asn Phe Thr Pro Ser Glu Leu Glu Gly Phe Lys Ser Leu Leu
    65                      70                      75                      80

Ala Ser Asp Ala Val Leu Arg Ser Val Ser Gly Glu Glu Ile Leu Pro
    85                      90                      95

Asp Asn Val Glu Val Val Gln Thr Asp Asn Val Gly Asp Glu Asp Pro
   100                      105                      110

Asn Val Ile Ser Pro Ala Ala Trp Gln Gly Ser Asp Tyr Ile Glu Gly
   115                      120                      125

Cys Leu Thr Asn Thr Leu Tyr Gly Ile Glu Val Leu Lys Val Cys Thr
   130                      135                      140

Gly Gly Thr Tyr Tyr Ser Asn Val Gly Ile Ala Thr Ser Val Ser Asn
   145                      150                      155                      160

Pro Arg Ser Tyr Val Lys Tyr Asn Ser Ala Pro Gly Leu Ala Val Thr
   165                      170                      175

Thr Ser Asn Pro Arg Gly Gly Ile Glu Gly Gly Leu Ala Ala Phe Tyr
   180                      185                      190

Gly Asp Val Asn Leu Val Ala Phe Pro Asn Ile Pro Trp Val Gly Pro
   195                      200                      205

Ile Ser Ser Ser Ala Gly Thr His Arg Val Val Ala Arg Ser Phe Pro
   210                      215                      220

Asn Ser Val Val Leu Asn Val Tyr Tyr
   225                      230

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<210> 1919

<211> 951

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(928)

<223> RXA00751

<400> 1919

cgcagcaacc ccgtccatga gggcaggga cgcacacat cctgtaccta tactgtgagg 60

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tgccatagag tatctctaatt ttagaaagtg gtgtagaagt atg ttg gta cgt tca    115
                Met Leu Val Arg Ser
                1                      5

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cgc acg ttg gtt acc gct gca ctg tca tgt tca ctg ttg ttc gga gca    163
Arg Thr Leu Val Thr Ala Ala Leu Ser Cys Ser Leu Leu Phe Gly Ala
                10                      15                      20

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acg gta aat ggc acg ggt gtt gcg att gca tat gaa aat gtg tct atg 211
 Thr Val Asn Gly Thr Gly Val Ala Ile Ala Tyr Glu Asn Val Ser Met
 25 30 35

gct gct cag tat gaa cca cgg tat gaa tcc tta gaa acg cgt ctc ggt 259
 Ala Ala Gln Tyr Glu Pro Arg Tyr Glu Ser Leu Glu Thr Arg Leu Gly
 40 45 50

tct agt gga gtc ttt ccc aag tcg gtt gaa cag tct gtt gaa aac ctt 307
 Ser Ser Gly Val Phe Pro Lys Ser Val Glu Gln Ser Val Glu Asn Leu
 55 60 65

gct gaa tta cca gag gag act cga ttt tta ctt gag ggt gat tcg ttt 355
 Ala Glu Leu Pro Glu Glu Thr Arg Phe Leu Leu Glu Gly Asp Ser Phe
 70 75 80 85

tca att att att gat gat ggt ctg ctc gct tct cga ttg gac cca aat 403
 Ser Ile Ile Ile Asp Asp Gly Leu Leu Ala Ser Arg Leu Asp Pro Asn
 90 95 100

aca ggg gag att cga cat act ctt ggg gct tcg ggg atc agc tac acc 451
 Thr Gly Glu Ile Arg His Thr Leu Gly Ala Ser Gly Ile Ser Tyr Thr
 105 110 115

cct ggt gaa atg aaa cga tct tat aca gat cga gtg act gtc aag gtg 499
 Pro Gly Glu Met Lys Arg Ser Tyr Thr Asp Arg Val Thr Val Lys Val
 120 125 130

gtc tac cct gat ggg tca ttt gat aga gtg aca ccc cat tca gtg gtt 547
 Val Tyr Pro Asp Gly Ser Phe Asp Arg Val Thr Pro His Ser Val Val
 135 140 145

tat gtg gct gac agt att tac tac ggc att gaa agc acg ggt tat cct 595
 Tyr Val Ala Asp Ser Ile Tyr Tyr Gly Ile Glu Ser Thr Gly Tyr Pro
 150 155 160 165

aaa gtc cgc aat ggt cag act gtc aag atc cca ttg agg gtg acg gat 643
 Lys Val Arg Asn Gly Gln Thr Val Lys Pro Leu Arg Val Thr Asp
 170 175 180

ggt ggt aca gga gcg gtt ggt ggg gtc cca cag gga tcg aag gtg gtc 691
 Gly Gly Thr Gly Ala Val Gly Gly Val Pro Gln Gly Ser Lys Val Val
 185 190 195

cga gat cgt tac ggc tca att gag aat gcg gag ttg atg ggt gca atc 739
 Arg Asp Arg Tyr Gly Ser Ile Glu Asn Ala Glu Leu Met Gly Ala Ile
 200 205 210

att ctc ata gat gag aag act ggc gat ctc acc ttc acg gcg cct gat 787
 Ile Leu Ile Asp Glu Lys Thr Gly Asp Leu Thr Phe Thr Ala Pro Asp
 215 220 225

gat cga acc ggt caa ctg tgg ttt cgt aca gaa gtg act ttc ccg gat 835
 Asp Arg Thr Gly Gln Leu Trp Phe Arg Thr Glu Val Thr Phe Pro Asp
 230 235 240 245

ggt tcg gac tca gag gtt caa tat gtg atc gag gtg acg gat cag cct 883
 Gly Ser Asp Ser Glu Val Gln Tyr Val Ile Glu Val Thr Asp Gln Pro
 250 255 260

gaa cct gtg gat gtc att cgt cct gcc gga tcg tct ctg agt tct 928

Glu Pro Val Asp Val Ile Arg Pro Ala Gly Ser Ser Leu Ser Ser
 265 270 275

tgatttatgc ctgagactta agc

951

<210> 1920

<211> 276

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1920

Met Leu Val Arg Ser Arg Thr Leu Val Thr Ala Ala Leu Ser Cys Ser
 1 5 10 15

Leu Leu Phe Gly Ala Thr Val Asn Gly Thr Gly Val Ala Ile Ala Tyr
 20 25 30

Glu Asn Val Ser Met Ala Ala Gln Tyr Glu Pro Arg Tyr Glu Ser Leu
 35 40 45

Glu Thr Arg Leu Gly Ser Ser Gly Val Phe Pro Lys Ser Val Glu Gln
 50 55 60

Ser Val Glu Asn Leu Ala Glu Leu Pro Glu Glu Thr Arg Phe Leu Leu
 65 70 75 80

Glu Gly Asp Ser Phe Ser Ile Ile Ile Asp Asp Gly Leu Leu Ala Ser
 85 90 95

Arg Leu Asp Pro Asn Thr Gly Glu Ile Arg His Thr Leu Gly Ala Ser
 100 105 110

Gly Ile Ser Tyr Thr Pro Gly Glu Met Lys Arg Ser Tyr Thr Asp Arg
 115 120 125

Val Thr Val Lys Val Val Tyr Pro Asp Gly Ser Phe Asp Arg Val Thr
 130 135 140

Pro His Ser Val Val Tyr Val Ala Asp Ser Ile Tyr Tyr Gly Ile Glu
 145 150 155 160

Ser Thr Gly Tyr Pro Lys Val Arg Asn Gly Gln Thr Val Lys Ile Pro
 165 170 175

Leu Arg Val Thr Asp Gly Gly Thr Gly Ala Val Gly Gly Val Pro Gln
 180 185 190

Gly Ser Lys Val Val Arg Asp Arg Tyr Gly Ser Ile Glu Asn Ala Glu
 195 200 205

Leu Met Gly Ala Ile Ile Leu Ile Asp Glu Lys Thr Gly Asp Leu Thr
 210 215 220

Phe Thr Ala Pro Asp Asp Arg Thr Gly Gln Leu Trp Phe Arg Thr Glu
 225 230 235 240

Val Thr Phe Pro Asp Gly Ser Asp Ser Glu Val Gln Tyr Val Ile Glu
 245 250 255

Val Thr Asp Gln Pro Glu Pro Val Asp Val Ile Arg Pro Ala Gly Ser

260

265

270

Ser Leu Ser Ser
275

<210> 1921

<211> 552

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(529)

<223> RXA00752

<400> 1921

aaggtcagcc gtatttcggt cagtcagcaa ctaactacgc ttatcttccg tgtagcatag 60

accgtagtta acataaggaa tggaatagga gaattgcggc atg tat tcc gac aag 115
Met Tyr Ser Asp Lys
1 5

ctg att ctc ttg ttc ctt tct gag cag gat tca agc tat gaa tgc tgc 163
Leu Ile Leu Leu Phe Leu Ser Glu Gln Asp Ser Ser Tyr Glu Cys Cys
10 15 20

gta ggt tta tta gat ggc tca gat gga ctt gat tat att gaa aag ctt 211
Val Gly Leu Leu Asp Gly Ser Asp Gly Leu Asp Tyr Ile Glu Lys Leu
25 30 35

ctg aag ggt agg aag ctg aag aac cat ttt ctt gaa tgg gaa gat att 259
Leu Lys Gly Arg Lys Leu Lys Asn His Phe Leu Glu Trp Glu Asp Ile
40 45 50

aac aag gct gat gtt gct cgt gaa gaa ata tat aaa ggg caa ttg gtg 307
Asn Lys Ala Asp Val Ala Arg Glu Glu Ile Tyr Lys Gly Gln Leu Val
55 60 65

cat ctg gtg ttt gtg acg gct ctt tcc acg cct ggt gaa att tct ttt 355
His Leu Val Phe Val Thr Ala Leu Ser Thr Pro Gly Glu Ile Ser Phe
70 75 80 85

gtt ttt cca ggt caa tct ctt atg agt gca aca ctc gaa gaa gac ttt 403
Val Phe Pro Gly Gln Ser Leu Met Ser Ala Thr Leu Glu Glu Asp Phe
90 95 100

gct gcg ctt gtg ctc gaa gag gag cgc aca tca ttt aga cct gaa ctg 451
Ala Ala Leu Val Leu Glu Glu Glu Arg Thr Ser Phe Arg Pro Glu Leu
105 110 115

tct cac ctg tgg tca ctc ccc gta ggg tgg gta gct ccg ggg ctt gag 499
Ser His Leu Trp Ser Leu Pro Val Gly Trp Val Ala Pro Gly Leu Glu
120 125 130

ggt ttc gtg gag cgt aat tcc gag gca gct tgaaccaccg ctttctgagc 549
Gly Phe Val Glu Arg Asn Ser Glu Ala Ala
135 140

cgg

552

<210> 1922

<211> 143

<212> PRT

<213> Corynebacterium glutamicum

<400> 1922

Met Tyr Ser Asp Lys Leu Ile Leu Leu Phe Leu Ser Glu Gln Asp Ser
1 5 10 15Ser Tyr Glu Cys Cys Val Gly Leu Leu Asp Gly Ser Asp Gly Leu Asp
20 25 30Tyr Ile Glu Lys Leu Leu Lys Gly Arg Lys Leu Lys Asn His Phe Leu
35 40 45Glu Trp Glu Asp Ile Asn Lys Ala Asp Val Ala Arg Glu Glu Ile Tyr
50 55 60Lys Gly Gln Leu Val His Leu Val Phe Val Thr Ala Leu Ser Thr Pro
65 70 75 80Gly Glu Ile Ser Phe Val Phe Pro Gly Gln Ser Leu Met Ser Ala Thr
85 90 95Leu Glu Glu Asp Phe Ala Ala Leu Val Leu Glu Glu Glu Arg Thr Ser
100 105 110Phe Arg Pro Glu Leu Ser His Leu Trp Ser Leu Pro Val Gly Trp Val
115 120 125Ala Pro Gly Leu Glu Gly Phe Val Glu Arg Asn Ser Glu Ala Ala
130 135 140

<210> 1923

<211> 1377

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1354)

<223> RXA00757

<400> 1923

cagggtttagc gaattcaatt tctaccactg ctgagggga atgtgctaatt tcaaggggttg 60

tgacctcgag caactttttta ttccgctcga tcaaaacaac gtg agt ttc ggc gtc 115
Val Ser Phe Gly Val
1 5gtt aag cgc ccc gat gcg tgc tac gcg ctt ttt gcc atc ctg atc aag 163
Val Lys Arg Pro Asp Ala Cys Tyr Ala Leu Phe Ala Ile Leu Ile Lys
10 15 20cgc aac cag gcg acc gcg gtt tct gcg cca atg gcg cgg cag cgt cag 211
Arg Asn Gln Ala Thr Ala Val Ser Ala Pro Met Ala Arg Gln Arg Gln
25 30 35

tgg gtt gtc cac gcc cgg cgt gga cac ttc gag cgt gta acc cgc tcc 259

Trp	Val	Val	His	Ala	Arg	Arg	Gly	His	Phe	Glu	Arg	Val	Thr	Arg	Ser		
		40					45					50					
gaa	gtt	gag	ctc	tcc	gcg	ctg	ctc	ggc	ggc	gtc	gaa	aag	ctc	tcc	gat	307	
Glu	Val	Glu	Leu	Ser	Ala	Leu	Leu	Gly	Gly	Val	Lys	Leu	Ser	Asp			
	55					60				65							
ttc	ttg	gct	gaa	tac	ttc	cag	ctg	gtc	gag	atc	ggg	gcg	gga	atc	cga	355	
Phe	Leu	Ala	Glu	Tyr		Phe	Gln	Leu	Val	Glu	Ile	Gly	Ala	Gly	Ile	Arg	
	70				75					80					85		
atc	tac	ctt	gat	ggc	gac	ggc	gga	ttt	tgg	acc	tgc	ttt	ggt	cac	ttt	403	
Ile	Tyr	Leu	Asp	Gly	Asp	Gly	Gly	Phe	Trp	Thr	Cys	Phe	Gly	His	Phe		
				90					95					100			
cag	gcc	ctc	gag	gtc	gaa	ttt	gtg	gga	tgc	ggc	gag	cgg	ctc	gat	gag	451	
Gln	Ala	Leu	Glu	Val	Glu	Phe	Val	Gly	Cys	Gly	Glu	Arg	Leu	Asp	Glu		
			105					110					115				
cgc	aga	cag	aat	ttc	agt	ggt	tgg	aaa	agc	cat	aaa	gac	aag	gat	aac	499	
Arg	Arg	Gln	Asn	Phe	Ser	Gly	Trp	Lys	Ser	His	Lys	Asp	Lys	Asp	Asn		
			120				125					130					
ctg	ccg	gca	aaa	atc	atc	ggg	cta	tta	cac	tgt	gaa	gcc	atg	cgt	agg	547	
Leu	Pro	Ala	Lys	Ile	Ile	Gly	Leu	Leu	His	Cys	Glu	Ala	Met	Arg	Arg		
	135					140				145							
cgt	atc	ccc	tct	gtc	ctt	ggt	gtt	tct	ctt	ctg	gct	gcc	ttt	ttg	gtg	595	
Arg	Ile	Pro	Ser	Val	Leu	Gly	Val	Ser	Leu	Leu	Ala	Ala	Phe	Leu	Val		
	150				155					160				165			
gcg	tgc	acc	ccc	tcc	ccc	aat	ccg	aat	gcg	gcg	ttg	gcc	cag	atg	tat	643	
Ala	Cys	Thr	Pro	Ser	Pro	Asn	Pro	Asn	Ala	Ala	Leu	Ala	Gln	Met	Tyr		
			170				175							180			
cag	gat	gcg	ctt	ttt	gat	tcc	cag	gcg	atg	tca	gag	gcc	gag	cct	gag	691	
Gln	Asp	Ala	Leu	Phe	Asp	Ser	Gln	Ala	Met	Ser	Glu	Ala	Glu	Pro	Glu		
			185				190						195				
ctt	gcc	act	ttg	gcg	agt	cag	cac	gca	gat	gaa	tta	ttg	gcc	gag	att	739	
Leu	Ala	Thr	Leu	Arg	Ser	Gln	His	Ala	Asp	Glu	Leu	Leu	Ala	Glu	Ile		
		200				205						210					
cgg	cgt	att	tgt	ggc	ttt	gat	gaa	ggc	cag	gtt	ccg	gaa	tgc	tgc	cag	787	
Arg	Arg	Ile	Cys	Gly	Phe	Asp	Glu	Gly	Gln	Val	Pro	Glu	Ser	Cys	Gln		
	215					220				225							
gta	acg	gtt	cct	gcg	atc	gct	att	ctg	ccc	acc	gat	gat	cca	gag	aag	835	
Val	Thr	Val	Pro	Ala	Ile	Ala	Ile	Leu	Pro	Thr	Asp	Asp	Pro	Glu	Lys		
	230				235					240				245			
tat	gtc	aac	gac	agt	cag	gcg	ttg	atc	ctt	gat	aat	ttg	gat	gac	att	883	
Tyr	Val	Asn	Asp	Ser	Gln	Ala	Leu	Ile	Leu	Asp	Asn	Leu	Asp	Asp	Ile		
		250						255						260			
cgg	gaa	gat	tcc	gtg	gct	tta	gtg	gtt	gag	caa	tac	atc	gcg	cag	gcg	931	
Pro	Glu	Asp	Ser	Val	Ala	Leu	Val	Val	Glu	Gln	Tyr	Ile	Ala	Gln	Ala		
		265					270						275				
gaa	ttt	gct	gaa	gga	tct	gag	gtg	tcc	gtt	cct	gtt	gat	ttg	gag	ctc	979	
Glu	Phe	Ala	Glu	Gly	Ser	Glu	Val	Ser	Val	Pro	Val	Asp	Leu	Glu	Leu		

280	285	290	
acc gag gca gaa tta gct gct gcg aag gac ttg gcg gac cgc gag ttt			1027
Thr Glu Ala Glu Leu Ala Ala Ala Lys Asp Leu Ala Asp Arg Glu Phe			
295	300	305	
tcc gcc gcg tgg tct ttg ggc gtg gct ttg gct cag ctt ccg gaa acc			1075
Ser Ala Ala Trp Ser Leu Gly Val Ala Leu Ala Gln Leu Pro Glu Thr			
310	315	320	325
gac cgc gag gag gtg gaa acg gcg atc agc aac cac cat gac cgc gcg			1123
Asp Arg Glu Glu Val Glu Thr Ala Ile Ser Asn His His Asp Arg Ala			
330	335	340	
tcg cag ctg caa att att acc tcc ggc act acc cca gcg cca ggt tac			1171
Ser Gln Leu Gln Ile Ile Thr Ser Gly Thr Thr Pro Ala Pro Gly Tyr			
345	350	355	
gtg agc gag ctg ccc gac ccc acc gac gag act tca gcg cga agc aac			1219
Val Ser Glu Leu Pro Asp Pro Thr Asp Glu Thr Ser Ala Arg Ser Asn			
360	365	370	
att gaa acc gtc gaa aac aac gtc acc cag gcc tgg cat gca gct gca			1267
Ile Glu Thr Val Glu Asn Asn Val Thr Gln Ala Trp His Ala Ala Ala			
375	380	385	
agc gcc gca acc acc gac gcc tgg cgt gtc ttc tgc gcg cac atc gcc			1315
Ser Ala Ala Thr Thr Asp Ala Trp Arg Val Phe Cys Ala His Ile Ala			
390	395	400	405
ggc gat acc gca cgc gaa tta acg ctt atc gac gtc tcc tagcagtttc			1364
Gly Asp Thr Ala Arg Glu Leu Thr Leu Ile Asp Val Ser			
410	415		
actgccatt ttt			1377
<210> 1924			
<211> 418			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 1924			
Val Ser Phe Gly Val Val Lys Arg Pro Asp Ala Cys Tyr Ala Leu Phe			
1	5	10	15
Ala Ile Leu Ile Lys Arg Asn Gln Ala Thr Ala Val Ser Ala Pro Met			
20	25	30	
Ala Arg Gln Arg Gln Trp Val Val His Ala Arg Arg Gly His Phe Glu			
35	40	45	
Arg Val Thr Arg Ser Glu Val Glu Leu Ser Ala Leu Leu Gly Gly Val			
50	55	60	
Glu Lys Leu Ser Asp Phe Leu Ala Glu Tyr Phe Gln Leu Val Glu Ile			
65	70	75	80
Gly Ala Gly Ile Arg Ile Tyr Leu Asp Gly Asp Gly Gly Phe Trp Thr			
85	90	95	

Cys Phe Gly His Phe Gln Ala Leu Glu Val Glu Phe Val Gly Cys Gly
 100 105 110
 Glu Arg Leu Asp Glu Arg Arg Gln Asn Phe Ser Gly Trp Lys Ser His
 115 120 125
 Lys Asp Lys Asp Asn Leu Pro Ala Lys Ile Ile Gly Leu Leu His Cys
 130 135 140
 Glu Ala Met Arg Arg Arg Ile Pro Ser Val Leu Gly Val Ser Leu Leu
 145 150 155 160
 Ala Ala Phe Leu Val Ala Cys Thr Pro Ser Pro Asn Pro Asn Ala Ala
 165 170 175
 Leu Ala Gln Met Tyr Gln Asp Ala Leu Phe Asp Ser Gln Ala Met Ser
 180 185 190
 Glu Ala Glu Pro Glu Leu Ala Thr Leu Arg Ser Gln His Ala Asp Glu
 195 200 205
 Leu Leu Ala Glu Ile Arg Arg Ile Cys Gly Phe Asp Glu Gly Gln Val
 210 215 220
 Pro Glu Ser Cys Gln Val Thr Val Pro Ala Ile Ala Ile Leu Pro Thr
 225 230 235 240
 Asp Asp Pro Glu Lys Tyr Val Asn Asp Ser Gln Ala Leu Ile Leu Asp
 245 250 255
 Asn Leu Asp Asp Ile Pro Glu Asp Ser Val Ala Leu Val Val Glu Gln
 260 265 270
 Tyr Ile Ala Gln Ala Glu Phe Ala Glu Gly Ser Glu Val Ser Val Pro
 275 280 285
 Val Asp Leu Glu Leu Thr Glu Ala Glu Leu Ala Ala Ala Lys Asp Leu
 290 295 300
 Ala Asp Arg Glu Phe Ser Ala Ala Trp Ser Leu Gly Val Ala Leu Ala
 305 310 315 320
 Gln Leu Pro Glu Thr Asp Arg Glu Glu Val Glu Thr Ala Ile Ser Asn
 325 330 335
 His His Asp Arg Ala Ser Gln Leu Gln Ile Ile Thr Ser Gly Thr Thr
 340 345 350
 Pro Ala Pro Gly Tyr Val Ser Glu Leu Pro Asp Pro Thr Asp Glu Thr
 355 360 365
 Ser Ala Arg Ser Asn Ile Glu Thr Val Glu Asn Asn Val Thr Gln Ala
 370 375 380
 Trp His Ala Ala Ala Ser Ala Ala Thr Thr Asp Ala Trp Arg Val Phe
 385 390 395 400
 Cys Ala His Ile Ala Gly Asp Thr Ala Arg Glu Leu Thr Leu Ile Asp
 405 410 415
 Val Ser

<210> 1925
 <211> 906
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(883)
 <223> RXA00763

<400> 1925
 agcgcgattt gaggctttt aatacgcg gaagtattca tgtcccagg ttatcccaa 60
 gtttgaatct cttgcaggaa cgtggggtaa agatatagat gtg gaa aaa tcc aga 115
 Val Glu Lys Ser Arg
 1 5
 aaa cga ctt gtg acc atc gca gca tcg aca att ggg gcc gtt gcg gtg 163
 Lys Arg Leu Val Thr Ile Ala Ala Ser Thr Ile Gly Ala Val Ala Val
 10 15 20
 gct ggc ggc gct ttt tgg atc gtt gat gct tcc atc gct gcg cac gcg 211
 Ala Gly Gly Ala Phe Trp Ile Val Asp Ala Ser Ile Ala Ala His Ala
 25 30 35
 gaa cgc aac ttg tct aaa gca gtt gcg gaa tcc gca gat ctt gaa aac 259
 Glu Arg Asn Leu Ser Lys Ala Val Ala Glu Ser Ala Asp Leu Glu Asn
 40 45 50
 gac ccg cga gta ttc ctc ggc agc tcc att tac tcc acg gcg ttt ttt 307
 Asp Pro Arg Val Phe Leu Gly Ser Ser Ile Tyr Ser Thr Ala Phe Phe
 55 60 65
 acc ggc aaa ctc gac tcc gta agc atc gac atg ctg gac gtg gaa atc 355
 Thr Gly Lys Leu Asp Ser Val Ser Ile Asp Met Leu Asp Val Glu Ile
 70 75 80 85
 ccc ggc gtc ggc atg gtg aat gca cgc aca gag gta gaa agc gtg gaa 403
 Pro Gly Val Gly Met Val Asn Ala Arg Thr Glu Val Glu Ser Val Glu
 90 95 100
 gtc tca cgg gat caa atc ctc tcc ggt gac ctc gac ggc acc act gcg 451
 Val Ser Arg Asp Gln Ile Leu Ser Gly Asp Leu Asp Gly Thr Thr Ala
 105 110 115
 gaa acc ttc acg cgc aca tta cgc atg gac ggc gtc gca atc ggc gcg 499
 Glu Thr Phe Thr Arg Thr Leu Arg Met Asp Gly Val Ala Ile Gly Ala
 120 125 130
 cag ctc gga atc acc gac ctc gac atc tcc cac ccc atc gac atc tcc 547
 Gln Leu Gly Ile Thr Asp Leu Asp Ile Ser His Pro Ile Asp Ile Ser
 135 140 145
 ccc tcc ggc ggc atc acc tca gaa gcg ctc ctg aca gga acc cca cca 595
 Pro Ser Gly Gly Ile Thr Ser Glu Ala Leu Leu Thr Gly Thr Pro Pro
 150 155 160 165
 gac atg gaa gac ccg gtc agt gtg ctg gtc acc ctt cgc cta gtc ggc 643

Asp Met Glu Asp Pro Val Ser Val Leu Val Thr Leu Arg Leu Val Gly
 170 175 180
 tca gaa ttc cag atg ctg ccg tac gag ctt atc gac gca ccc tcc gga 691
 Ser Glu Phe Gln Met Leu Pro Tyr Glu Leu Ile Asp Ala Pro Ser Gly
 185 190 195
 ctc acc ctc gac gat gtc gcc ccc gac ttc acg tgg aaa atc gac acc 739
 Leu Thr Leu Asp Asp Val Ala Pro Asp Phe Thr Trp Lys Ile Asp Thr
 200 205 210
 ctg caa cta ccc ctc gca gat cgg gca atg gcg gtt tac cta tct ggt 787
 Leu Gln Leu Pro Leu Ala Asp Arg Ala Met Ala Val Tyr Leu Ser Gly
 215 220 225
 ggc tcc gtc cat ttc caa tct gaa gcc cgc aac gtc cag ctc acc acc 835
 Gly Ser Val His Phe Gln Ser Glu Ala Arg Asn Val Gln Leu Thr Thr
 230 235 240 245
 cgc gaa cta tca cca cta gct gca ccg gaa gaa aac tcc gat gaa tcc 883
 Arg Glu Leu Ser Pro Leu Ala Ala Pro Glu Glu Asn Ser Asp Glu Ser
 250 255 260
 tagatgccaa acgtgcgcac ccg 906
 <210> 1926
 <211> 261
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 1926
 Val Glu Lys Ser Arg Lys Arg Leu Val Thr Ile Ala Ala Ser Thr Ile
 1 5 10 15
 Gly Ala Val Ala Val Ala Gly Gly Ala Phe Trp Ile Val Asp Ala Ser
 20 25 30
 Ile Ala Ala His Ala Glu Arg Asn Leu Ser Lys Ala Val Ala Glu Ser
 35 40 45
 Ala Asp Leu Glu Asn Asp Pro Arg Val Phe Leu Gly Ser Ser Ile Tyr
 50 55 60
 Ser Thr Ala Phe Phe Thr Gly Lys Leu Asp Ser Val Ser Ile Asp Met
 65 70 75 80
 Leu Asp Val Glu Ile Pro Gly Val Gly Met Val Asn Ala Arg Thr Glu
 85 90 95
 Val Glu Ser Val Glu Val Ser Arg Asp Gln Ile Leu Ser Gly Asp Leu
 100 105 110
 Asp Gly Thr Thr Ala Glu Thr Phe Thr Arg Thr Leu Arg Met Asp Gly
 115 120 125
 Val Ala Ile Gly Ala Gln Leu Gly Ile Thr Asp Leu Asp Ile Ser His
 130 135 140
 Pro Ile Asp Ile Ser Pro Ser Gly Gly Ile Thr Ser Glu Ala Leu Leu
 145 150 155 160

Thr Gly Thr Pro Pro Asp Met Glu Asp Pro Val Ser Val Leu Val Thr
 165 170 175
 Leu Arg Leu Val Gly Ser Glu Phe Gln Met Leu Pro Tyr Glu Leu Ile
 180 185 190
 Asp Ala Pro Ser Gly Leu Thr Leu Asp Asp Val Ala Pro Asp Phe Thr
 195 200 205
 Trp Lys Ile Asp Thr Leu Gln Leu Pro Leu Ala Asp Arg Ala Met Ala
 210 215 220
 Val Tyr Leu Ser Gly Gly Ser Val His Phe Gln Ser Glu Ala Arg Asn
 225 230 235 240
 Val Gln Leu Thr Thr Arg Glu Leu Ser Pro Leu Ala Ala Pro Glu Glu
 245 250 255
 Asn Ser Asp Glu Ser
 260

<210> 1927

<211> 810

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(787)

<223> RXA00765

<400> 1927

acggaaaagt ttctgcgtct gcgtgggtcga ctcaggattc gcaatcagaa gaacatgcac 60

gttatctaag agtagtgcca aaacgctagt cttgagtgtc atg agc gaa aat tcc 115
 Met Ser Glu Asn Ser 5
 1

acc cct aat aat cca gtc gtc cca ggt gca ggc gca gac ggc cca tca 163
 Thr Pro Asn Asn Pro Val Val Pro Gly Ala Gly Ala Asp Gly Pro Ser 20
 10 15

ctg tcc gat tct gca agc atc agc gga tcc gac gca gta aac ctc gct 211
 Leu Ser Asp Ser Ala Ser Ile Ser Gly Ser Asp Ala Val Asn Leu Ala 35
 25 30

gcc gaa caa tcc aag agc acc gct cac cgc aac atc cca ggc cta ggt 259
 Ala Glu Gln Ser Lys Ser Thr Ala His Arg Asn Ile Pro Gly Leu Gly 50
 40 45

gac ctt cct atc cct gac gac acc gct aac ctc cgc gaa ggc ccc aac 307
 Asp Leu Pro Ile Pro Asp Asp Thr Ala Asn Leu Arg Glu Gly Pro Asn 65
 55 60

ctc cac gac gga ctc ctc gcg ctc ctc cct ctc gtc ggc gtc tgg cgc 355
 Leu His Asp Gly Leu Leu Ala Leu Leu Pro Leu Val Gly Val Trp Arg 85
 70 75 80

ggc gaa ggc caa gcc gac acc gca gaa gac gga caa tac gca ttc ggc 403

[illegible]

<211> 229

<213> Cor

Met Ser Glu Asn Ser Thr Pro Asn Asn Pro Val Val Pro Gly Ala Gly
1 5 10 15

Ala Asp Gly Pro Ser Leu Ser Asp Ser Ala Ser Ile Ser Gly Ser Asp
20 25 30

Ala Val Asn Leu Ala Ala Glu Gln Ser Lys Ser Thr Ala His Arg Asn
35 40 45

Ile Pro Gly Leu Gly Asp Leu Pro Ile Pro Asp Asp Thr Ala Asn Leu
50 55 60

Arg Glu Gly Pro Asn Leu His Asp Gly Leu Leu Ala Leu Leu Pro Leu
65 70 75 80

Val Gly Val Trp Arg Gly Glu Gly Gln Ala Asp Thr Ala Glu Asp Gly
85 90 95

Gln Tyr Ala Phe Gly Gln Gln Ile Thr Phe Ala His Asp Gly Glu Asn
 100 105 110
 Tyr Leu Ser Phe Glu Ser Arg Met Trp Lys Leu Asp Glu Glu Gly Asn
 115 120 125
 Pro Thr Gly Val Asp Gln Arg Glu Ser Gly Phe Trp Arg Ile Asn Leu
 130 135 140
 Lys Asp Glu Ile Glu Phe Val Cys Thr His Ala Gly Gly Val Val Glu
 145 150 155 160
 Ile Tyr Tyr Gly Gln Pro Leu Asn Glu Arg Ala Trp Gln Leu Glu Ser
 165 170 175
 Ala Ser Thr Met Val Thr Ala Thr Gly Pro Ser Thr Leu Gly Pro Gly
 180 185 190
 Lys Arg Leu Tyr Gly Leu Leu Pro Thr Asn Glu Leu Gly Trp Val Asp
 195 200 205
 Glu Arg Leu Val Gly Asp Ala Leu Lys Pro Arg Met Ser Ala Gln Leu
 210 215 220
 Thr Arg Val Ile Gly
 225
 <210> 1929
 <211> 411
 <212> DNA
 <213> Corynebacterium glutamicum
 <220>
 <221> CDS
 <222> (101)..(388)
 <223> RXA00781
 <400> 1929
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 cgggttaattc caccgggatg agataccgag gagaacgcac atg agc gag aac aaa 115
 Met Ser Glu Asn Lys
 1 5
 aac att gag att gtc cac aat gaa gga cag aag cgc ttt gtt atc agc 163
 Asn Ile Glu Ile Val His Asn Glu Gly Gln Lys Arg Phe Val Ile Ser
 10 15 20
 gtt gat gga acg cca gct gga ttt gcc agc tat tta gac ggc ccg gat 211
 Val Asp Gly Thr Pro Ala Gly Phe Ala Ser Tyr Leu Asp Gly Pro Asp
 25 30 35
 atc cgc aac ttc aac cac act gtt att aag cct gaa ttc cgt gga cag 259
 Ile Arg Asn Phe Asn His Thr Val Ile Lys Pro Glu Phe Arg Gly Gln
 40 45 50
 gga ctg tct gcg cca ttg atc aag ttt gct ttg gat gat gca cgt gag 307
 Gly Leu Ser Ala Pro Leu Ile Lys Phe Ala Leu Asp Asp Ala Arg Glu
 55 60 65

```

tcc ggt atc cgt att cat gat gct tgc tct gca gtc gct ggc ttc att 355
Ser Gly Ile Arg Ile His Asp Ala Cys Ser Ala Val Ala Gly Phe Ile
70 75 80 85

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cag aag aac cct gag tat aag gat cta aag aac tagctggcac aggggggtgg 408
Gln Lys Asn Pro Glu Tyr Lys Asp Leu Lys Asn
90 95

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ttc 411

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<210> 1930

<211> 96

<212> PRT

<213> Corynebacterium glutamicum

<400> 1930

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Met Ser Glu Asn Lys Asn Ile Glu Ile Val His Asn Glu Gly Gln Lys
1 5 10 15

```

```

Arg Phe Val Ile Ser Val Asp Gly Thr Pro Ala Gly Phe Ala Ser Tyr
20 25 30

```

```

Leu Asp Gly Pro Asp Ile Arg Asn Phe Asn His Thr Val Ile Lys Pro
35 40 45

```

```

Glu Phe Arg Gly Gln Gly Leu Ser Ala Pro Leu Ile Lys Phe Ala Leu
50 55 60

```

```

Asp Asp Ala Arg Glu Ser Gly Ile Arg Ile His Asp Ala Cys Ser Ala
65 70 75 80

```

```

Val Ala Gly Phe Ile Gln Lys Asn Pro Glu Tyr Lys Asp Leu Lys Asn
85 90 95

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<210> 1931

<211> 348

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(325)

<223> RXA00788

<400> 1931

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cgcacccctc tagttttcca tcacctcaat gaacggcgct aactccggtt cattgcgcaa 60

```

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ttgatccagc actgcttgca gtgaggccctc attagtgtggc atg gcc tcc tcc atc 115
Met Ala Ser Ser Ile
1 5

```

```

aac atc gga gtg ttc aac ctt gga aat gct gtt gct gcc tgg ctt gct 163
Asn Ile Gly Val Phe Asn Leu Gly Asn Ala Val Ala Ala Trp Leu Ala
10 15 20

```

```

ggt gca acc atc acc act tcc ctt gga ctc aca tca gcc gga tta gtt 211
Gly Ala Thr Ile Thr Thr Ser Leu Gly Leu Thr Ser Ala Gly Leu Val
      25          30          35

ggc ggt ttg atg acg tcc ctc gga cta gtg ttg gcc atc gtg gct gtg 259
Gly Gly Leu Met Thr Ser Leu Gly Leu Val Leu Ala Ile Val Ala Val
      40          45          50

gtt ttg cgt cga aaa gcg caa ggc acc caa gcg acc atc agc gtt gtg 307
Val Leu Arg Arg Lys Ala Gln Gly Thr Gln Ala Thr Ile Ser Val Val
      55          60          65

gag cac cag ccc gcc caa taaataattt ctctcttcta att 348
Glu His Gln Pro Ala Gln
      70          75

```

<210> 1932

<211> 75

<212> PRT

<213> Corynebacterium glutamicum

<400> 1932

```

Met Ala Ser Ser Ile Asn Ile Gly Val Phe Asn Leu Gly Asn Ala Val
  1          5          10          15

Ala Ala Trp Leu Ala Gly Ala Thr Ile Thr Thr Ser Leu Gly Leu Thr
      20          25          30

Ser Ala Gly Leu Val Gly Gly Leu Met Thr Ser Leu Gly Leu Val Leu
      35          40          45

Ala Ile Val Ala Val Val Leu Arg Arg Lys Ala Gln Gly Thr Gln Ala
      50          55          60

Thr Ile Ser Val Val Glu His Gln Pro Ala Gln
      65          70          75

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<210> 1933

<211> 567

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(544)

<223> RXA00804

<400> 1933

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aatctagtagc aagttccagc gaaaaccttc caaaactgac caagttaag aagattcgct 60

accctatgaa tcagttgtag gagtaagagg ggagttagag atg aag atc aga agt 115
      Met Lys Ile Arg Ser
      1          5

gca cgt gaa atc gcg gag tgg ttc gtt gcc tgg gga gat gaa ctc gat 163
Ala Arg Glu Ile Ala Glu Trp Phe Val Ala Trp Gly Asp Glu Leu Asp
      10          15          20

gct gaa gtc tcc cct ttg aaa ttg cag aag ctc ctt tat tac tcc cag 211

```

Ala Glu Val Ser Pro Leu Lys Leu Gln Lys Leu Leu Tyr Tyr Ser Gln
25 30 35

ggg gag cat ata gct gca aca ggg cga aaa ctt ttc tcg gat aag att 259
Gly Glu His Ile Ala Ala Thr Gly Arg Lys Leu Phe Ser Asp Lys Ile
40 45 50

ctg gcg tgg cag cac gga cct gtc act ccg ggc gtt tat tca gat aca 307
Leu Ala Trp Gln His Gly Pro Val Thr Pro Gly Val Tyr Ser Asp Thr
55 60 65

aaa tca tac gcc cga aac cca att gat cct gat gag ttt gtg tca gat 355
Lys Ser Tyr Gly Arg Asn Pro Ile Asp Pro Asp Glu Phe Val Ser Asp
70 75 80 85

gaa ttt aac tgg gat gac tac tca gat gtg tca gat gag ctt gta acc 403
Glu Phe Asn Trp Asp Asp Tyr Ser Asp Val Ser Asp Glu Leu Val Thr
90 95 100

gta tgg cga aaa tac gcc atc tat tcg gcg tgg gca ctg agg gaa aaa 451
Val Trp Arg Lys Tyr Gly Ile Tyr Ser Ala Trp Ala Leu Arg Glu Lys
105 110 115

act cac agt gaa tcg ccg tgg ctc gat gcc tgg gca caa ggg caa aat 499
Thr His Ser Glu Ser Pro Trp Leu Asp Ala Trp Ala Gln Gly Gln Asn
120 125 130

att gaa att aca gat gct gcg ctg aaa gat ttc ttc ttg gtg cat 544
Ile Glu Ile Thr Asp Ala Ala Leu Lys Asp Phe Phe Leu Val His
135 140 145

tagaaatttg aaaaagaaac gaa 567

<210> 1934
<211> 148
<212> PRT
<213> Corynebacterium glutamicum

<400> 1934
Met Lys Ile Arg Ser Ala Arg Glu Ile Ala Glu Trp Phe Val Ala Trp
1 5 10 15

Gly Asp Glu Leu Asp Ala Glu Val Ser Pro Leu Lys Leu Gln Lys Leu
20 25 30

Leu Tyr Tyr Ser Gln Gly Glu His Ile Ala Ala Thr Gly Arg Lys Leu
35 40 45

Phe Ser Asp Lys Ile Leu Ala Trp Gln His Gly Pro Val Thr Pro Gly
50 55 60

Val Tyr Ser Asp Thr Lys Ser Tyr Gly Arg Asn Pro Ile Asp Pro Asp
65 70 75 80

Glu Phe Val Ser Asp Glu Phe Asn Trp Asp Asp Tyr Ser Asp Val Ser
85 90 95

Asp Glu Leu Val Thr Val Trp Arg Lys Tyr Gly Ile Tyr Ser Ala Trp
100 105 110

Ala Leu Arg Glu Lys Thr His Ser Glu Ser Pro Trp Leu Asp Ala Trp
 115 120 125

Ala Gln Gly Gln Asn Ile Glu Ile Thr Asp Ala Ala Leu Lys Asp Phe
 130 135 140

Phe Leu Val His
 145

<210> 1935

<211> 1005

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(982)

<223> RXA00805

<400> 1935

tgctccgctg acagtgggtgc gcctgagcag cccaaaagag acaaacgcgt ggttgagggc 60

atatggggaa agcgtgaaac tctgataggg tgccatatcc atg gca gaa agt ttt 115
 Met Ala Glu Ser Phe
 1 5

ata gag gtc tcg gcg ggg cat gcg gat cgg cgg ata gat aag ttt ttg 163
 Ile Glu Val Ser Ala Gly His Ala Asp Arg Arg Ile Asp Lys Phe Leu
 10 15 20

cgg gca cag cta aag gcc gtg ccc gcg tcg ttg att ttc cgt caa atg 211
 Arg Ala Gln Leu Lys Gly Val Pro Ala Ser Leu Ile Phe Arg Gln Met
 25 30 35

cgt aaa gcc gac att cgg gtg aat ggt cgt aaa gtg gat ccg aat tac 259
 Arg Lys Gly Asp Ile Arg Val Asn Gly Arg Lys Val Asp Pro Asn Tyr
 40 45 50

cgg ttg caa gaa gcc gac cga att cga atg tgg cag atg gat ttg ctg 307
 Arg Leu Gln Glu Gly Asp Arg Ile Arg Met Trp Gln Met Asp Leu Leu
 55 60 65

gca gat ttg ccg cca ccg gtc gtc gat aag cat att ttt aag gct gtc 355
 Ala Asp Leu Pro Pro Val Val Val Asp Lys His Ile Phe Lys Ala Val
 70 75 80 85

gca gac agc gtg ctt ttt gag gac gcc gaa tta ctg gtg atc aat aag 403
 Ala Asp Ser Val Leu Phe Glu Asp Ala Glu Leu Leu Val Ile Asn Lys
 90 95 100

cca gct gga att cct gtg cac ggt gcc acg ggg cac gcc ggt gcc gtg 451
 Pro Ala Gly Ile Pro Val His Gly Gly Thr Gly His Gly Gly Val
 105 110 115

att gag gcg ctg cgg cag aag ttt ccg cag gaa cgc gac ctg gaa ttg 499
 Ile Glu Ala Leu Arg Gln Lys Phe Pro Gln Glu Arg Asp Leu Glu Leu
 120 125 130

gtg cat cgt ttg gat cgg gac acc tca ggt ttg ttg ctg gtt tct aaa 547
 Val His Arg Leu Asp Arg Asp Thr Ser Gly Leu Leu Leu Val Ser Lys

135	140	145	
acg aca tct gtg ttg cgc gag ttg cag gaa att ttg cga gac cgc gaa			595
Thr Thr Ser Val Leu Arg Glu Leu Gln Glu Ile Leu Arg Asp Arg Glu			
150	155	160	165
gag gag att ttt cgg ggg tat tta ctc aag gtc gag ggg gct tgg cct			643
Glu Glu Ile Phe Arg Gly Tyr Leu Leu Lys Val Glu Gly Ala Trp Pro			
170	175	180	
ggc gat ttg cga caa att gat gtg ccg ttg aag cgg acg gag aca act			691
Gly Asp Leu Arg Gln Ile Asp Val Pro Leu Lys Arg Thr Glu Thr Thr			
185	190	195	
gtt gtg cca cat tcg gat ggt ttg cgg gcg cgg acg tat ttt gag gtt			739
Val Val Pro His Ser Asp Gly Leu Arg Ala Arg Thr Tyr Phe Glu Val			
200	205	210	
gta aag cgt ttg ccg ggt gcg acc ttg gtg aag gcg cag ttg gcg acc			787
Val Lys Arg Leu Pro Gly Ala Thr Leu Val Lys Ala Gln Leu Ala Thr			
215	220	225	
ggg cgg aaa cat cag att cgg gtc cat gcg cag tat gcg ggt cac cct			835
Gly Arg Lys His Gln Ile Arg Val His Ala Gln Tyr Ala Gly His Pro			
230	235	240	245
att gtt ggc gat cca cga tac ggg tcg cgt ggg ggc aga gct gcg acg			883
Ile Val Gly Asp Pro Arg Tyr Gly Ser Arg Gly Gly Arg Ala Ala Thr			
250	255	260	
atg cat ttg cat gcg gcg gaa ttg gtg gcg cct cgt ggg gcg ggg aag			931
Met His Leu His Ala Ala Glu Leu Val Ala Pro Arg Gly Ala Gly Lys			
265	270	275	
cgt cag aaa ttc act gca ccg ttg ccg aag gag tgg ggt atg gga cgg			979
Arg Gln Lys Phe Thr Ala Pro Leu Pro Lys Glu Trp Gly Met Gly Arg			
280	285	290	
gtc tgagtcgggc cttcgtggaa tcg			1005
Val			
<210> 1936			
<211> 294			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 1936			
Met Ala Glu Ser Phe Ile Glu Val Ser Ala Gly His Ala Asp Arg Arg			
1	5	10	15
Ile Asp Lys Phe Leu Arg Ala Gln Leu Lys Gly Val Pro Ala Ser Leu			
20	25	30	
Ile Phe Arg Gln Met Arg Lys Gly Asp Ile Arg Val Asn Gly Arg Lys			
35	40	45	
Val Asp Pro Asn Tyr Arg Leu Gln Glu Gly Asp Arg Ile Arg Met Trp			
50	55	60	

Gln Met Asp Leu Leu Ala Asp Leu Pro Pro Pro Val Val Asp Lys His
 65 70 75 80
 Ile Phe Lys Ala Val Ala Asp Ser Val Leu Phe Glu Asp Ala Glu Leu
 85 90 95
 Leu Val Ile Asn Lys Pro Ala Gly Ile Pro Val His Gly Gly Thr Gly
 100 105 110
 His Gly Gly Gly Val Ile Glu Ala Leu Arg Gln Lys Phe Pro Gln Glu
 115 120 125
 Arg Asp Leu Glu Leu Val His Arg Leu Asp Arg Asp Thr Ser Gly Leu
 130 135 140
 Leu Leu Val Ser Lys Thr Thr Ser Val Leu Arg Glu Leu Gln Glu Ile
 145 150 155 160
 Leu Arg Asp Arg Glu Glu Glu Ile Phe Arg Gly Tyr Leu Leu Lys Val
 165 170 175
 Glu Gly Ala Trp Pro Gly Asp Leu Arg Gln Ile Asp Val Pro Leu Lys
 180 185 190
 Arg Thr Glu Thr Thr Val Val Pro His Ser Asp Gly Leu Arg Ala Arg
 195 200 205
 Thr Tyr Phe Glu Val Val Lys Arg Leu Pro Gly Ala Thr Leu Val Lys
 210 215 220
 Ala Gln Leu Ala Thr Gly Arg Lys His Gln Ile Arg Val His Ala Gln
 225 230 235 240
 Tyr Ala Gly His Pro Ile Val Gly Asp Pro Arg Tyr Gly Ser Arg Gly
 245 250 255
 Gly Arg Ala Ala Thr Met His Leu His Ala Ala Glu Leu Val Ala Pro
 260 265 270
 Arg Gly Ala Gly Lys Arg Gln Lys Phe Thr Ala Pro Leu Pro Lys Glu
 275 280 285
 Trp Gly Met Gly Arg Val
 290

<210> 1937

<211> 701

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(678)

<223> RXA00808

<400> 1937

gct ggc ttc aat gag atg atg cgt ggc ctg cgt gaa cgt cag cgc gtc 48
 Ala Gly Phe Asn Glu Met Met Arg Gly Leu Arg Glu Arg Gln Arg Val
 1 5 10 15


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cgt gac ctt ttc ggt cgc tac gtg ggc gct gaa gtg gcc aag cgt gcg   96
Arg Asp Leu Phe Gly Arg Tyr Val Gly Ala Glu Val Ala Lys Arg Ala
      20                      25                      30

ctg gag gaa cgc ccc act ctg ggt ggc gag gac cgt aag gtt gcc gtg   144
Leu Glu Glu Glu Arg Pro Thr Leu Gly Gly Glu Asp Arg Lys Val Ala Val
      35                      40                      45

ttg ttt gtc gat gtc atc ggc tcc act acc ttt gcc gtc aac cac act   192
Leu Phe Val Asp Val Ile Gly Ser Thr Thr Phe Ala Val Asn His Thr
      50                      55                      60

cct gaa gag gtt gtg gag cgc ctc aat gag ttc ttc gag cac gtc gtg   240
Pro Glu Glu Val Val Glu Ala Leu Asn Glu Phe Phe Glu His Val Val
      65                      70                      75                      80

gag gtt gtg cac cgc aac aag ggt gtt atc aac aag ttc cag ggt gac   288
Glu Val Val His Arg Asn Lys Gly Val Ile Asn Lys Phe Gln Gly Asp
      85                      90                      95

gcg gcg ttg gcg att ttc ggc gct ccc ctg ccc ctg tct gat gcc acc   336
Ala Ala Leu Ala Ile Phe Gly Ala Pro Leu Pro Leu Ser Asp Ala Thr
      100                      105                      110

ggt cat gcg ctt gcg gct gcc cgt gag ctc cgc gca gag ctg aaa gat   384
Gly His Ala Leu Ala Ala Arg Glu Leu Arg Ala Glu Leu Lys Asp
      115                      120                      125

ctc cag ctc aag gcc gga att ggt gtg gct gct gcc cat gtc gtt gct   432
Leu Glu Leu Lys Ala Gly Ile Gly Val Ala Ala Gly His Val Val Ala
      130                      135                      140

ggt cat atc gcc ggt cac gcg agg ttt gag tac act gtg atc gcc gac   480
Gly His Ile Gly Gly His Ala Arg Phe Glu Tyr Thr Val Ile Gly Asp
      145                      150                      155                      160

gcg gtg aac cag gct gcg cgc ctg acg gag atc gcg aaa acg acc cca   528
Ala Val Asn Gln Ala Ala Arg Leu Thr Glu Ile Ala Lys Thr Thr Pro
      165                      170                      175

ggc cgc acc gtc acc aac gct tcc acg ctg cgt gag gcc aac gag gcg   576
Gly Arg Thr Val Thr Asn Ala Ser Thr Leu Arg Glu Ala Asn Glu Ala
      180                      185                      190

gag cag gct cgc tgg acg ctc atg aag tcc gtg gag ctg cgc gga cgt   624
Glu Gln Ala Arg Trp Thr Leu Met Lys Ser Val Glu Leu Arg Gly Arg
      195                      200                      205

agc cag atg acg cag att gcg cgg cct att cgg ccg acg ttg gcg gat   672
Ser Gln Met Thr Gln Ile Ala Arg Pro Ile Arg Pro Thr Leu Ala Asp
      210                      215                      220

agg tcc taatacgttt ttcgacgcaa aaa   701
Arg Ser
225

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<210> 1938

<211> 226

<212> PRT

<213> Corynebacterium glutamicum

<400> 1938

Ala Gly Phe Asn Glu Met Met Arg Gly Leu Arg Glu Arg Gln Arg Val
 1 5 10 15

Arg Asp Leu Phe Gly Arg Tyr Val Gly Ala Glu Val Ala Lys Arg Ala
 20 25 30

Leu Glu Glu Arg Pro Thr Leu Gly Glu Asp Arg Lys Val Ala Val
 35 40 45

Leu Phe Val Asp Val Ile Gly Ser Thr Thr Phe Ala Val Asn His Thr
 50 55 60

Pro Glu Glu Val Val Glu Ala Leu Asn Glu Phe Phe Glu His Val Val
 65 70 75 80

Glu Val Val His Arg Asn Lys Gly Val Ile Asn Lys Phe Gln Gly Asp
 85 90 95

Ala Ala Leu Ala Ile Phe Gly Ala Pro Leu Pro Leu Ser Asp Ala Thr
 100 105 110

Gly His Ala Leu Ala Ala Ala Arg Glu Leu Arg Ala Glu Leu Lys Asp
 115 120 125

Leu Gln Leu Lys Ala Gly Ile Gly Val Ala Ala Gly His Val Val Ala
 130 135 140

Gly His Ile Gly Gly His Ala Arg Phe Glu Tyr Thr Val Ile Gly Asp
 145 150 155 160

Ala Val Asn Gln Ala Ala Arg Leu Thr Glu Ile Ala Lys Thr Thr Pro
 165 170 175

Gly Arg Thr Val Thr Asn Ala Ser Thr Leu Arg Glu Ala Asn Glu Ala
 180 185 190

Glu Gln Ala Arg Trp Thr Leu Met Lys Ser Val Glu Leu Arg Gly Arg
 195 200 205

Ser Gln Met Thr Gln Ile Ala Arg Pro Ile Arg Pro Thr Leu Ala Asp
 210 215 220

Arg Ser
 225

<210> 1939

<211> 1182

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1159)

<223> RXA00812

<400> 1939

ttcacaggtg agcgtatcgc gggcggttga gaggtgagtt atccacaggc cgcagagggg 60

gtcgttgaaa gcacgtaagc ctcaggccac agtaggtgcc atg aac acc atc aca 115
Met Asn Thr Ile Thr
1 5

cac caa gca att ctc atc gca gtg gaa gat ccg gtc ctg cac cca gag 163
His Gln Ala Ile Leu Ile Ala Val Glu Asp Pro Val Leu His Pro Glu
10 15 20

gcc atg cac gta gct gca gcc act ggt cgg ccg gtt att gaa aca aca 211
Ala Met His Val Ala Ala Ala Thr Gly Arg Pro Val Ile Glu Thr Thr
25 30 35

aat ttg atg gac atc tcc agg cat ttt cac cgc aca tcg gca gtg ctc 259
Asn Leu Met Asp Ile Ser Arg His Phe His Arg Thr Ser Ala Val Leu
40 45 50

att gat gcg tcg atg gcc tct caa tta tca cct ggg aaa cgc cgc gac 307
Ile Asp Ala Ser Met Ala Ser Gln Leu Ser Pro Gly Lys Arg Arg Asp
55 60 65

agg gtg ttt ctt ctc gat tct gat cca ggg ccc tct gat tgg aaa acg 355
Arg Val Phe Leu Leu Asp Ser Asp Pro Gly Pro Ser Asp Trp Lys Thr
70 75 80 85

gcg atg aaa atc cac gct gag caa gcc atg ttg ctt ccc gct cag gca 403
Ala Met Lys Ile His Ala Glu Gln Ala Met Leu Leu Pro Ala Gln Ala
90 95 100

ggg gag ttg ctc agc gct tta ggc aga gat gac aaa caa ctg ccg gtg 451
Gly Glu Leu Leu Ser Ala Leu Gly Arg Asp Asp Lys Gln Leu Pro Val
105 110 115

gct tcg ggc cat gtc atc ggt gtt gcc ggg gtg gtg gga gga aca ggc 499
Ala Ser Gly His Val Ile Gly Val Ala Gly Val Val Gly Gly Thr Gly
120 125 130

gcg agc acg ttt gct gcg gcg ctc gca aag cgg cgt gcg gag tca gtc 547
Ala Ser Thr Phe Ala Ala Ala Leu Ala Lys Arg Arg Ala Glu Ser Val
135 140 145

acc act gtg ctt atc gac gcc gac cct tcc tct ggc ggc atc gac ctg 595
Thr Thr Val Leu Ile Asp Ala Asp Pro Ser Ser Gly Gly Ile Asp Leu
150 155 160 165

ttg cta gga atc gaa gat gtg ccc ggc gcg tgg cct gat gtg ggg 643
Leu Asp Gly Ile Glu Asp Val Pro Gly Ala Arg Trp Pro Asp Val Gly
170 175 180

ttg cgt cgc gga act gtc cag gct gct gat gtg ttg aaa gcg ctg ccg 691
Leu Arg Arg Gly Thr Val Gln Ala Ala Asp Val Leu Lys Ala Leu Pro
185 190 195

agc act cct gat gag gtc gtg gtg ttg tct acg gcg cgg tct aat att 739
Ser Thr Pro Asp Glu Val Val Leu Ser Thr Ala Arg Ser Asn Ile
200 205 210

ctg gat cct ttt gca tta tcc gag tct gat gtt tca gcg gcg att gat 787
Leu Asp Pro Phe Ala Leu Ser Glu Ser Asp Val Ser Ala Ala Ile Asp
215 220 225

tgt ttc tta agc gcc gat agg tcg gtg gat gtg gtg gtg gat ctg cct 835

Cys Phe Leu Ser Ala Asp Arg Ser Val Asp Val Val Val Asp Leu Pro
 230 235 240 245
 cat gcg aga gtg cat cca gat att gcg gag cgc tta tcc cac ctg gtg 883
 His Ala Arg Val His Pro Asp Ile Ala Glu Arg Leu Ser His Leu Val
 250 255 260
 tta gtc atc cct gca gag gtc cga gcg gtg gct gct gcc agg gct cgg 931
 Leu Val Ile Pro Ala Glu Val Arg Ala Val Ala Ala Arg Ala Arg
 265 270 275
 tgt ctg gaa tta caa caa ttg cat gta tcc atc acg tgc gtg ttg agg 979
 Cys Leu Glu Leu Gln Gln Leu His Val Ser Ile Thr Cys Val Leu Arg
 280 285 290
 cat cgc ggg tgg tca ggt ttg gat gtt gca gaa gtg gaa gag att tta 1027
 His Arg Gly Trp Ser Gly Leu Asp Val Ala Glu Val Glu Glu Ile Leu
 295 300 305
 ggt gcg gat att acc gcg gag gtt ggc tgc atc cag cgg ctg gct aag 1075
 Gly Ala Asp Ile Thr Ala Glu Val Gly Ser Ile Gln Arg Leu Ala Lys
 310 315 320 325
 tcc gtg gag atg cat ggg ctg acc ggt tct ttg cgg agg gtt tta agc 1123
 Ser Val Glu Met His Gly Leu Thr Gly Ser Leu Pro Arg Val Leu Ser
 330 335 340
 tca gca tgc gac gcg gtc ctc ggg gag gtg gcg gca tgactgacat 1169
 Ser Ala Cys Asp Ala Val Leu Gly Glu Val Ala Ala
 345 350
 tgatctggtg gtg 1182
 <210> 1940
 <211> 353
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 1940
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 1 5 10 15
 Val Leu His Pro Glu Ala Met His Val Ala Ala Ala Thr Gly Arg Pro
 20 25 30
 Val Ile Glu Thr Thr Asn Leu Met Asp Ile Ser Arg His Phe His Arg
 35 40 45
 Thr Ser Ala Val Leu Ile Asp Ala Ser Met Ala Ser Gln Leu Ser Pro
 50 55 60
 Gly Lys Arg Arg Asp Arg Val Phe Leu Leu Asp Ser Asp Pro Gly Pro
 65 70 75 80
 Ser Asp Trp Lys Thr Ala Met Lys Ile His Ala Glu Gln Ala Met Leu
 85 90 95
 Leu Pro Ala Gln Ala Gly Glu Leu Leu Ser Ala Leu Gly Arg Asp Asp
 100 105 110

Lys Gln Leu Pro Val Ala Ser Gly His Val Ile Gly Val Ala Gly Val
 115 120 125
 Val Gly Gly Thr Gly Ala Ser Thr Phe Ala Ala Ala Leu Ala Lys Arg
 130 135 140
 Arg Ala Glu Ser Val Thr Thr Val Leu Ile Asp Ala Asp Pro Ser Ser
 145 150 155 160
 Gly Gly Ile Asp Leu Leu Leu Gly Ile Glu Asp Val Pro Gly Ala Arg
 165 170 175
 Trp Pro Asp Val Gly Leu Arg Arg Gly Thr Val Gln Ala Ala Asp Val
 180 185 190
 Leu Lys Ala Leu Pro Ser Thr Pro Asp Glu Val Val Val Leu Ser Thr
 195 200 205
 Ala Arg Ser Asn Ile Leu Asp Pro Phe Ala Leu Ser Glu Ser Asp Val
 210 215 220
 Ser Ala Ala Ile Asp Cys Phe Leu Ser Ala Asp Arg Ser Val Asp Val
 225 230 235 240
 Val Val Asp Leu Pro His Ala Arg Val His Pro Asp Ile Ala Glu Arg
 245 250 255
 Leu Ser His Leu Val Leu Val Ile Pro Ala Glu Val Arg Ala Val Ala
 260 265 270
 Ala Ala Arg Ala Arg Cys Leu Glu Leu Gln Gln Leu His Val Ser Ile
 275 280 285
 Thr Cys Val Leu Arg His Arg Gly Trp Ser Gly Leu Asp Val Ala Glu
 290 295 300
 Val Glu Glu Ile Leu Gly Ala Asp Ile Thr Ala Glu Val Gly Ser Ile
 305 310 315 320
 Gln Arg Leu Ala Lys Ser Val Glu Met His Gly Leu Thr Gly Ser Leu
 325 330 335
 Pro Arg Val Leu Ser Ser Ala Cys Asp Ala Val Leu Gly Glu Val Ala
 340 345 350

Ala

<210> 1941
 <211> 897
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(874)
 <223> RXA00814

<400> 1941
 gccgcaggct agctcaactc ggggtgctcc gcggaaatcc tgtgaccacg caggtggtgt 60

gggatttgga	ccacggcatg	cacgaaggga	gcgaagaggc	atg	gtt	tat	gcc	cta	115
				Met	Val	Tyr	Ala	Leu	
				1				5	
ggc	ctt	ctt	agc	gtg	gcg	gtg	ttg	atc	163
Gly	Leu	Leu	Ser	Val	Ala	Val	Leu	Ile	
				10				15	
gcg	cgt	acc	agg	cca	cca	aca	cct	ggg	211
Ala	Arg	Thr	Arg	Pro	Pro	Thr	Pro	Gly	
				25				30	
cta	att	gca	cta	ttt	tgc	ctg	gcc	atg	259
Leu	Ile	Ala	Leu	Phe	Cys	Leu	Ala	Thr	
				40				45	
gcc	tac	acg	atg	atc	gcc	ggc	atc	atc	307
Ala	Tyr	Thr	Met	Ile	Ala	Gly	Ile	Ile	
				55				60	
tat	ctc	cgc	cag	aca	cac	gcc	gca	gcc	355
Tyr	Leu	Arg	Gln	Thr	His	Ala	Ala	Ala	
				70				75	
caa	tta	gcc	agc	ttc	tta	agc	ctc	tgc	403
Gln	Leu	Ala	Ser	Phe	Leu	Ser	Leu	Cys	
				90				95	
gtc	acc	atg	gtc	gac	gcc	atg	gac	tac	451
Val	Thr	Met	Val	Asp	Ala	Met	Asp	Tyr	
				105				110	
gac	aaa	ttc	tta	agc	ccc	acg	ttg	cag	499
Asp	Lys	Phe	Leu	Ser	Pro	Thr	Leu	Gln	
				120				125	
tcg	ggc	ggc	agc	ggg	ccg	cga	gtg	ctt	547
Ser	Gly	Gly	Ser	Gly	Pro	Arg	Val	Leu	
				135				140	
ctt	caa	cgc	ctc	ggc	cat	ttg	tgg	gaa	595
Leu	Gln	Arg	Leu	Gly	His	Leu	Trp	Glu	
				150				155	
ccg	ctg	gtc	gcc	ctc	att	gat	caa	atg	643
Pro	Leu	Val	Ala	Leu	Ile	Asp	Gln	Met	
				170				175	
caa	cgc	cac	ggc	gaa	tcc	acc	cga	gct	691
Gln	Arg	His	Gly	Glu	Ser	Thr	Arg	Ala	
				185				190	
acc	gca	gtg	atc	ctt	acc	gtg	ttg	cca	739
Thr	Ala	Val	Ile	Leu	Thr	Val	Leu	Pro	
				200				205	
aca	gcc	atg	gga	gca	aac	ccc	ctt	ggg	787
Thr	Ala	Met	Gly	Ala	Asn	Pro	Leu	Gly	
				215				220	

ggt ggg ttc ctg ctt gtc atc ggt gtg ggc ctc gat gct gca ggg ttt 835
 Gly Gly Phe Leu Leu Val Ile Gly Val Gly Leu Asp Ala Ala Gly Phe
 230 235 240 245
 gtg ctc acc cac aaa att ctc cag agc gcg agc ccc tca tgattacagc 884
 Val Leu Thr His Lys Ile Leu Gln Ser Ala Ser Pro Ser
 250 255
 actagttctt gca 897

<210> 1942

<211> 258

<212> PRT

<213> Corynebacterium glutamicum

<400> 1942

Met Val Tyr Ala Leu Gly Leu Leu Ser Val Ala Val Leu Ile Ser Gly
 1 5 10 15

Ser Arg Gly Pro Gly Ala Arg Thr Arg Pro Pro Thr Pro Gly Asn Gly
 20 25 30

Val His Leu Phe Ala Leu Ile Ala Leu Phe Cys Leu Ala Thr Val Leu
 35 40 45

Phe Ile Val Val Asp Ala Tyr Thr Met Ile Ala Gly Ile Ile Ile Ala
 50 55 60

Thr Thr Leu Phe Trp Tyr Leu Arg Gln Thr His Ala Ala Ala Gln Arg
 65 70 75 80

Thr Lys Gln Ser Leu Gln Leu Ala Ser Phe Leu Ser Leu Cys Ala Gly
 85 90 95

Asn Leu Arg Ala Gly Val Thr Met Val Asp Ala Met Asp Tyr Ala Leu
 100 105 110

Asp Asn Thr Thr Pro Asp Lys Phe Leu Ser Pro Thr Leu Gln Thr Ala
 115 120 125

Ala Arg Gln Ala Arg Ser Gly Gly Ser Gly Pro Arg Val Leu Ile Asp
 130 135 140

Ala Ser Leu Pro Asp Leu Gln Arg Leu Gly His Leu Trp Glu Thr Ser
 145 150 155 160

Glu Arg His Gly Ile Pro Leu Val Ala Leu Ile Asp Gln Met Arg Ser
 165 170 175

Arg Ile Ser Ser Lys Gln Arg His Gly Glu Ser Thr Arg Ala Ala Leu
 180 185 190

Gln Gly Pro Gln Ala Thr Ala Val Ile Leu Thr Val Leu Pro Leu Ala
 195 200 205

Gly Met Leu Met Gly Thr Ala Met Gly Ala Asn Pro Leu Gly Leu Leu
 210 215 220

Thr Gly Gly Gly Ile Gly Gly Phe Leu Leu Val Ile Gly Val Gly Leu
 225 230 235 240

Asp Ala Ala Gly Phe Val Leu Thr His Lys Ile Leu Gln Ser Ala Ser
 245 250 255

Pro Ser

<210> 1943

<211> 696

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(673)

<223> RXA00815

<400> 1943

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ttgtgctcac ccacaaaatt ctccagagcg cgagcccctc atg att aca gca cta 115
 Met Ile Thr Ala Leu 5

gtt ctt gca gca gtg gcc atg ttc ctc ggt tca ccc aac cct gga gtt 163
 Val Leu Ala Ala Val Ala Met Phe Leu Gly Ser Pro Asn Pro Gly Val 20

cgc ggt gga ttg ata agc ccc aaa tcc ggt aaa agc ctg cgt atc cga 211
 Arg Gly Gly Leu Ile Ser Pro Lys Ser Gly Lys Ser Leu Arg Ile Arg 35

gct ggc cca aaa aag ctg ggc aac gct gac cca gtg gat gtc tct gca 259
 Ala Gly Pro Lys Lys Leu Gly Asn Ala Asp Pro Val Asp Val Ser Ala 40

gat atc gaa ctg ttt tca gcg tgt ttg gat gcg ggt tta aac aca cgt 307
 Asp Ile Glu Leu Phe Ser Ala Cys Leu Asp Ala Gly Leu Asn Thr Arg 55

gat gca gcg cag gtg gtg gct cat gtt gca gcc att acg cac cgc gaa 355
 Asp Ala Ala Gln Val Val Ala His Val Ala Ala Ile Thr His Arg Glu 70

ctg tgg aca cat gtg gtg gca ttg cta tcg att gga gtg agt gcc cct 403
 Leu Trp Thr His Val Val Ala Leu Leu Ser Ile Gly Val Ser Ala Pro 90

caa gca ttc gcc ctg atg gca gga gtt gat ggg ctg gat gaa cta gcc 451
 Gln Ala Phe Ala Leu Met Ala Gly Val Asp Gly Leu Asp Glu Leu Ala 105

aat tta gcc acc gtg tcg cac agg tcg ggc agt gca tta agt gat ggg 499
 Asn Leu Ala Thr Val Ser His Arg Ser Gly Ser Ala Leu Ser Asp Gly 120

tgc agg aac att tcc acc tcg ttg ttg gcc tct gct ggt gac aag cgc 547
 Cys Arg Asn Ile Ser Thr Ser Leu Leu Ala Ser Ala Gly Asp Lys Arg 135


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acc gcc gca gca gaa cgc gca gga gtg ttc atc gcc ctg cca ctt gct 595
Thr Ala Ala Ala Glu Arg Ala Gly Val Phe Ile Ala Leu Pro Leu Ala
150 155 160 165

ctg tgt ttc ctc ccc gca ttc atg att gtc ggg ctt gca cca gtg gtg 643
Leu Cys Phe Leu Pro Ala Phe Met Ile Val Gly Leu Ala Pro Val Val
170 175 180

ctc agc ttg ggt acg caa ctt atc aat ttc tagaaaacac acacaggaga 693
Leu Ser Leu Gly Thr Gln Leu Ile Asn Phe
185 190

aaa 696

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<210> 1944

<211> 191

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1944

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Met Ile Thr Ala Leu Val Leu Ala Ala Val Ala Met Phe Leu Gly Ser
1 5 10 15

Pro Asn Pro Gly Val Arg Gly Gly Leu Ile Ser Pro Lys Ser Gly Lys
20 25 30

Ser Leu Arg Ile Arg Ala Gly Pro Lys Lys Leu Gly Asn Ala Asp Pro
35 40 45

Val Asp Val Ser Ala Asp Ile Glu Leu Phe Ser Ala Cys Leu Asp Ala
50 55 60

Gly Leu Asn Thr Arg Asp Ala Ala Gln Val Val Ala His Val Ala Ala
65 70 75 80

Ile Thr His Arg Glu Leu Trp Thr His Val Val Ala Leu Leu Ser Ile
85 90 95

Gly Val Ser Ala Pro Gln Ala Phe Ala Leu Met Ala Gly Val Asp Gly
100 105 110

Leu Asp Glu Leu Ala Asn Leu Ala Thr Val Ser His Arg Ser Gly Ser
115 120 125

Ala Leu Ser Asp Gly Cys Arg Asn Ile Ser Thr Ser Leu Leu Ala Ser
130 135 140

Ala Gly Asp Lys Arg Thr Ala Ala Ala Glu Arg Ala Gly Val Phe Ile
145 150 155 160

Ala Leu Pro Leu Ala Leu Cys Phe Leu Pro Ala Phe Met Ile Val Gly
165 170 175

Leu Ala Pro Val Val Leu Ser Leu Gly Thr Gln Leu Ile Asn Phe
180 185 190

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<210> 1945

<211> 420

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(397)

<223> RXA00816

<400> 1945

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ttcccggtgg	aaaactagct	gtgcaaatga	cgaaggctac	atg	acc	atc	gcc	agc	115
				Met	Thr	Ile	Ala	Ser	
				1				5	

gct	ggt	gtc	gcc	tcc	atc	ctc	att	agc	ctg	ctg	gtg	gtg	ctg	gcc	tgg	163
Ala	Gly	Val	Ala	Ser	Ile	Leu	Ile	Ser	Leu	Leu	Val	Val	Leu	Ala	Trp	
			10						15					20		

cag	gcg	gga	aac	ctc	gtg	gcc	agg	gaa	caa	gca	cag	gta	gcg	gcc	gat	211
Gln	Ala	Gly	Asn	Leu	Val	Ala	Arg	Glu	Gln	Ala	Gln	Val	Ala	Ala	Asp	
			25					30					35			

gtt	tca	gct	gtt	gcc	gga	gcc	tac	gcc	ttt	gcc	cgc	ggg	gaa	cta	ccc	259
Val	Ser	Ala	Val	Ala	Gly	Ala	Tyr	Ala	Phe	Ala	Arg	Gly	Glu	Leu	Pro	
			40				45					50				

gac	gct	gcc	tgc	gcc	acc	gcg	aaa	cac	aca	gcc	gaa	gca	aac	aac	gca	307
Asp	Ala	Ala	Cys	Ala	Thr	Ala	Lys	His	Thr	Ala	Glu	Ala	Asn	Asn	Ala	
		55				60					65					

caa	cta	gaa	aac	tgc	gca	aca	gaa	ggg	gag	gat	ctc	acg	ctc	acc	gtc	355
Gln	Leu	Glu	Asn	Cys	Ala	Thr	Glu	Gly	Glu	Asp	Leu	Thr	Leu	Thr	Val	
	70			75				80							85	

acc	gtt	cgt	gga	caa	gaa	gcc	cac	gca	aaa	gca	gga	cct	tta			397
Thr	Val	Arg	Gly	Gln	Glu	Ala	His	Ala	Lys	Ala	Gly	Pro	Leu			
			90					95								

tgagggtccc	aacaagggtca	cca	420
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<210> 1946

<211> 99

<212> PRT

<213> Corynebacterium glutamicum

<400> 1946

Met	Thr	Ile	Ala	Ser	Ala	Gly	Val	Ala	Ser	Ile	Leu	Ile	Ser	Leu	Leu
1				5					10					15	

Val	Val	Leu	Ala	Trp	Gln	Ala	Gly	Asn	Leu	Val	Ala	Arg	Glu	Gln	Ala
		20				25						30			

Gln	Val	Ala	Ala	Asp	Val	Ser	Ala	Val	Ala	Gly	Ala	Tyr	Ala	Phe	Ala
		35				40					45				

Arg	Gly	Glu	Leu	Pro	Asp	Ala	Ala	Cys	Ala	Thr	Ala	Lys	His	Thr	Ala
	50					55				60					

Glu	Ala	Asn	Asn	Ala	Gln	Leu	Glu	Asn	Cys	Ala	Thr	Glu	Gly	Glu	Asp
	65				70				75						80

Leu Thr Leu Thr Val Thr Val Arg Gly Gln Glu Ala His Ala Lys Ala
 85 90 95

Gly Pro Leu

<210> 1947

<211> 654

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(631)

<223> RXA00826

<400> 1947

tcggcgcgcg cgatctggtg ctcatcttgg tgtgtgctgc catttccgcg atcgctctaa 60

ccgtgtccat tcagactggt ttctttaagt tcttgggcac atg atc aca gtt tta 115
 Met Ile Thr Val Leu
 1 5

att gat gga caa tcc ggt gcg ggc aaa acc acc ttg gcg ggt gag tta 163
 Ile Asp Gly Gln Ser Gly Ala Gly Lys Thr Thr Leu Ala Gly Glu Leu
 10 15 20

gct gcc cgc acc ggg ttt cag ttg gtt cat ttg gat gac ttt tat cct 211
 Ala Ala Arg Thr Gly Phe Gln Leu Val His Leu Asp Asp Phe Tyr Pro
 25 30 35

ggt tgg act ggc ctt gaa gcg gca tcg gag att gtt gca cgc cat gtt 259
 Gly Trp Thr Gly Leu Glu Ala Ala Ser Glu Ile Val Ala Arg His Val
 40 45 50

ttg gac gcg gac aac ccc ggt ttc ttc acg tgg gat tgg cac aac aat 307
 Leu Asp Ala Asp Asn Pro Gly Phe Phe Thr Trp Asp Trp His Asn Asn
 55 60 65

tgc caa ggc gat tgg atc aag ttg gag cct ggt cga agt ctc att atc 355
 Cys Gln Gly Asp Trp Ile Lys Leu Glu Pro Gly Arg Ser Leu Ile Ile
 70 75 80 85

gaa ggc tct gga tca atc act gct gca aca aaa cgc aag gca tcg ctg 403
 Glu Gly Ser Gly Ser Ile Thr Ala Ala Thr Lys Arg Lys Ala Ser Leu
 90 95 100

ttg ggc gag ctg gtg acc gtt cgt atc act ggt cct gag gct tta aga 451
 Leu Gly Glu Leu Val Thr Val Arg Ile Thr Gly Pro Glu Ala Leu Arg
 105 110 115

aaa cag cgc gcc ctc aac cgc gat cct gat tac gca cca ttt tgg aaa 499
 Lys Gln Arg Ala Leu Asn Arg Asp Pro Asp Tyr Ala Pro Phe Trp Lys
 120 125 130

gtg tgg gcg cag cag gag caa cgc cat ttc tct tta ggc gtt gag gtg 547
 Val Trp Ala Gln Gln Glu Gln Arg His Phe Ser Leu Gly Val Glu Val
 135 140 145

gat cat gag att gtg cta ggt tct gat gag gct tcg gga cga ccc gaa 595
 Asp His Glu Ile Val Leu Gly Ser Asp Glu Ala Ser Gly Arg Pro Glu
 150 155 160 165

gaa atc tat gac agc ctg gga acg gcc cag agt tct taagaaagtt 641
 Glu Ile Tyr Asp Ser Leu Gly Thr Ala Gln Ser Ser
 170 175

tgactagaga aca 654

<210> 1948

<211> 177

<212> PRT

<213> Corynebacterium glutamicum

<400> 1948

Met Ile Thr Val Leu Ile Asp Gly Gln Ser Gly Ala Gly Lys Thr Thr
 1 5 10 15

Leu Ala Gly Glu Leu Ala Ala Arg Thr Gly Phe Gln Leu Val His Leu
 20 25 30

Asp Asp Phe Tyr Pro Gly Trp Thr Gly Leu Glu Ala Ala Ser Glu Ile
 35 40 45

Val Ala Arg His Val Leu Asp Ala Asp Asn Pro Gly Phe Phe Thr Trp
 50 55 60

Asp Trp His Asn Asn Cys Gln Gly Asp Trp Ile Lys Leu Glu Pro Gly
 65 70 75 80

Arg Ser Leu Ile Ile Glu Gly Ser Gly Ser Ile Thr Ala Ala Thr Lys
 85 90 95

Arg Lys Ala Ser Leu Leu Gly Glu Leu Val Thr Val Arg Ile Thr Gly
 100 105 110

Pro Glu Ala Leu Arg Lys Gln Arg Ala Leu Asn Arg Asp Pro Asp Tyr
 115 120 125

Ala Pro Phe Trp Lys Val Trp Ala Gln Gln Glu Gln Arg His Phe Ser
 130 135 140

Leu Gly Val Glu Val Asp His Glu Ile Val Leu Gly Ser Asp Glu Ala
 145 150 155 160

Ser Gly Arg Pro Glu Glu Ile Tyr Asp Ser Leu Gly Thr Ala Gln Ser
 165 170 175

Ser

<210> 1949

<211> 846

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(823)

<223> RXA00830

<400> 1949

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aacgagcgc cacccttaag cttatgtaga ttatgtttctt atg gaa aac cct ggt 115
 Met Glu Asn Pro Gly
 1 5

gat ctg ggc gct atg cca cag tac ggt ttt gag cat att tcg atg ctc 163
 Asp Leu Gly Ala Met Pro Gln Tyr Gly Phe Glu His Ile Ser Met Leu
 10 15 20

atc acc gct gtg gtt tta gcg att ctt gtc gtc ccc att gct cgt cga 211
 Ile Thr Ala Val Val Leu Ala Ile Leu Val Val Pro Ile Ala Arg Arg
 25 30 35

ttc aac ttc gca ccg gca ttt ggc tgg gtg cta ctg atc gca aca ctt 259
 Phe Asn Phe Ala Pro Ala Phe Gly Trp Val Leu Leu Ile Ala Thr Leu
 40 45 50

ctg tcg aac ctg tgg aat ttt atg ccc ggc tat tac acg ctg gac caa 307
 Leu Ser Asn Leu Trp Asn Phe Met Pro Gly Tyr Tyr Thr Leu Asp Gln
 55 60 65

tct tgg cca ttc cac ttc tca gat gca ttg cgc att att gct gcc atc 355
 Ser Trp Pro Phe His Phe Ser Asp Ala Leu Arg Ile Ile Ala Ala Ile
 70 75 80 85

gca ttg att aat cgc gcg cgg tgg gca gtt tca gtg act att ttg tgg 403
 Ala Leu Ile Asn Arg Ala Arg Trp Ala Val Ser Val Thr Ile Leu Trp
 90 95 100

ggc acc acg atc aac ctg atg tca ctg ctg act cca gat gtt cag tat 451
 Gly Thr Thr Ile Asn Leu Met Ser Leu Leu Thr Pro Asp Val Gln Tyr
 105 110 115

tta cag gtt ccc tgg ctg gag ttt tta atg tac tgg ttt atg cac att 499
 Leu Gln Val Pro Trp Leu Glu Phe Leu Met Tyr Trp Phe Met His Ile
 120 125 130

tct gtg ttc cta gca gct ata att ctg att ttc gct ttt gga gaa aag 547
 Ser Val Phe Leu Ala Ala Ile Ile Leu Ile Phe Ala Phe Gly Glu Lys
 135 140 145

cca ggg ctg tcc gga gtg gtt atg tcc gtt gca gtg gcg att agc tgg 595
 Pro Gly Leu Ser Gly Val Val Met Ser Val Ala Val Ala Ile Ser Trp
 150 155 160 165

ggc atc atg tgc ctg atg gtc aac gca ttt ttg gga acc aac tac ggg 643
 Gly Ile Met Cys Leu Met Val Asn Ala Phe Leu Gly Thr Asn Tyr Gly
 170 175 180

tac ctg tcc aca gaa cca gaa tca gcg tca att ctg gat ttg ttg gga 691
 Tyr Leu Ser Thr Glu Pro Glu Ser Ala Ser Ile Leu Asp Leu Leu Gly
 185 190 195

gga tgg ccg ttc tac atc gtc gcg gaa gta tta ctg ctg tgt gca gtg 739
 Gly Trp Pro Phe Tyr Ile Val Ala Glu Val Leu Leu Leu Cys Ala Val
 200 205 210

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tgg gct ttg tgg tct tat ctg att gat aag ctg cct atc acg tat cgc 787
 Trp Ala Leu Trp Ser Tyr Leu Ile Asp Lys Leu Pro Ile Thr Tyr Arg
 215 220 225

cct gct tac cgt cgg aaa act cgg aag gcc gct gcg taaccgcct 833
 Pro Ala Tyr Arg Pro Lys Thr Arg Lys Ala Ala Ala
 230 235 240

ctacctcgag aaa 846

<210> 1950

<211> 241

<212> PRT

<213> Corynebacterium glutamicum

<400> 1950

Met Glu Asn Pro Gly Asp Leu Gly Ala Met Pro Gln Tyr Gly Phe Glu
 1 5 10 15

His Ile Ser Met Leu Ile Thr Ala Val Val Leu Ala Ile Leu Val Val
 20 25 30

Pro Ile Ala Arg Arg Phe Asn Phe Ala Pro Ala Phe Gly Trp Val Leu
 35 40 45

Leu Ile Ala Thr Leu Leu Ser Asn Leu Trp Asn Phe Met Pro Gly Tyr
 50 55 60

Tyr Thr Leu Asp Gln Ser Trp Pro Phe His Phe Ser Asp Ala Leu Arg
 65 70 75 80

Ile Ile Ala Ala Ile Ala Leu Ile Asn Arg Ala Arg Trp Ala Val Ser
 85 90 95

Val Thr Ile Leu Trp Gly Thr Thr Ile Asn Leu Met Ser Leu Leu Thr
 100 105 110

Pro Asp Val Gln Tyr Leu Gln Val Pro Trp Leu Glu Phe Leu Met Tyr
 115 120 125

Trp Phe Met His Ile Ser Val Phe Leu Ala Ala Ile Ile Leu Ile Phe
 130 135 140

Ala Phe Gly Glu Lys Pro Gly Leu Ser Gly Val Val Met Ser Val Ala
 145 150 155 160

Val Ala Ile Ser Trp Gly Ile Met Cys Leu Met Val Asn Ala Phe Leu
 165 170 175

Gly Thr Asn Tyr Gly Tyr Leu Ser Thr Glu Pro Glu Ser Ala Ser Ile
 180 185 190

Leu Asp Leu Leu Gly Gly Trp Pro Phe Tyr Ile Val Ala Glu Val Leu
 195 200 205

Leu Leu Cys Ala Val Trp Ala Leu Trp Ser Tyr Leu Ile Asp Lys Leu
 210 215 220

Pro Ile Thr Tyr Arg Pro Ala Tyr Arg Pro Lys Thr Arg Lys Ala Ala

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<210> 1951

<211> 726

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(703)

<223> RXA00853

<400> 1951

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 Met Pro Thr Ser Ser
 1 5

tct cct gca act gtg act ccg cta aag aag cag tct tca cgt aaa cag 163
 Ser Pro Ala Thr Val Thr Pro Leu Lys Lys Gln Ser Ser Arg Lys Gln
 10 15 20

ctc caa gac atc gcg ctt att gca gtt ttt gca gca ctg atc att gtg 211
 Leu Gln Asp Ile Ala Leu Ile Ala Val Phe Ala Ala Leu Ile Ile Val
 25 30 35

ctt gct ttt gtt tcc atc cca gtt ggc aca gcg gga gtg cct att gtt 259
 Leu Ala Phe Val Ser Ile Pro Val Gly Thr Ala Gly Val Pro Ile Val
 40 45 50

ttg cag aat gcc tcc atc gtt ttg gct ggc ctg att ctt ggt ggt cga 307
 Leu Gln Asn Ala Ser Ile Val Leu Ala Gly Leu Ile Leu Gly Gly Arg
 55 60 65

cgt ggt ttt ctc act gct ttg ctg ttc ctg gca ctc ggc ctg att ggc 355
 Arg Gly Phe Leu Thr Ala Leu Leu Phe Leu Ala Leu Gly Leu Ile Gly
 70 75 80 85

ctg cct gtc ctt gca ggt ggt cgt acc act ttg gcc gca ctt gct ggc 403
 Leu Pro Val Leu Ala Gly Gly Arg Thr Thr Leu Ala Ala Leu Ala Gly
 90 95 100

cca aca gct ggc tac atc gtg ggt tac ctc att tcc cca ctt gtt gca 451
 Pro Thr Ala Gly Tyr Ile Val Gly Tyr Leu Ile Ser Pro Leu Val Ala
 105 110 115

ggc atc atc gct tac ctc gca cct aaa aag cgt ggc gct gga atg ttc 499
 Gly Ile Ile Ala Tyr Leu Ala Pro Lys Lys Arg Gly Ala Gly Met Phe
 120 125 130

atc gtt tta ggc ctg gcg ggt ctc gcg ggt ctg atc acc caa tac gct 547
 Ile Val Leu Gly Leu Ala Gly Leu Ala Gly Leu Ile Thr Gln Tyr Ala
 135 140 145

tgc ggc atc gtg ggt ctc gtc ctt cgt gcg ggt cta agc ttg agt gaa 595
 Cys Gly Ile Val Gly Leu Val Leu Arg Ala Gly Leu Ser Leu Ser Glu

<210> 1953
 <211> 426
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (1)..(426)
 <223> RXA00861

<400> 1953
 atg gct cct cac aag gtc atg ctg att acc act ggt act cag ggt gag 48
 Met Ala Pro His Lys Val Met Leu Ile Thr Thr Gly Thr Gln Gly Glu
 1 5 10 15
 cct atg gct gcg ctg tct cgc atg gcg cgt cgt gag cag cga cag atc 96
 Pro Met Ala Ala Leu Ser Arg Met Ala Arg Arg Glu His Arg Gln Ile
 20 25 30
 act gtc cgt gat gga gac ttg att atc ctt tct tcc tcc ctg gtt cca 144
 Thr Val Arg Asp Gly Asp Leu Ile Ile Leu Ser Ser Ser Leu Val Pro
 35 40 45
 ggt aac gaa gaa gca gtg ttc ggt gtc atc aac atg ctg gct cag atc 192
 Gly Asn Glu Glu Ala Val Phe Gly Val Ile Asn Met Leu Ala Gln Ile
 50 55 60
 ggt gca act gtt gtt acc ggt cgc gac gcc aag gtg cac acc tcg ggc 240
 Gly Ala Thr Val Val Thr Gly Arg Asp Ala Lys Val His Thr Ser Gly
 65 70 75 80
 cac ggc tac tcc gga gag ctg ttg ttc ttg tac aac gcc gct cgt ccg 288
 His Gly Tyr Ser Gly Glu Leu Leu Phe Leu Tyr Asn Ala Ala Arg Pro
 85 90 95
 aag aac gct atg cct gtc cac ggc gag tgg cgc cac ctg cgc gcc aac 336
 Lys Asn Ala Met Pro Val His Gly Glu Trp Arg His Leu Arg Ala Asn
 100 105 110
 aag gaa ctg gct atc tcc act ggt gtt aac cgc gac aac gtt gtg ctt 384
 Lys Glu Leu Ala Ile Ser Thr Gly Val Asn Arg Asp Asn Val Val Leu
 115 120 125
 gca caa aac ggt gtt gtg gtt gat atg gtc aac ggt cgc gca 426
 Ala Gln Asn Gly Val Val Val Asp Met Val Asn Gly Arg Ala
 130 135 140

<210> 1954
 <211> 142
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 1954
 Met Ala Pro His Lys Val Met Leu Ile Thr Thr Gly Thr Gln Gly Glu
 1 5 10 15
 Pro Met Ala Ala Leu Ser Arg Met Ala Arg Arg Glu His Arg Gln Ile
 20 25 30
 Thr Val Arg Asp Gly Asp Leu Ile Ile Leu Ser Ser Ser Leu Val Pro

	35		40		45	
Gly Asn Glu Glu Ala Val Phe Gly Val Ile Asn Met Leu Ala Gln Ile	50		55		60	
Gly Ala Thr Val Val Thr Gly Arg Asp Ala Lys Val His Thr Ser Gly	65		70		75	80
His Gly Tyr Ser Gly Glu Leu Leu Phe Leu Tyr Asn Ala Ala Arg Pro		85		90		95
Lys Asn Ala Met Pro Val His Gly Glu Trp Arg His Leu Arg Ala Asn	100		105		110	
Lys Glu Leu Ala Ile Ser Thr Gly Val Asn Arg Asp Asn Val Val Leu	115		120		125	
Ala Gln Asn Gly Val Val Val Asp Met Val Asn Gly Arg Ala	130		135		140	

<210> 1955

<211> 680

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(664)

<223> RXA00862

<400> 1955

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cggtcacaacg cctacaacct ctgctagctc tgctccagtt gtg aca gaa act gaa	115
Val Thr Glu Thr Glu	5

acc gct aac ccg gtc acc aca act cgc acg cct tca gat gct gcc ccg	163
Thr Ala Asn Pro Val Thr Thr Thr Arg Thr Pro Ser Asp Ala Ala Pro	
10 15 20	

tcg cct acc act tca gag ccc act ggt tca gag tcc acc aac tcc cct	211
Ser Pro Thr Thr Ser Glu Pro Thr Gly Ser Glu Ser Thr Asn Ser Pro	
25 30 35	

tcc ccc act gct ttg ccg ccg ttg ggt tcc ccg tcg atg gat cag aag	259
Ser Pro Thr Ala Leu Pro Pro Leu Gly Ser Pro Ser Met Asp Gln Lys	
40 45 50	

cag cag gct caa gtt ggt gac tcc gat atg tcg atc gct gcc atc cgc	307
Gln Gln Ala Gln Val Gly Asp Ser Asp Met Ser Ile Ala Gly Ile Arg	
55 60 65	

gtt gcc gag cac gaa acg ttc aca cga gtt gtt ttt gat atc gcc ggt	355
Val Ala Glu His Glu Thr Phe Thr Arg Val Val Phe Asp Ile Ala Gly	
70 75 80 85	

aat gcc caa cct ggt tgg tgg gtc gat tgg gcc act gat cca att cag	403
Asn Gly Gln Pro Gly Trp Trp Val Asp Trp Ala Thr Asp Pro Ile Gln	
90 95 100	

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cag gcg tca ggt ctt cca gtt gag atg gct ggt gat tcc ttc ctc aac 451
Gln Ala Ser Gly Leu Pro Val Glu Met Ala Gly Asp Ser Phe Leu Asn
      105                      110                      115

gtc aat att caa ggc act gga tat cct gat cag gtt gtc gtt cca ggt 499
Val Asn Ile Gln Gly Thr Gly Tyr Pro Asp Gln Val Val Val Pro Gly
      120                      125                      130

atc gat acc gga tca tat cct ggt gca ggc att gtt gaa gac atc aac 547
Ile Asp Thr Gly Ser Tyr Pro Gly Ala Gly Ile Val Glu Asp Ile Asn
      135                      140                      145

ttc acc agt att ttt gaa gcc cgt tcc caa gtt ctc att ggt gta tct 595
Phe Thr Ser Ile Phe Glu Ala Arg Ser Gln Val Leu Ile Gly Val Ser
      150                      155                      160

ggg caa ccc cga aat tac tcg gtc tca ttg ctg cag gaa cca acc agg 643
Gly Gln Pro Arg Asn Tyr Ser Val Ser Leu Leu Gln Glu Pro Thr Arg
      170                      175                      180

ctt gtg gtg gac atc gtt cac tagcgctgga acgccg 680
Leu Val Val Asp Ile Val His
      185

<210> 1956
<211> 188
<212> PRT
<213> Corynebacterium glutamicum

#
<400> 1956
Val Thr Glu Thr Glu Thr Ala Asn Pro Val Thr Thr Thr Arg Thr Pro
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Ser Asp Ala Ala Pro Ser Pro Thr Thr Ser Glu Pro Thr Gly Ser Glu
      20          25          30

Ser Thr Asn Ser Pro Ser Pro Thr Ala Leu Pro Pro Leu Gly Ser Pro
      35          40          45

Ser Met Asp Gln Lys Gln Gln Ala Gln Val Gly Asp Ser Asp Met Ser
      50          55          60

Ile Ala Gly Ile Arg Val Ala Glu His Glu Thr Phe Thr Arg Val Val
      65          70          75          80

Phe Asp Ile Ala Gly Asn Gly Gln Pro Gly Trp Trp Val Asp Trp Ala
      85          90          95

Thr Asp Pro Ile Gln Gln Ala Ser Gly Leu Pro Val Glu Met Ala Gly
      100          105          110

Asp Ser Phe Leu Asn Val Asn Ile Gln Gly Thr Gly Tyr Pro Asp Gln
      115          120          125

Val Val Val Pro Gly Ile Asp Thr Gly Ser Tyr Pro Gly Ala Gly Ile
      130          135          140

Val Glu Asp Ile Asn Phe Thr Ser Ile Phe Glu Ala Arg Ser Gln Val
      145          150          155          160

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Leu Ile Gly Val Ser Gly Gln Pro Arg Asn Tyr Ser Val Ser Leu Leu
 165 170

Gln Glu Pro Thr Arg Leu Val Val Asp Ile Val His
 180 185

<210> 1957

<211> 1212

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1189)

<223> RXA00874

<400> 1957

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tctggtttga tctcaccgcc gatgaaaagg acgatatgga atg agc att ggc caa 115
 Met Ser Ile Gly Gln
 1 5

cac atc atc acc gag cgt ttc tac ggc gcc aag tcc cac acc atc gac 163
 His Ile Ile Thr Glu Arg Phe Tyr Gly Ala Lys Ser His Thr Ile Asp
 10 15 20

aac gta gat att gtg ttg tcc cgc gaa tgt ggc gag aac act ttg gct 211
 Asn Val Asp Ile Val Leu Ser Arg Glu Cys Gly Glu Asn Thr Leu Ala
 25 30 35

gta gtg cgc atc aac aat gcg ctg tat cag ttg ttg gtc aat gat gat 259
 Val Val Arg Ile Asn Asn Ala Leu Tyr Gln Leu Leu Val Asn Asp Asp
 40 45 50

ggc aaa gat gtt ctc aac gac cac gta gaa gag gtc ggt gcg agt ttc 307
 Gly Lys Asp Val Leu Asn Asp His Val Glu Glu Val Gly Ala Ser Phe
 55 60 65

gga gca tgg act ggc agc tct gct ttt ccc att ggc cct ttc act cca 355
 Gly Ala Trp Thr Gly Ser Ser Ala Phe Pro Ile Gly Pro Phe Thr Pro
 70 75 80 85

ctc ggc aca gaa caa tcc aat agc tct ttc atc acc gcc gac aat aaa 403
 Leu Gly Thr Glu Gln Ser Asn Ser Ser Phe Ile Thr Ala Asp Asn Lys
 90 95 100

gcg atc gtg aaa tac ttc cgc aaa tta gaa tcc ggg caa aac ccc gat 451
 Ala Ile Val Lys Tyr Phe Arg Lys Leu Glu Ser Gly Gln Asn Pro Asp
 105 110 115

gtg gag cta att tct aaa att tcc tcc tgc ccc aac atc gcg ccc atc 499
 Val Glu Leu Ile Ser Lys Ile Ser Ser Cys Pro Asn Ile Ala Pro Ile
 120 125 130

ctg ggt ttt tcc tcc gct gag atc tcc ggg gct aac tac acc ctg gtc 547
 Leu Gly Phe Ser Ser Ala Glu Ile Ser Gly Ala Asn Tyr Thr Leu Val
 135 140 145

atg gcg cag cag tac gtt cca ggt ttg gat ggc tgg tca cac gcg ctg 595
Met Ala Gln Gln Tyr Val Pro Gly Leu Asp Gly Trp Ser His Ala Leu
150 155 160 165

act act acc tct ggc agc ttt gca gag gat gca gaa aag atc ggc gaa 643
Thr Thr Thr Ser Gly Ser Phe Ala Glu Asp Ala Glu Lys Ile Gly Glu
170 175 180

gcc acc cgc aat gtt cac act gct ctt gca tgg gcc ttc cct act cgg 691
Ala Thr Arg Asn Val His Thr Ala Leu Ala Ser Ala Phe Pro Thr Arg
185 190 195

gta gtt ccc gta gaa gca ctc gcc gat gcg ctc act acc cgc ctt aat 739
Val Val Pro Val Glu Ala Leu Ala Asp Ala Leu Thr Thr Arg Leu Asn
200 205 210

gaa cta atc tcc caa gca ccc gaa atc gcc gcg ttc aaa gaa gca gcc 787
Glu Leu Ile Ser Gln Ala Pro Glu Ile Ala Arg Phe Lys Glu Ala Ala
215 220 225

atc gac ctc tac caa tgg ttg gaa ggc gaa gcc cac atc caa gcg atc 835
Ile Asp Leu Tyr Gln Ser Leu Glu Gly Glu Ala His Ile Gln Arg Ile
230 235 240 245

cac ggt gac ctc cac ttg ggg cag ctc atc aaa acc ccc gaa gcg tac 883
His Gly Asp Leu His Leu Gly Gln Leu Ile Lys Thr Pro Glu Arg Tyr
250 255 260

atc ctc atc gat ttc gaa ggc gaa cct gcc gcg cca ctt aat caa cga 931
Ile Leu Ile Asp Phe Glu Gly Glu Pro Ala Arg Pro Leu Asn Gln Arg
265 270 275

gcg ctc ccc gac tct ccc ctg aaa gat ctc gcc gcc atc atc aga tcc 979
Arg Leu Pro Asp Ser Pro Leu Lys Asp Leu Ala Gly Ile Ile Arg Ser
280 285 290

atc gac tac gca gcc tac ttc gac ggc gaa cac acc caa tgg gcc aac 1027
Ile Asp Tyr Ala Ala Tyr Phe Asp Gly Glu His Thr Gln Trp Ala Asn
295 300 305

gaa gcc acc gcg cta ttc ctc gac ggc tac gga tca att gaa gac caa 1075
Glu Ala Thr Ala Leu Phe Leu Asp Gly Tyr Gly Ser Ile Glu Asp Gln
310 315 320 325

gaa ctc ctc aat gcc tac att ctg gac aag gcg ttg tac gag gtt gcc 1123
Glu Leu Leu Asn Ala Tyr Ile Leu Asp Lys Ala Leu Tyr Glu Val Ala
330 335 340

tat gaa ata aac aac gcg ccc gac tgg gtg aaa atc cca ctc gag gcg 1171
Tyr Glu Ile Asn Arg Pro Asp Trp Val Lys Ile Pro Leu Glu Ala
345 350 355

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Val Glu Arg Leu Leu Asp
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<210> 1958

<211> 363

<212> PRT

<213> Corynebacterium glutamicum

<400> 1958

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Glu Asn Thr Leu Ala Val Val Arg Ile Asn Asn Ala Leu Tyr Gln Leu
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Leu Val Asn Asp Asp Gly Lys Asp Val Leu Asn Asp His Val Glu Glu
          50           55           60

Val Gly Ala Ser Phe Gly Ala Trp Thr Gly Ser Ser Ala Phe Pro Ile
          65           70           75           80

Gly Pro Phe Thr Pro Leu Gly Thr Glu Gln Ser Asn Ser Ser Phe Ile
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Thr Ala Asp Asn Lys Ala Ile Val Lys Tyr Phe Arg Lys Leu Glu Ser
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Gly Gln Asn Pro Asp Val Glu Leu Ile Ser Lys Ile Ser Ser Cys Pro
          115          120          125

Asn Ile Ala Pro Ile Leu Gly Phe Ser Ser Ala Glu Ile Ser Gly Ala
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Asn Tyr Thr Leu Val Met Ala Gln Gln Tyr Val Pro Gly Leu Asp Gly
          145          150          155          160

Trp Ser His Ala Leu Thr Thr Thr Ser Gly Ser Phe Ala Glu Asp Ala
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Glu Lys Ile Gly Glu Ala Thr Arg Asn Val His Thr Ala Leu Ala Ser
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Ala Phe Pro Thr Arg Val Val Pro Val Glu Ala Leu Ala Asp Ala Leu
          195          200          205

Thr Thr Arg Leu Asn Glu Leu Ile Ser Gln Ala Pro Glu Ile Ala Arg
          210          215          220

Phe Lys Glu Ala Ala Ile Asp Leu Tyr Gln Ser Leu Glu Gly Glu Ala
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His Ile Gln Arg Ile His Gly Asp Leu His Leu Gly Gln Leu Ile Lys
          245          250          255

Thr Pro Glu Arg Tyr Ile Leu Ile Asp Phe Glu Gly Glu Pro Ala Arg
          260          265          270

Pro Leu Asn Gln Arg Arg Leu Pro Asp Ser Pro Leu Lys Asp Leu Ala
          275          280          285

Gly Ile Ile Arg Ser Ile Asp Tyr Ala Ala Tyr Phe Asp Gly Glu His
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Thr Gln Trp Ala Asn Glu Ala Thr Ala Leu Phe Leu Asp Gly Tyr Gly
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Ser Ile Glu Asp Gln Glu Leu Leu Asn Ala Tyr Ile Leu Asp Lys Ala
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Leu Tyr Glu Val Ala Tyr Glu Ile Asn Asn Arg Pro Asp Trp Val Lys
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<210> 1959
 <211> 1878
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1855)
 <223> RXA00876

<400> 1959
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 Met Thr Leu Lys Ile
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gat ccc tcg tcc atc agt agt gct gtg tct cgc ttg aat gag ctt cag 163
 Asp Pro Ser Ser Ile Ser Ser Ala Val Ser Arg Leu Asn Glu Leu Gln
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 His Gln Ala Ile Thr Ala Ser Gln Val Gly Met Lys Ser Thr Ile Leu
 25 30 35

tcc gcg ttt tcg ccc gtc tct gga ctc gat caa ttg ggt tcc ggt cac 259
 Ser Ala Phe Ser Pro Val Ser Gly Leu Asp Gln Leu Gly Ser Gly His
 40 45 50

ggg aat gtg att aat ggt ggg gca ggc gca gca aac tct gtg ctg aat 307
 Gly Asn Val Ile Asn Gly Gly Ala Gly Ala Ala Asn Ser Val Leu Asn
 55 60 65

tcc tat gcc gaa caa atc gag tgg ttg tct gcg gct ttg cag gct tct 355
 Ser Tyr Ala Glu Gln Ile Glu Trp Leu Ser Ala Ala Leu Gln Ala Ser
 70 75 80 85

ggt gcg gct ttg act ggc cag gat gaa tta ttc gct agg ggt atg gat 403
 Gly Ala Ala Leu Thr Gly Gln Asp Glu Leu Phe Ala Arg Gly Met Asp
 90 95 100

gta gcg gat acc ggt ggc agg gtt gta gaa gag tca gta atg ttc ccg 451
 Val Ala Asp Thr Gly Gly Arg Val Val Glu Glu Ser Val Met Phe Pro
 105 110 115

gcg cgg ccg gca cct cgg ttt gag tct ttc gtt ttt aat cca cca gct 499
 Ala Arg Pro Ala Pro Arg Phe Glu Ser Phe Val Phe Asn Pro Pro Ala
 120 125 130

gtt agt cct tcg ttg tcg ttg gat gcg ttg tgt agt cag ttt tcc gga 547

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Thr Asn Ser Gly Ala Val Leu Glu Ala Gln Gly Ser Trp Gly Ser Met																	
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Ala Ser Ala Ile Ser Asn Val Ser Ala Ser Leu Ser Ser Ile Ala Gly																	
			170					175							180		
gag att ttg gcg gag aac tca ggc gaa acg ttt gag cag gct gct gct	691																
Glu Ile Leu Ala Glu Asn Ser Gly Glu Thr Phe Glu Gln Ala Ala Ala																	
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cgg att aat gag gtg gcg gct gcg ggg gcg acg ttt gct gcg aat gcg	739																
Arg Ile Asn Glu Val Ala Ala Ala Gly Ala Thr Phe Ala Ala Asn Ala																	
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aaa atg atg ggg gcg tcg gtg ggg acg ctg aat cgg att tat atg ggg	787																
Lys Met Met Gly Ala Ser Val Gly Thr Leu Asn Arg Ile Tyr Met Gly																	
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cat cgc atg cag gtg ttt atg gct gcg acg tcg att aag cgc att ttg	835																
His Arg Met Gln Val Phe Met Ala Ala Thr Ser Ile Lys Ala Ile Leu																	
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gat ccg gtg cag agg ctt gct gcg gag agg gcg ttt ttg gcg tcg ttt	883																
Asp Pro Val Gln Arg Leu Ala Ala Glu Arg Ala Phe Leu Ala Ser Phe																	
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cag gct act ttt cag gcg gat gtg ttg acg ggt atg cct cct gtg agc	931																
Gln Ala Thr Phe Gln Ala Asp Val Leu Thr Gly Met Pro Pro Val Ser																	
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aat ttg atg cag atg aag ggg gcg aat ggt tct gcg ggg gaa att gct	979																
Asn Leu Met Gln Met Lys Gly Ala Asn Gly Ser Ala Gly Glu Ile Ala																	
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ctg ggg atg gat gag att gct ggc agt ggg cag gca tgg tct gcg gcg	1027																
Leu Gly Met Asp Glu Ile Ala Gly Ser Gly Gln Ala Trp Ser Ala Ala																	
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Gly Leu Thr Pro Ser Gly Ala Ala Gln Gly Gly Val Ala Asn Ala Gly																	
		310			315				320						325		
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Ser Ile Ala Pro Asp Ala Ala Val Gln Gly Ala Ala Gly Gln Ser Gly																	
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gtt gga agt ttt ggc act gtc act gat cag ttg gat ggc atc aat att	1171																
Val Gly Ser Phe Gly Thr Val Thr Asp Gln Leu Asp Gly Ile Asn Ile																	
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Gly Asp Met Leu Thr Ser Ala Ala Ser Ala Gly Gln Ser Leu Ala Asn																	
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Gly Leu Ala Met Pro Thr Ser Thr Pro Asn Ser Ala Ser Gly Ala Ile																	

375	380	385	
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gca ggg ttg ggc gca cag ggt ggc tcg att gga tct tcg gca cct gga Ala Gly Leu Gly Ala Gln Gly Gly Ser Ile Gly Ser Ser Ala Pro Gly 410 415 420			1363
gcg atc agt agt cga gcg gcc gga tcc gca ggt ggt tcg gta ccg gga Ala Ile Ser Ser Arg Ala Ala Gly Ser Ala Gly Gly Ser Val Pro Gly 425 430 435			1411
atg act ggt ggt cct ggc gcg ccg ggg att acc tcg gat tcg ttg atg Met Thr Gly Gly Pro Gly Ala Pro Gly Ile Thr Ser Asp Ser Leu Met 440 445 450			1459
gga gct cga act cat ggt gct tct tcc gcg gga gct gtc gct ccg atg Gly Ala Arg Thr His Gly Ala Ser Ser Ala Gly Ala Val Ala Pro Met 455 460 465			1507
atg ggt ggt gct ggc gga atg tct ggt ggc gtc gtt ggt gca ggt ggt Met Gly Gly Ala Gly Gly Met Ser Gly Gly Val Val Gly Ala Gly Gly 470 475 480 485			1555
act ggt tct cag agc aag tat gcg cgc cag act gga tcg tcg gtt gga Thr Gly Ser Gln Ser Lys Tyr Ala Arg Gln Thr Ser Ser Val Gly 490 495 500			1603
tct agt tcg cag tcg ggt tct ggc ctg ggg atg gtg gga tca ggg agt Ser Ser Ser Gln Ser Gly Ser Gly Leu Gly Met Val Gly Ser Gly Ser 505 510 515			1651
ggg aag ccg tcg ata agc aat ttt ggg cgc ggc atg atg ccg atg atg Gly Lys Pro Ser Ile Ser Asn Phe Gly Arg Gly Met Met Pro Met Met 520 525 530			1699
ccc atg atg ccc atg gga ggc gcc ggc ggt ggg cag aag aat acc ggc Pro Met Met Pro Met Gly Gly Ala Gly Gly Gln Lys Asn Thr Gly 535 540 545			1747
aag gtg aaa acg gtg acg tct gcg gtg gag gaa gac cgc aat ttg gcg Lys Val Lys Thr Val Thr Ser Ala Val Glu Glu Asp Arg Asn Leu Ala 550 555 560 565			1795
gcg ctg ctg ggt gat ccg ggg ccg gtt gtt ccg ggt gtg att ggt gac Ala Leu Leu Gly Asp Arg Gly Pro Val Val Pro Gly Val Ile Gly Asp 570 575 580			1843
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<210> 1960

<211> 585

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1960

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 Lys Ser Thr Ile Leu Ser Ala Phe Ser Pro Val Ser Gly Leu Asp Gln
 35 40 45
 Leu Gly Ser Gly His Gly Asn Val Ile Asn Gly Gly Ala Gly Ala Ala
 50 55 60
 Asn Ser Val Leu Asn Ser Tyr Ala Glu Gln Ile Glu Trp Leu Ser Ala
 65 70 75 80
 Ala Leu Gln Ala Ser Gly Ala Ala Leu Thr Gly Gln Asp Glu Leu Phe
 85 90 95
 Ala Arg Gly Met Asp Val Ala Asp Thr Gly Gly Arg Val Val Glu Glu
 100 105 110
 Ser Val Met Phe Pro Ala Arg Pro Ala Pro Arg Phe Glu Ser Phe Val
 115 120 125
 Phe Asn Pro Pro Ala Val Ser Pro Ser Leu Ser Leu Asp Ala Leu Cys
 130 135 140
 Ser Gln Phe Ser Gly Thr Asn Ser Gly Ala Val Leu Glu Ala Gln Gly
 145 150 155 160
 Ser Trp Gly Ser Met Ala Ser Ala Ile Ser Asn Val Ser Ala Ser Leu
 165 170 175
 Ser Ser Ile Ala Gly Glu Ile Leu Ala Glu Asn Ser Gly Glu Thr Phe
 180 185 190
 Glu Gln Ala Ala Ala Arg Ile Asn Glu Val Ala Ala Ala Gly Ala Thr
 195 200 205
 Phe Ala Ala Asn Ala Lys Met Met Gly Ala Ser Val Gly Thr Leu Asn
 210 215 220
 Arg Ile Tyr Met Gly His Arg Met Gln Val Phe Met Ala Ala Thr Ser
 225 230 235 240
 Ile Lys Ala Ile Leu Asp Pro Val Gln Arg Leu Ala Ala Glu Arg Ala
 245 250 255
 Phe Leu Ala Ser Phe Gln Ala Thr Phe Gln Ala Asp Val Leu Thr Gly
 260 265 270
 Met Pro Pro Val Ser Asn Leu Met Gln Met Lys Gly Ala Asn Gly Ser
 275 280 285
 Ala Gly Glu Ile Ala Leu Gly Met Asp Glu Ile Ala Gly Ser Gly Gln
 290 295 300
 Ala Trp Ser Ala Ala Gly Leu Thr Pro Ser Gly Ala Ala Gln Gly Gly
 305 310 315 320
 Val Ala Asn Ala Gly Ser Ile Ala Pro Asp Ala Ala Val Gln Gly Ala

	325		330		335
Ala Gly Gln Ser	Gly Val Gly Ser	Phe Gly Thr Val Thr	Asp Gln Leu		
	340	345	350		
Asp Gly Ile Asn Ile	Gly Asp Met Leu Thr	Ser Ala Ala Ser	Ala Gly		
	355	360	365		
Gln Ser Leu Ala Asn Gly	Leu Ala Met Pro Thr	Ser Thr Pro Asn Ser			
	370	375	380		
Ala Ser Gly Ala Ile	Pro Ser Ser Met Ser	Ala Ala Ser Pro	Leu Gly		
	385	390	395	400	
Ala Phe Gly Ser	Gly Ala Gly Leu Gly	Ala Gln Gly Gly	Ser Ile Gly		
	405	410	415		
Ser Ser Ala Pro	Gly Ala Ile Ser	Ser Arg Ala Ala	Gly Ser Ala Gly		
	420	425	430		
Gly Ser Val Pro	Gly Met Thr Gly	Gly Pro Gly Ala	Pro Gly Ile Thr		
	435	440	445		
Ser Asp Ser Leu Met	Gly Ala Arg Thr His	Gly Ala Ser Ser	Ala Gly		
	450	455	460		
Ala Val Ala Pro	Met Met Gly Gly	Ala Gly Met Ser	Gly Gly Val		
	465	470	475	480	
Val Gly Ala Gly	Gly Thr Gly Ser	Gln Ser Lys Tyr	Ala Arg Gln Thr		
	485	490	495		
Gly Ser Ser Val	Gly Ser Ser Ser	Gln Ser Gly Ser	Gly Leu Gly Met		
	500	505	510		
Val Gly Ser Gly	Ser Gly Lys Pro	Ser Ile Ser Asn	Phe Gly Arg Gly		
	515	520	525		
Met Met Pro Met	Met Pro Met Met	Pro Met Gly Gly	Ala Gly Gly Gly		
	530	535	540		
Gln Lys Asn Thr	Gly Lys Val Lys Thr	Val Thr Ser Ala	Val Glu Glu		
	545	550	555	560	
Asp Arg Asn Leu	Ala Ala Leu Leu	Gly Asp Arg Gly	Pro Val Val Pro		
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<210> 1961

<211> 501

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(478)

<223> RXA00881

[illegible]

2008-09-01 10:00:00

1998 年 12 月 10 日

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Ser Arg Leu Ser Asp Glu Glu Ser Arg Gly Glu Pro Thr Arg Ile Leu						
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Asn Glu Leu Val Ser Ala Met Glu Leu Pro Ala Leu Pro Trp						
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<210> 1963

<211> 801

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(778)

<223> RXA00882

<400> 1963

aaatagctga gaaattggct agaggacggc tagcaaaccg gatcaagacc ggctagaact 60

ttagctacga ggcaagaaaa ggaaggtgtg ttggaacgcg atg agc agt aca acc	115
Met Ser Ser Thr Thr	
1 5	

gca cag cta cgc cac cga gag ctg acc cag gag atc tac aac atc ggc	163
Ala Gln Leu Arg His Arg Glu Leu Thr Gln Glu Ile Tyr Asn Ile Gly	
10 15 20	

gac gag gtc gct gaa tac att gag cac atc atg gaa gca gtc tcc gac	211
Asp Glu Val Ala Glu Tyr Ile Glu His Ile Met Glu Ala Val Ser Asp	
25 30 35	

tgg gat ctg gag ctc gtg gaa gat tgc ctc gct gaa ttc gat gag atc	259
Trp Asp Leu Glu Leu Val Glu Asp Cys Leu Ala Glu Phe Asp Glu Ile	
40 45 50	

atc act gaa gcc cgc gat gac tcc cgc act gtt gtg gct gaa ctt tca	307
Ile Thr Glu Ala Arg Asp Ser Arg Thr Val Val Ala Glu Leu Ser	
55 60 65	

ggc ctg cgt cac gca cta acc act ggt atc cgt cag gcc acc gtg agc	355
Gly Leu Arg His Ala Leu Thr Thr Gly Ile Arg Gln Gly Thr Val Ser	
70 75 80 85	

gct aga gcc acg gtg gag gtg gac gtc gat aag ccg gaa cgc ctg acc	403
Ala Arg Ala Thr Val Glu Val Asp Val Asp Lys Pro Glu Arg Leu Thr	
90 95 100	

gcc tcc gag ctg gag cgc gac ttc gat att gat gcc gcc ctc gtt gat	451
Ala Ser Glu Leu Glu Arg Asp Phe Asp Ile Asp Ala Gly Leu Val Asp	
105 110 115	

gta cgc gat ctg tcg acc gcg ctc aat gcg cgc aca gac gct gtg gtt	499
Val Arg Asp Leu Ser Thr Ala Leu Asn Ala Arg Thr Asp Ala Val Val	
120 125 130	

aag cgc ctg gag gcc act gtg gag tgg gtg ctg cgc gaa act gac aag 547
 Lys Arg Leu Glu Ala Thr Val Glu Trp Val Leu Ala Glu Thr Asp Lys
 135 140 145

gtg gcc aac gat ctg gat tcc ctg tct ctg cca ctg ctt tat gcc cgc 595
 Val Ala Asn Asp Leu Asp Ser Leu Ser Leu Pro Leu Leu Tyr Gly Arg
 150 155 160 165

gtt gca cgc gtg atc gaa agc gcc acc agc gca tgg atc aac gca gtg 643
 Val Ala Ala Val Ile Glu Ser Ala Thr Ser Ala Trp Ile Asn Ala Val
 170 175 180

ggc acc gcc aat ccg cgc tat gtg cgc acc atg cga gcc agc aac ccg 691
 Gly Thr Ala Asn Pro Ala Tyr Val Arg Thr Met Arg Gly Ser Asn Pro
 185 190 195

cca cgt ttc ctg ctt gag cgt cgc cgt atc gac gct gtc gtg gcc cgg 739
 Pro Arg Phe Leu Leu Glu Arg Ala Arg Ile Asp Ala Val Val Ala Arg
 200 205 210

gtt gca gac aag ctt cgc caa aag cgc aac gct gtt tcc tagaaatctc 788
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<210> 1964

<211> 226

<212> PRT

<213> Corynebacterium glutamicum

<400> 1964

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 35 40 45

Glu Phe Asp Glu Ile Ile Thr Glu Ala Arg Asp Asp Ser Arg Thr Val
 50 55 60

Val Ala Glu Leu Ser Gly Leu Arg His Ala Leu Thr Thr Gly Ile Arg
 65 70 75 80

Gln Gly Thr Val Ser Ala Arg Ala Thr Val Glu Val Asp Val Asp Lys
 85 90 95

Pro Glu Arg Leu Thr Ala Ser Glu Leu Glu Arg Asp Phe Asp Ile Asp
 100 105 110

Ala Gly Leu Val Asp Val Arg Asp Leu Ser Thr Ala Leu Asn Ala Arg
 115 120 125

Thr Asp Ala Val Val Lys Arg Leu Glu Ala Thr Val Glu Trp Val Leu
 130 135 140

Ala Glu Thr Asp Lys Val Ala Asn Asp Leu Asp Ser Leu Ser Leu Pro

145		150		155		160
Leu Leu Tyr Gly Arg Val Ala Ala Val Ile Glu Ser Ala Thr Ser Ala						
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Trp Ile Asn Ala Val Gly Thr Ala Asn Pro Ala Tyr Val Arg Thr Met						
		180		185		190
Arg Gly Ser Asn Pro Pro Arg Phe Leu Leu Glu Arg Ala Arg Ile Asp						
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Val Ser						
225						

<210> 1965

<211> 642

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(619)

<223> RXA00883

<400> 1965

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	1 5	

cgg aag atg gtc gca gcg gcg ctg gca aca gcg ctt ctt ttt ggg gct	163
Arg Lys Met Val Ala Ala Ala Leu Ala Thr Ala Leu Leu Phe Gly Ala	
	10 15 20

gca cct gcg cac gct tcc gaa ttg gta gag ccc acc aca gtt gca gag	211
Ala Pro Ala His Ala Ser Glu Leu Val Glu Pro Thr Thr Val Ala Glu	
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tca gtg gca ctc gat ccc aac aaa gca atc aat att ctc acc cca gat	259
Ser Val Ala Leu Asp Pro Asn Lys Ala Ile Asn Ile Leu Thr Pro Asp	
	40 45 50

ctc tgg gaa gac att gag gca aaa cca ggc gat atc gtc cac atc ccc	307
Leu Trp Glu Asp Ile Glu Ala Lys Pro Gly Asp Ile Val His Ile Pro	
	55 60 65

tac cag ggc acc cga aac tac gag gac ctc acc gta gaa gtc gcg aaa	355
Tyr Gln Gly Thr Arg Asn Tyr Glu Asp Leu Thr Val Glu Val Ala Lys	
	70 75 80 85

cct ttc gaa gat ttc caa atc ctc gtc gga ctc gac aac agc atc gtc	403
Pro Phe Glu Asp Phe Gln Ile Leu Val Gly Leu Asp Asn Ser Ile Val	
	90 95 100

atc gca gtg cca aag aac tta agt ggc gca gca tca gtc gcc cca gtt	451
Ile Ala Val Pro Lys Asn Leu Ser Gly Ala Ala Ser Val Ala Pro Val	

105	110	115	
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Phe Thr Val Ser Asp Lys Asn Gly Glu Ile Asp Ser Phe Thr Ile Lys			
120	125	130	
gta agc gtc gag cca cgc cgc caa agc gac gaa gaa aag cgc tcc gca			547
Val Ser Val Glu Pro Arg Arg Gln Ser Asp Glu Glu Lys Arg Ser Ala			
135	140	145	
cta ttt gat gtc atc tct gag ctt gcc tac cgc atg cct cat ctg cca			595
Leu Phe Asp Val Ile Ser Glu Leu Ala Tyr Arg Met Pro His Leu Pro			
150	155	160	165
ttc gtg tca gag ttg ctg aag tac tagaacagta acgagaaaaac ccc			642
Phe Val Ser Glu Leu Leu Lys Tyr			
170			

<210> 1966
 <211> 173
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1966	
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20 25 30	
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35 40 45	
Ile Leu Thr Pro Asp Leu Trp Glu Asp Ile Glu Ala Lys Pro Gly Asp	
50 55 60	
Ile Val His Ile Pro Tyr Gln Gly Thr Arg Asn Tyr Glu Asp Leu Thr	
65 70 75 80	
Val Glu Val Ala Lys Pro Phe Glu Asp Phe Gln Ile Leu Val Gly Leu	
85 90 95	
Asp Asn Ser Ile Val Ile Ala Val Pro Lys Asn Leu Ser Gly Ala Ala	
100 105 110	
Ser Val Ala Pro Val Phe Thr Val Ser Asp Lys Asn Gly Glu Ile Asp	
115 120 125	
Ser Phe Thr Ile Lys Val Ser Val Glu Pro Arg Arg Gln Ser Asp Glu	
130 135 140	
Glu Lys Arg Ser Ala Leu Phe Asp Val Ile Ser Glu Leu Ala Tyr Arg	
145 150 155 160	
Met Pro His Leu Pro Phe Val Ser Glu Leu Leu Lys Tyr	
165 170	

<210> 1967

<211> 846

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(823)

<223> RXA00887

<400> 1967

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ccggtttctt tgacaagctc cgaacaacgt tccgcaaata atg tca ctg cca gta 115
                                     Met Ser Leu Pro Val
                                     1 5

ttt atc tct gat tcc gca gcc gga cca ggc gaa acc att gag ctc gcc 163
Phe Ile Ser Asp Ser Ala Ala Gly Pro Gly Glu Thr Ile Glu Leu Ala
                                     10 15 20

ggg ccg gaa ggc cgg cac gcc gtc acc gtc aaa cgg atc cag gta ggc 211
Gly Pro Glu Gly Arg His Ala Val Thr Val Lys Arg Ile Gln Val Gly
                                     25 30 35

gaa aag att tcg ctt atc gac gcc cgg ggt aca gcg cgc acc tgc acg 259
Glu Lys Ile Ser Leu Ile Asp Gly Arg Gly Thr Ala Arg Thr Cys Thr
                                     40 45 50

gtc acc gcc ttg cag gcc aaa gac cgc ctg aac gct gtg gtg gat ttg 307
Val Thr Ala Leu Gln Gly Lys Asp Arg Leu Asn Ala Val Val Asp Leu
                                     55 60 65

gtc gag gaa atc ccc gca ccg aac cca cag gtc acc atc gtg cag gct 355
Val Glu Glu Ile Pro Ala Pro Asn Pro Gln Val Thr Ile Val Gln Ala
                                     70 75 80 85

atc ccc aaa tca gag cgt tcc gag ctg acc atc gac ctg ctc acc caa 403
Ile Pro Lys Ser Glu Arg Ser Glu Leu Thr Ile Asp Leu Leu Thr Gln
                                     90 95 100

gct ggc gcc gat cgg att gtt gcg tgg caa gca tcg cgc tgc gta gca 451
Ala Gly Ala Asp Arg Ile Val Ala Trp Gln Ala Ser Arg Cys Val Ala
                                     105 110 115

aaa tgg ggc gcc aag gaa gca aaa tca ctg gct aaa tgg cag gtg gct 499
Lys Trp Gly Gly Lys Glu Ala Lys Ser Leu Ala Lys Trp Gln Val Ala
                                     120 125 130

gcg gaa gca gcc gcc aag caa tcg cgg cgc gca acg atc cct gaa att 547
Ala Glu Ala Ala Ala Lys Gln Ser Arg Arg Ala Thr Ile Pro Glu Ile
                                     135 140 145

ctt ggc gta gtg ggg gag gag gcc gtc gaa aag ctt atc gac gaa tcc 595
Leu Gly Val Val Gly Glu Glu Gly Val Glu Lys Leu Ile Asp Glu Ser
                                     150 155 160 165

gac ctg gcc atc atc ctg cac gaa gaa gca acc gcc gcg atc cgt gaa 643
Asp Leu Ala Ile Ile Leu His Glu Glu Ala Thr Ala Ala Ile Arg Glu
                                     170 175 180

ctg gaa ttt tcc gcc aac gtc gtg gtg atc atc gga ccc gaa ggt ggc 691
Leu Glu Phe Ser Gly Asn Val Val Val Ile Ile Gly Pro Glu Gly Gly

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185	190	195	
gtc gcg cca tcg gaa att tca cgc ttc gtc gac gct ggc gca cac acc			739
Val Ala Pro Ser Glu Ile Ser Arg Phe Val Asp Ala Gly Ala His Thr			
200	205	210	
gtg aaa cta ggc cct gag gtg ttg cgc act gcc tcc gca ggc atg gtg			787
Val Lys Leu Gly Pro Glu Val Leu Arg Thr Ala Ser Ala Gly Met Val			
215	220	225	
gcg ctc gca gct atc ggc gtg ctg tct gac cgc tgg taacatttct			833
Ala Leu Ala Ala Ile Gly Val Leu Ser Asp Arg Trp			
230	235	240	
ctgacataac ctt			846
<210> 1968			
<211> 241			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 1968			
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Thr Ile Glu Leu Ala Gly Pro Glu Gly Arg His Ala Val Thr Val Lys			
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Arg Ile Gln Val Gly Glu Lys Ile Ser Leu Ile Asp Gly Arg Gly Thr			
35	40	45	
Ala Arg Thr Cys Thr Val Thr Ala Leu Gln Gly Lys Asp Arg Leu Asn			
50	55	60	
Ala Val Val Asp Leu Val Glu Glu Ile Pro Ala Pro Asn Pro Gln Val			
65	70	75	80
Thr Ile Val Gln Ala Ile Pro Lys Ser Glu Arg Ser Glu Leu Thr Ile			
85	90	95	
Asp Leu Leu Thr Gln Ala Gly Ala Asp Arg Ile Val Ala Trp Gln Ala			
100	105	110	
Ser Arg Cys Val Ala Lys Trp Gly Gly Lys Glu Ala Lys Ser Leu Ala			
115	120	125	
Lys Trp Gln Val Ala Ala Glu Ala Ala Ala Lys Gln Ser Arg Arg Ala			
130	135	140	
Thr Ile Pro Glu Ile Leu Gly Val Val Gly Glu Glu Gly Val Glu Lys			
145	150	155	160
Leu Ile Asp Glu Ser Asp Leu Ala Ile Ile Leu His Glu Glu Ala Thr			
165	170	175	
Ala Ala Ile Arg Glu Leu Glu Phe Ser Gly Asn Val Val Val Ile Ile			
180	185	190	
Gly Pro Glu Gly Gly Val Ala Pro Ser Glu Ile Ser Arg Phe Val Asp			
195	200	205	

Ala Gly Ala His Thr Val Lys Leu Gly Pro Glu Val Leu Arg Thr Ala
210 215 220

Ser Ala Gly Met Val Ala Leu Ala Ala Ile Gly Val Leu Ser Asp Arg
225 230 235 240

Trp

<210> 1969

<211> 711

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(688)

<223> RXA00889

<400> 1969

tggtccgcc ccaactgggt ggacacattg tggatgcata cgaagactat gaagaacgcg 60

aggccccgca attgaaacgc aaacgccagg agacacggcc atg agc att gag gta 115
Met Ser Ile Glu Val
1 5

ttc aac gaa tca gga tac gac ggc gtc aat gaa gaa atg ctc att gat 163
Phe Asn Glu Ser Gly Tyr Asp Gly Val Asn Glu Glu Met Leu Ile Asp
10 15 20

gtc ctc tcc ttc gca ctc ggg gaa atg gac atc cac ccc gac gcc gaa 211
Val Leu Ser Phe Ala Leu Gly Glu Met Asp Ile His Pro Asp Ala Glu
25 30 35

gca tcc atc cac atc gtc gac gtc gac acc atc gcc gat ctc cac gtg 259
Ala Ser Ile His Ile Val Asp Val Asp Thr Ile Ala Asp Leu His Val
40 45 50

aaa tgg ctt gat ctt gaa ggc cca acc gac gtg atg agc ttc ccg atg 307
Lys Trp Leu Asp Leu Glu Gly Pro Thr Asp Val Met Ser Phe Pro Met
55 60 65

gat gag ctc acc ccc ggc tac tcc cgc ccc gac ggc gcc acc ccc ggc 355
Asp Glu Leu Thr Pro Gly Tyr Ser Arg Pro Asp Gly Ala Thr Pro Gly
70 75 80 85

ccc gcc atg ctg ggc gac att gtg ctg tgc cca gag ttc gcg gca aag 403
Pro Ala Met Leu Gly Asp Ile Val Leu Cys Pro Glu Phe Ala Leu Lys
90 95 100

caa gcg acc aaa gca ggc cac gac tta gcc cac gag cta gct ttg ctg 451
Gln Ala Thr Lys Ala Gly His Asp Leu Ala His Glu Leu Ala Leu Leu
105 110 115

acc gtg cac ggc agc ctg cac ctg ctt ggc tac gac cac gtc gat cca 499
Thr Val His Gly Ser Leu His Leu Leu Gly Tyr Asp His Val Asp Pro
120 125 130

gcc gaa gag cgt gaa atg ttc gcc ctt caa aac gag ctg ctt gcc gat 547

Ala Glu Glu Arg Glu Met Phe Ala Leu Gln Asn Glu Leu Leu Ala Asp
 135 140 145

tgg tac gac aac gtc gaa gcc cgt ggc gtc acc tac cag cca aaa cca 595
 Trp Tyr Asp Asn Val Glu Ala Arg Gly Val Thr Tyr Gln Pro Lys Pro
 150 155 160 165

tcc ggc gcc ggt gca ttc ccc acc gct gct gat cgt ctg gaa ttg gac 643
 Ser Gly Ala Gly Ala Phe Pro Thr Ala Ala Asp Arg Leu Glu Leu Asp
 170 175 180

gaa aag atg gaa gcg gat gac tct ggc ttt gga ggc gtt gag tcc 688
 Glu Lys Met Glu Ala Asp Asp Ser Gly Phe Gly Gly Val Glu Ser
 185 190 195

taggtggaat cctcagttat atg 711

<210> 1970
 <211> 196
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 1970
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Glu Met Leu Ile Asp Val Leu Ser Phe Ala Leu Gly Glu Met Asp Ile
 20 25 30

His Pro Asp Ala Glu Ala Ser Ile His Ile Val Asp Val Asp Thr Ile
 35 40 45

Ala Asp Leu His Val Lys Trp Leu Asp Leu Glu Gly Pro Thr Asp Val
 50 55 60

Met Ser Phe Pro Met Asp Glu Leu Thr Pro Gly Tyr Ser Arg Pro Asp
 65 70 75 80

Gly Ala Thr Pro Gly Pro Ala Met Leu Gly Asp Ile Val Leu Cys Pro
 85 90 95

Glu Phe Ala Ala Lys Gln Ala Thr Lys Ala Gly His Asp Leu Ala His
 100 105 110

Glu Leu Ala Leu Leu Thr Val His Gly Ser Leu His Leu Leu Gly Tyr
 115 120 125

Asp His Val Asp Pro Ala Glu Glu Arg Glu Met Phe Ala Leu Gln Asn
 130 135 140

Glu Leu Leu Ala Asp Trp Tyr Asp Asn Val Glu Ala Arg Gly Val Thr
 145 150 155 160

Tyr Gln Pro Lys Pro Ser Gly Ala Gly Ala Phe Pro Thr Ala Ala Asp
 165 170 175

Arg Leu Glu Leu Asp Glu Lys Met Glu Ala Asp Asp Ser Gly Phe Gly
 180 185 190

Gly Val Glu Ser

195

<210> 1971
 <211> 720
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(697)
 <223> RXA00893

<400> 1971
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 cgacgaactc aacgacctca aagcactgga ctaaatagct atg gtg gaa tcc caa 115
 Met Val Glu Ser Gln
 1 5
 cac atc att ttc atc ccg gaa tcc caa caa aca ccc gac gag ttt acc 163
 His Ile Ile Phe Ile Pro Glu Ser Gln Gln Thr Pro Asp Glu Phe Thr
 10 15 20
 gag gta gtc aac gag att ccc gcc gga atc aaa cca cgg atc gta ccg 211
 Glu Val Val Asn Glu Ile Pro Ala Gly Ile Lys Pro Arg Ile Val Pro
 25 30 35
 tgg agc ggt agt gtt tcc gca ggt gtg cag gct gtg gaa tcc atc ctc 259
 Trp Ser Gly Ser Val Ser Ala Gly Val Gln Ala Val Glu Ser Ile Leu
 40 45 50
 gac cgt gaa gaa atc ccg cgc gtc atc ctg gtc gcc gct gga acc gga 307
 Asp Arg Glu Glu Ile Arg Arg Val Ile Leu Val Gly Ala Gly Thr Gly
 55 60 65
 gct gga gtg gcg ttg gaa att gcc aag aac caa ccc cgc cgc gtg gaa 355
 Ala Gly Val Ala Leu Glu Ile Ala Lys Asn Gln Pro Arg Arg Val Glu
 70 75 80 85
 cgc ctc gtg ctg gat tca ccg ttg gtg acc ttt gat gag aaa caa ctc 403
 Arg Leu Val Leu Asp Ser Pro Leu Val Thr Phe Asp Glu Lys Gln Leu
 90 95 100
 aaa gcc atg agc acc gca ctg aaa atg atg cca gga ttc ttc ttc cga 451
 Lys Gly Met Ser Thr Ala Leu Lys Met Met Pro Gly Phe Phe Phe Arg
 105 110 115
 aag aag aac aag aaa gac ctc ctg cag cag gta gaa gaa gcc cgt act 499
 Lys Lys Asn Lys Lys Asp Leu Leu Gln Gln Val Glu Glu Ala Arg Thr
 120 125 130
 gca gtt ccg atg gga ttt tcc gag att acc atg ccg acg tta atc atc 547
 Ala Val Pro Met Gly Phe Ser Glu Ile Thr Met Pro Thr Leu Ile Ile
 135 140 145
 cga gcc tcc gct gcg aag gct gga att gat tct gac ttg gaa aaa caa 595
 Arg Gly Ser Ala Ala Lys Ala Gly Ile Asp Ser Asp Leu Glu Lys Gln
 150 155 160 165
 atc ccg agc gct ccg gct acc acc att att ggt gcc aat tgg ctg act 643

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Ile Pro Ser Ala Arg Ala Thr Thr Ile Ile Gly Ala Asn Trp Leu Thr
      170                      175                      180

tac aca acg cat gga cgc caa act ggt gct gcg att gcg gaa ttc ctc   691
Tyr Thr Thr His Gly Arg Gln Thr Gly Ala Ala Ile Ala Glu Phe Leu
      185                      190                      195

gcc caa tagaaggcca cgcctaaacg cca                               720
Ala Gln

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<210> 1972

<211> 199

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1972

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Met Val Glu Ser Gln His Ile Ile Phe Ile Pro Glu Ser Gln Gln Thr
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Pro Asp Glu Phe Thr Glu Val Val Asn Glu Ile Pro Ala Gly Ile Lys
      20                      25                      30

Pro Arg Ile Val Pro Trp Ser Gly Ser Val Ser Ala Gly Val Gln Ala
      35                      40                      45

Val Glu Ser Ile Leu Asp Arg Glu Glu Ile Arg Arg Val Ile Leu Val
      50                      55                      60

Gly Ala Gly Thr Gly Ala Gly Val Ala Leu Glu Ile Ala Lys Asn Gln
      65                      70                      75                      80

Pro Arg Arg Val Glu Arg Leu Val Leu Asp Ser Pro Leu Val Thr Phe
      85                      90                      95

Asp Glu Lys Gln Leu Lys Gly Met Ser Thr Ala Leu Lys Met Met Pro
      100                     105                     110

Gly Phe Phe Phe Arg Lys Lys Asn Lys Lys Asp Leu Leu Gln Gln Val
      115                     120                     125

Glu Glu Ala Arg Thr Ala Val Pro Met Gly Phe Ser Glu Ile Thr Met
      130                     135                     140

Pro Thr Leu Ile Ile Arg Gly Ser Ala Ala Lys Ala Gly Ile Asp Ser
      145                     150                     155                     160

Asp Leu Glu Lys Gln Ile Pro Ser Ala Arg Ala Thr Thr Ile Ile Gly
      165                     170                     175

Ala Asn Trp Leu Thr Tyr Thr Thr His Gly Arg Gln Thr Gly Ala Ala
      180                     185                     190

Ile Ala Glu Phe Leu Ala Gln
      195

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<210> 1973

<211> 714

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(691)

<223> RXA00895

<400> 1973

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ctcggccacg ccttcagaag aaaacaagg cggactgccc atg cgc ggt ttg gcc 115
 Met Arg Gly Leu Ala
 1 5

atg att ttg atc gcc gtg gcc gta ttg ctc gca gcg tgg gca ctg tgg 163
 Met Ile Leu Ile Ala Val Ala Val Leu Leu Ala Ala Trp Ala Leu Trp
 10 15 20

tca atg cag ggc aaa gac gac acc tcc acc acc agc gcc gga caa acc 211
 Ser Met Gln Gly Lys Asp Asp Thr Ser Thr Thr Ser Ala Gly Gln Thr
 25 30 35

cag tcc acg gaa acc aac gcg gga act att gct gaa tct tct ggc tct 259
 Gln Ser Thr Glu Thr Asn Ala Gly Thr Ile Ala Glu Ser Ser Gly Ser
 40 45 50

tcg gat tcc gag cag gca tca gca gaa cct gga acc tcc gaa gaa acc 307
 Ser Asp Ser Ser Glu Gln Ala Ser Ala Glu Pro Gly Thr Ser Glu Glu Thr
 55 60 65

tct gct gag cag cca gct gca gat ggc gaa gcc gct aat gct gct ggg 355
 Ser Ala Glu Gln Pro Ala Ala Asp Gly Glu Ala Ala Asn Ala Ala Gly
 70 75 80 85

gcc gct gct gct ggt ggc gct agt tcg gct aac ggc aac tcc acc cca 403
 Ala Ala Ala Ala Gly Gly Ala Ser Ser Ala Asn Gly Asn Ser Thr Pro
 90 95 100

gtg aac act ctg tac gtg ctc aac aac tcc acc gtc cca caa ctt gca 451
 Val Asn Thr Leu Tyr Val Leu Asn Asn Ser Thr Val Pro Gln Leu Ala
 105 110 115

gca cga gtg gca gac agc cta agc ggt gac tac caa aag gta gag tcc 499
 Ala Arg Val Ala Asp Ser Leu Ser Gly Asp Tyr Gln Lys Val Glu Ser
 120 125 130

gga aac ctt cca gac acc atc att ccg cag aac act gtg tac ttc acc 547
 Gly Asn Leu Pro Asp Thr Ile Ile Pro Gln Asn Thr Val Tyr Phe Thr
 135 140 145

gct gga aac acc gaa gct gaa aag gct gca cgt gaa ctc gct gac cgc 595
 Ala Gly Asn Thr Glu Ala Glu Lys Ala Ala Arg Glu Leu Ala Asp Arg
 150 155 160 165

gtc agt ggc gta gca atg gaa cgc agc gat gca ctg cca acc gaa aca 643
 Val Ser Gly Val Ala Met Glu Arg Ser Asp Ala Leu Pro Thr Glu Thr
 170 175 180

gaa ggc aaa gat gcc ctc gtt ttg gtg ctg gtc caa gac gta gcg ctg 691
 Glu Gly Lys Asp Ala Leu Val Leu Val Leu Val Gln Asp Val Ala Leu
 185 190 195

tagttttctc ggatttggtg gaa

714

<210> 1974

<211> 197

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1974

Met	Arg	Gly	Leu	Ala	Met	Ile	Leu	Ile	Ala	Val	Ala	Val	Leu	Leu	Ala
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Ala	Trp	Ala	Leu	Trp	Ser	Met	Gln	Gly	Lys	Asp	Asp	Thr	Ser	Thr	Thr
		20						25					30		

Ser	Ala	Gly	Gln	Thr	Gln	Ser	Thr	Glu	Thr	Asn	Ala	Gly	Thr	Ile	Ala
		35					40					45			

Glu	Ser	Ser	Gly	Ser	Ser	Asp	Ser	Glu	Gln	Ala	Ser	Ala	Glu	Pro	Gly
	50					55					60				

Thr	Ser	Glu	Glu	Thr	Ser	Ala	Glu	Gln	Pro	Ala	Ala	Asp	Gly	Glu	Ala
	65					70				75				80	

Ala	Asn	Ala	Ala	Gly	Ala	Ala	Ala	Ala	Gly	Gly	Ala	Ser	Ser	Ala	Asn
			85						90					95	

Gly	Asn	Ser	Thr	Pro	Val	Asn	Thr	Leu	Tyr	Val	Leu	Asn	Asn	Ser	Thr
			100				105						110		

Val	Pro	Gln	Leu	Ala	Ala	Arg	Val	Ala	Asp	Ser	Leu	Ser	Gly	Asp	Tyr
		115				120						125			

Gln	Lys	Val	Glu	Ser	Gly	Asn	Leu	Pro	Asp	Thr	Ile	Ile	Pro	Gln	Asn
	130					135					140				

Thr	Val	Tyr	Phe	Thr	Ala	Gly	Asn	Thr	Glu	Ala	Glu	Lys	Ala	Ala	Arg
	145				150				155					160	

Glu	Leu	Ala	Asp	Arg	Val	Ser	Gly	Val	Ala	Met	Glu	Arg	Ser	Asp	Ala
			165					170						175	

Leu	Pro	Thr	Glu	Thr	Glu	Gly	Lys	Asp	Ala	Leu	Val	Leu	Val	Leu	Val
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Gln	Asp	Val	Ala	Leu
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<210> 1975

<211> 815

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (37) .. (792)

<223> RXA00904

<400> 1975

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				1				5	
tcc gaa tgg acc aaa ctt gtc acc acc aaa tcc ttc tgg tgg aca acc	102								
Ser Glu Trp Thr Lys Leu Val Thr Thr Lys Ser Phe Trp Trp Thr Thr									
	10		15				20		
gca cta att ctg gtc ttc agc ctg gga tac gca gcg ctc acc gga tca	150								
Ala Leu Ile Leu Val Phe Ser Leu Gly Tyr Ala Ala Leu Thr Gly Ser									
	25		30				35		
ctc gcc acc ggc gaa agc ttt gca tca ctg ttc ctt ctc gca ggc agc	198								
Leu Ala Thr Gly Glu Ser Phe Ala Ser Leu Phe Leu Leu Ala Gly Ser									
	40		45				50		
aca gtc acc ggc ctt tac ctc ctt ggc ttc gtg gtg atc atg atc caa	246								
Thr Val Thr Gly Leu Tyr Leu Leu Gly Phe Val Val Ile Met Ile Gln									
	55		60				65		70
tcc atc atg atg ttc acc acc gaa ttt cga ttc ggc tac caa acc caa	294								
Ser Ile Met Met Phe Thr Thr Glu Phe Arg Phe Gly Tyr Gln Thr Gln									
	75		80				85		
acc ttc ctc gcc aca cca aaa cgc tgg gtt gtc gcc gtt tcc aaa tgg	342								
Thr Phe Leu Ala Thr Pro Lys Arg Trp Val Val Ala Val Ser Lys Trp									
	90		95				100		
ttg ctg tac ctc gtg ttc gcc gta gtg ttg acc ttc atc acc gtg att	390								
Leu Leu Tyr Leu Val Phe Ala Val Val Leu Thr Phe Ile Thr Val Ile									
	105		110				115		
ctg tgc ttc tat cta gcc aaa gcc ctg gca tca gac act gca agc tcc	438								
Leu Cys Phe Tyr Leu Ala Lys Ala Leu Ala Ser Asp Thr Ala Ser Ser									
	120		125				130		
acc ctg gtg gtg tgg gaa gat acg caa gca cga cga atc atg tgg caa	486								
Thr Leu Val Val Trp Glu Asp Thr Gln Ala Arg Arg Ile Met Trp Gln									
	135		140				145		150
tac cca ctg gca gca gca cta ttg gta act ttc tgt tcc gga att gcg	534								
Tyr Pro Leu Ala Ala Ala Leu Leu Val Thr Phe Cys Ser Gly Ile Ala									
	155		160				165		
ctc ctg ctg cgt caa act gca gga gca gtg gca ctg gtg ctt atg tgg	582								
Leu Leu Leu Arg Gln Thr Ala Gly Ala Val Ala Leu Val Leu Met Trp									
	170		175				180		
cac ttc gct atc gaa aac ctc ctg tct ttc ttg cca cgc atc ggc gaa	630								
His Phe Ala Ile Glu Asn Leu Leu Ser Phe Leu Pro Arg Ile Gly Glu									
	185		190				195		
tac gtc ggc aag tat ggt ccc ttc acc aac ctc tac gca ttc atc acc	678								
Tyr Val Gly Lys Tyr Gly Pro Phe Thr Asn Leu Tyr Ala Phe Ile Thr									
	200		205				210		
gac tat caa tca att gat cca gga tgg tcc acc acc atg gga gcg gtg	726								
Asp Tyr Gln Ser Ile Asp Pro Gly Trp Ser Thr Thr Met Gly Ala Val									
	215		220				225		230
tac ttc gga gcg tgg gca ttc gtg ctg ttc gca ctc gga atc gtc gtc	774								

Tyr Phe Gly Ala Trp Ala Phe Val Leu Phe Ala Leu Gly Ile Val Val
 235 240 245

cta gaa aag aaa gac gcc taaaatgccc tctaaaatat cgc 815
 Leu Glu Lys Lys Asp Ala
 250

<210> 1976

<211> 252

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1976

Met Ile Asn Thr Ile Arg Ser Glu Trp Thr Lys Leu Val Thr Thr Lys
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Ser Phe Trp Trp Thr Thr Ala Leu Ile Leu Val Phe Ser Leu Gly Tyr
 20 25 30

Ala Ala Leu Thr Gly Ser Leu Ala Thr Gly Glu Ser Phe Ala Ser Leu
 35 40 45

Phe Leu Leu Ala Gly Ser Thr Val Thr Gly Leu Tyr Leu Leu Gly Phe
 50 55 60

Val Val Ile Met Ile Gln Ser Ile Met Met Phe Thr Thr Glu Phe Arg
 65 70 75 80

Phe Gly Tyr Gln Thr Gln Thr Phe Leu Ala Thr Pro Lys Arg Trp Val
 85 90 95

Val Ala Val Ser Lys Trp Leu Leu Tyr Leu Val Phe Ala Val Val Leu
 100 105 110

Thr Phe Ile Thr Val Ile Leu Cys Phe Tyr Leu Ala Lys Ala Leu Ala
 115 120 125

Ser Asp Thr Ala Ser Ser Thr Leu Val Val Trp Glu Asp Thr Gln Ala
 130 135 140

Arg Arg Ile Met Trp Gln Tyr Pro Leu Ala Ala Ala Leu Leu Val Thr
 145 150 155 160

Phe Cys Ser Gly Ile Ala Leu Leu Leu Arg Gln Thr Ala Gly Ala Val
 165 170 175

Ala Leu Val Leu Met Trp His Phe Ala Ile Glu Asn Leu Leu Ser Phe
 180 185 190

Leu Pro Arg Ile Gly Glu Tyr Val Gly Lys Tyr Gly Pro Phe Thr Asn
 195 200 205

Leu Tyr Ala Phe Ile Thr Asp Tyr Gln Ser Ile Asp Pro Gly Trp Ser
 210 215 220

Thr Thr Met Gly Ala Val Tyr Phe Gly Ala Trp Ala Phe Val Leu Phe
 225 230 235 240

Ala Leu Gly Ile Val Val Leu Glu Lys Lys Asp Ala
 245 250

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<221> CDS
<222> (101)..(658)
<223> RXA00908
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400> 1977																	
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				Met	Ser	Leu	Tyr	Thr	5								
cgt	act	caa	aat	acc	cgt	cac	tcc	acc	atc	atc	gag	ttc	cgc	cgc	gag	163	
Arg	Thr	Gln	Asn	Thr	Arg	His	Ser	Thr	Ile	Ile	Glu	Phe	Arg	Arg	Glu		
				10					15					20			
cag	act	cgt	aat	cac	acg	atg	gag	cca	atc	cag	tcc	gag	cca	cgg	atc	211	
Gln	Thr	Arg	Asn	His	Thr	Met	Glu	Pro	Ile	Gln	Ser	Glu	Pro	Arg	Ile		
				25					30					35			
tac	gct	gac	gat	cct	ttc	cgt	gca	cgc	ttc	gga	cac	caa	ctc	ccc	cgc	259	
Tyr	Ala	Asp	Asp	Pro	Phe	Arg	Ala	Arg	Phe	Gly	His	Gln	Leu	Pro	Arg		
				40					45					50			
gga	ctt	cgc	gaa	gaa	gca	cgc	ggc	atg	gaa	tgg	cgc	acc	ttc	acc	aac	307	
Gly	Leu	Arg	Glu	Glu	Ala	Arg	Gly	Met	Glu	Trp	Arg	Thr	Phe	Thr	Asn		
				55					60					65			
acc	tac	gca	cca	acc	ggc	aac	ctg	cgc	atc	agc	aac	ctc	gag	tcc	gag	355	
Thr	Tyr	Ala	Pro	Thr	Gly	Asn	Leu	Arg	Ile	Ser	Asn	Leu	Glu	Ser	Glu		
				70					75					80			85
gca	cgc	cgc	gga	gga	atg	ttc	cac	ttc	aac	gca	acc	ctg	atc	aac	aac	403	
Ala	Arg	Arg	Gly	Gly	Met	Phe	His	Phe	Asn	Ala	Thr	Leu	Ile	Asn	Asn		
				90					95					100			
tgc	cag	ggc	gag	cgc	acc	acc	acc	gac	gct	cac	atc	atg	gca	acc	ggc	451	
Cys	Gln	Gly	Glu	Arg	Thr	Thr	Thr	Asp	Ala	His	Ile	Met	Ala	Thr	Gly		
				105					110					115			
cca	gtt	tcc	gca	tgc	acc	aac	ttg	ctt	gcc	gac	gcc	ggc	cgt	cgc	gtt	499	
Pro	Val	Ser	Ala	Cys	Thr	Asn	Leu	Leu	Ala	Asp	Ala	Gly	Arg	Arg	Val		
				120					125					130			
gaa	atc	ctc	gaa	ttc	cac	caa	ttc	gac	atc	ttt	gaa	gca	acc	gtc	acc	547	
Glu	Ile	Leu	Glu	Phe	His	Gln	Phe	Asp	Ile	Phe	Glu	Ala	Thr	Val	Thr		
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Phe	Ile	Tyr	Thr	Cys	Asn	Asn	Val	Ser	Arg	Thr	Trp	Ala	Met	Gly	Phe		
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Gly	Gly	Thr	Pro	Glu	Gln	Ser	Ala	Ala	Ser	Ala	Met	Ser	Ser	Ala	Ala		

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<210> 1978

<211> 186

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<400> 1978

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35 40 45His Gln Leu Pro Arg Gly Leu Arg Glu Glu Ala Arg Gly Met Glu Trp
50 55 60Arg Thr Phe Thr Asn Thr Tyr Ala Pro Thr Gly Asn Leu Arg Ile Ser
65 70 75 80Asn Leu Glu Ser Glu Ala Arg Arg Gly Gly Met Phe His Phe Asn Ala
85 90 95Thr Leu Ile Asn Asn Cys Gln Gly Glu Arg Thr Thr Thr Asp Ala His
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115 120 125Ala Gly Arg Arg Val Glu Ile Leu Glu Phe His Gln Phe Asp Ile Phe
130 135 140Glu Ala Thr Val Thr Phe Ile Tyr Thr Cys Asn Asn Val Ser Arg Thr
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Met Lys Lys Val Leu
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Val Val Gly Cys Gly Gly Ser Gly Ala Lys Thr Leu Ala Tyr Met Met
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gac cag ctc aag acc acc ctg gcg gat agt ctt ccc gag cgt tac cca 211
Asp Gln Leu Lys Thr Thr Leu Ala Asp Ser Leu Pro Glu Arg Tyr Pro
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Asn Pro Lys Glu Ala Lys Leu Pro Gly Ala Trp Gln Phe Val Ser Val
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gat gtt ccg acc tcc cca gaa agc ccc gcc ccg aac ctt ccg aat gtt 307
Asp Val Pro Thr Ser Pro Glu Ser Pro Gly Pro Asn Leu Pro Asn Val
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cca gaa gcc ggt gga cgt tat att tcc tgt ggt tcc tcg gat cgc tat 355
Pro Glu Ala Gly Gly Arg Tyr Ile Ser Cys Gly Ser Ser Asp Arg Tyr
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gcc acc gtt gat act gcg gtg tcc aac cag ctc tcc tcc agg gcc gcg 403
Ala Thr Val Asp Thr Ala Val Ser Asn Gln Leu Ser Ser Arg Gly Ala
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Leu Gly Gly Val Ser Ser Trp Ala Leu Arg Asn Pro Asp Ser Glu Thr
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acc cca att agt aaa ggt gcg gcc cag tac cgc tcc att gcc cgt atg 499
Thr Pro Ile Ser Lys Gly Ala Gly Gln Tyr Arg Ser Ile Gly Arg Met
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Leu Ile Leu Ser Arg Leu Gln Glu Ile Gln Ala Glu Leu Arg Lys Ser
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Trp Asp Val Leu Phe Ser Gly Glu Thr Glu Arg Glu Leu Ala Asp Leu
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gag cag cca att atc ttc ggt gtc tcc tcc atg gct ggt gcc gcc ggt 691
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gct tcg atg gct cta gat atc tgc cgc ctg ctc acc ggt ctt gaa gcc 739
Ala Ser Met Ala Leu Asp Ile Cys Arg Leu Leu Thr Gly Leu Glu Gly
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Asn Ala Val Gly Leu Ser Ser Leu Phe Met Val Thr Pro Asp Ile Phe
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Lys Leu Gly Val Pro Tyr Gly Val Ser Val Ile Glu Ser Leu Ser Ala	
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Ile Val Ser Arg Ser Thr Gly Gln Leu His Thr Arg Ala Val Gln Tyr	
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Ile Ala Asp His Met Ala Ser Val Leu Asp Asp Phe Leu Lys Asn Phe	
600 605 610	
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Ile Tyr Pro Leu Gln Arg Thr Ile Gln Arg Glu His Ser Leu Glu	
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Lys Thr Asn Val Pro Ala Leu Trp Pro Asp Glu Ser Gln Thr Thr Val	
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cgt	cgc	gcg	cgc	cgt	cag	cag	gtg	ctg	agc	aag	ttc	agt	gag	gca	atg	2563
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Thr	Tyr	Ala	Leu	Pro	Leu	Ala	Gln	Ile	Asn	Pro	Gln	Leu	Val	Arg	Ala	
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Phe	Ala	Gly	Asp	Glu	Leu	Gly	Ser	Ser	Leu	Glu	Gln	Ala	Val	Arg	Asp	
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Lys	Gln	Trp	Arg	Gln	Ile	Thr	Gly	Asp	Arg	Thr	Glu	Phe	Trp	His	Gly	
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Arg	Arg	Thr	Arg	Pro	Leu	Thr	Ala	Ala	Leu	Pro	Met	Thr	Asp	Leu	Glu	
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Val Phe Phe Pro Ala Thr Leu Asp Thr Ala Asp Thr Thr Pro Val Gln	970	975	980	
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Ile Tyr Asp Glu Lys Ser Asp Ser Trp Ile Asn Phe Ser Thr Pro Met	985	990	995	
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Leu Thr Pro Val Ser Arg Phe Arg Gly Ser Leu Asp Trp Leu Pro Asn	1000	1005	1010	
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Leu Leu Glu Ser Ala Ser Leu Ala Trp Ala Arg Ala Gly Glu Arg Pro	1015	1020	1025	
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Val Phe Glu Ser Val Glu Pro Tyr Ile Gln Leu Arg Gln Leu Trp Asp	1030	1035	1040	1045
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Asp Ala Ala Ser Pro Ser Leu Pro Gly Arg Thr Thr Arg Gly Glu Lys	1050	1055	1060	
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Leu Leu His Trp Leu Phe Asp Gly Asn Arg Met Ala Ala Asn Val	1065	1070	1075	
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Leu Gln Ile Pro Gly Thr Glu Ala Gly Val Thr Pro Ala Ala Arg Phe	1080	1085	1090	
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Glu Ala Ala Lys Asn Phe Leu Gln Arg Gln Asn Glu Ile Ser Gln Asn	1095	1100	1105	
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Tyr Val Pro Ser Asp Lys Leu Arg Gln Gly Arg Leu Phe Thr Thr Ala	1110	1115	1120	1125
gat cgt cca ttt ggc gac gtc aag gat cgt gaa cta gca gca cag att				3523
Asp Arg Pro Phe Gly Asp Val Lys Asp Arg Glu Leu Ala Ala Gln Ile	1130	1135	1140	
cca gtg ttt gct gac ctt gca gcc gat gtt ttt gat ggc acc caa gaa				3571
Pro Val Phe Ala Asp Leu Ala Ala Asp Val Phe Asp Gly Thr Gln Glu	1145	1150	1155	
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Ile Ile Asp Ile Leu Glu Lys Cys Leu Ala Ala Gly Pro Pro Ser Ala	1160	1165	1170	
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Gln Val Phe Asp Met Asn Val Ala Arg Arg Asp Val Ser Ser Gly Pro	1175	1180	1185	
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Gln Phe Val Ser Val Asp Val Pro Thr Ser Pro Glu Ser Pro Gly Pro
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Asn Leu Pro Asn Val Pro Glu Ala Gly Gly Arg Tyr Ile Ser Cys Gly
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Ser Ile Gly Arg Met Leu Ile Leu Ser Arg Leu Gln Glu Ile Gln Ala
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Glu Leu Arg Lys Ser Trp Asp Val Leu Phe Ser Gly Glu Thr Glu Arg
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Glu Leu Ala Asp Leu Arg Ser Ala Leu Tyr Gly Thr Ser Val Ser Ser
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Gly Glu Thr Ser Lys Glu Gln Pro Ile Ile Phe Gly Val Ser Ser Met
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Ala Gly Gly Ala Gly Ala Ser Met Ala Leu Asp Ile Cys Arg Leu Leu
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Thr Gly Leu Glu Gly Asn Ala Val Gly Leu Ser Ser Leu Phe Met Val
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Thr Pro Asp Ile Phe Ser Gln Leu Ser Pro Asp Gln Val Ala Gly Thr
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 245 250 255

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 Ser Asp Gln Gln Leu Gln Lys Arg Leu Glu Asn Asn Arg Pro Ser Leu
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 Met Lys Ala Ile Ile Lys Ser Gln Ile Pro Ala Ala Asn Gly Gln Arg
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 Gln Met Ile Asp Asn Asp Ser Arg His Glu Leu Tyr Met Gly Val Ala
 485 490 495
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 Arg Asp Glu Ile Ala Lys Leu Gly Val Pro Tyr Gly Val Ser Val Ile
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 Arg Ala Val Gln Tyr Ile Ala Asp His Met Ala Ser Val Leu Asp Asp
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Phe Leu Lys Asn Phe Ile Tyr Pro Leu Gln Arg Thr Ile Gln Arg Glu
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 His His Ser Leu Glu Lys Asp Tyr Gln Leu Thr Asn Asp Val Asn Leu
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 Gly Ile Ser Gln Leu Lys Thr Asn Val Pro Ala Leu Trp Pro Asp Glu
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 Ser Gln Thr Thr Val Pro Ser Arg Phe Ser Gln Ala Ala Asn Glu Val
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 675 680 685
 Arg Ser Ser Thr Asp Asp Ile Asn Glu Gln Asn Asp Tyr Ser Ser Ala
 690 695 700
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 Ser Gly Ser Glu Lys Ala Pro Arg Asp Leu Ile Arg Leu Ile Asp Val
 725 730 735
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 755 760 765
 Val Leu Glu Arg Ser Arg Gln Tyr Ile Arg Arg Pro Gly Phe Ser Phe
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 865 870 875 880
 Pro Leu Gly Lys Ala Leu Val Ser Gln Gly Glu Glu Arg Ser Ile Asp
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 Ile Phe Gly Ser Tyr Pro Asn Tyr Ala Pro Ile Val Phe Asp Ser Leu
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 Glu Phe Trp His Gly Arg Arg Thr Arg Pro Leu Thr Ala Ala Leu Pro

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Asp	Trp	Leu	Pro	Asn	Leu	Leu	Glu	Ser	Ala	Ser	Leu	Ala	Trp	Ala	Arg
	1010						1015					1020			
Ala	Gly	Glu	Arg	Pro	Val	Phe	Glu	Ser	Val	Glu	Pro	Tyr	Ile	Gln	Leu
1025					1030					1035					1040
Arg	Gln	Leu	Trp	Asp	Asp	Ala	Ala	Ser	Pro	Ser	Leu	Pro	Gly	Arg	Thr
				1045					1050					1055	
Thr	Arg	Gly	Glu	Lys	Leu	Leu	His	Asp	Trp	Leu	Phe	Asp	Gly	Asn	Arg
			1060					1065					1070		
Met	Ala	Gly	Asn	Val	Leu	Gln	Ile	Pro	Gly	Thr	Glu	Ala	Gly	Val	Thr
		1075					1080					1085			
Pro	Ala	Ala	Arg	Phe	Glu	Ala	Ala	Lys	Asn	Phe	Leu	Gln	Arg	Gln	Asn
			1090			1095						1100			
Glu	Ile	Ser	Gln	Asn	Tyr	Val	Pro	Ser	Asp	Lys	Leu	Arg	Gln	Gly	Arg
1105				1110					1115						1120
Leu	Phe	Thr	Thr	Ala	Asp	Arg	Pro	Phe	Gly	Asp	Val	Lys	Asp	Arg	Glu
				1125					1130					1135	
Leu	Ala	Ala	Gln	Ile	Pro	Val	Phe	Ala	Asp	Leu	Ala	Ala	Asp	Val	Phe
			1140					1145					1150		
Asp	Gly	Thr	Gln	Glu	Ile	Ile	Asp	Ile	Leu	Glu	Lys	Cys	Leu	Ala	Ala
	1155					1160						1165			
Gly	Pro	Pro	Ser	Ala	Gln	Val	Phe	Asp	Met	Asn	Val	Ala	Arg	Arg	Asp
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<210> 1981
<211> 486
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> {101}..(463)
<223> RXA00926
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gggtggccagg atgttccatg gtctggcaaa ctaactaacc atg gac atc gtt ttc 115
Met Asp Ile Val Phe
1 5

ctc ata att ctt cta gcc att ttt atc gtt ccc act ttc ctc atg agc 163
Leu Ile Ile Leu Leu Ala Ile Phe Ile Val Pro Thr Phe Leu Met Ser
10 15 20

cgc cgc cag cgc gca cgg atg act gaa atc caa aag ctg cag gac tct 211
Arg Arg Gln Arg Ala Arg Met Thr Glu Ile Gln Lys Leu Gln Asp Ser
25 30 35

gtc gtc cca ggc gac cgc atc gtc acc acc gcg gga cag cac gca acg 259
Val Val Pro Gly Asp Arg Ile Val Thr Thr Ala Gly Gln His Ala Thr
40 45 50

gtc att tcc acc act gca gaa acc gtt gat cta gag atc gcg ccg ggt 307
Val Ile Ser Thr Thr Ala Glu Thr Val Asp Leu Glu Ile Ala Pro Gly
55 60 65

atg atc agc act ttt gaa aag ctt gct atc gtg cgt gtg ctg tcc aag 355
Met Ile Ser Thr Phe Glu Lys Leu Ala Ile Val Arg Val Leu Ser Lys
70 75 80 85

gcc aat gaa cct cag atg ttg gat gag ccg acg ctg ttt gat cag cca 403
Ala Asn Glu Pro Gln Met Leu Asp Glu Pro Thr Leu Phe Asp Gln Pro
90 95 100

gaa gac gat cag ccg aac gat ggt ttc gat gga cgc act gac gga cat 451
Glu Asp Asp Gln Pro Asn Asp Gly Phe Asp Gly Arg Thr Asp Gly His
105 110 115

cct gag aat cgt tagaaattaa taataattca gca 486
Pro Glu Asn Arg
120

<210> 1982

<211> 121

<212> PRT

<213> Corynebacterium glutamicum

<400> 1982

Met Asp Ile Val Phe Leu Ile Ile Leu Leu Ala Ile Phe Ile Val Pro
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Thr Phe Leu Met Ser Arg Arg Gln Arg Ala Arg Met Thr Glu Ile Gln
20 25 30

Lys Leu Gln Asp Ser Val Val Pro Gly Asp Arg Ile Val Thr Thr Ala
35 40 45

Gly Gln His Ala Thr Val Ile Ser Thr Thr Ala Glu Thr Val Asp Leu
50 55 60

Glu Ile Ala Pro Gly Met Ile Ser Thr Phe Glu Lys Leu Ala Ile Val
65 70 75 80

Arg Val Leu Ser Lys Ala Asn Glu Pro Gln Met Leu Asp Glu Pro Thr
 85 90 95

Leu Phe Asp Gln Pro Glu Asp Asp Gln Pro Asn Asp Gly Phe Asp Gly
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Arg Thr Asp Gly His Pro Glu Asn Arg
 115 120

<210> 1983

<211> 876

<212> DNA

<213> *Corynebacterium glutamicum*

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<222> (101)..(853)

<223> RXA00930

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ttccggtgga tgatggaagc tagacgacga aagggagcat atg tct ggc cac tca 115
 Met Ser Gly His Ser
 1 5

aaa tgg gcg act acc aag cac aag aag gct gct aac gac gcc aag cga 163
 Lys Trp Ala Thr Thr Lys His Lys Lys Ala Ala Asn Asp Ala Lys Arg
 10 15 20

ggc aag gaa ttt gcc aag ctg atc aag aac atc gaa gtt gcg gca cgt 211
 Gly Lys Glu Phe Ala Lys Leu Ile Lys Asn Ile Glu Val Ala Ala Arg
 25 30 35

aca ggc ggt gga gat ccg tct gcg aac cca acg ctt gat gac atg atc 259
 Thr Gly Gly Gly Asp Pro Ser Ala Asn Pro Thr Leu Asp Asp Met Ile
 40 45 50

aag aaa gcc aag aag gct tct gtg ccg aac gat aac atc gaa cgt gca 307
 Lys Lys Ala Lys Lys Ala Ser Val Pro Asn Asp Asn Ile Glu Arg Ala
 55 60 65

cgc aag cgt ggc tcc gcc gaa gaa gct ggt gcc gct gac tgg atg aac 355
 Arg Lys Arg Gly Ser Gly Glu Glu Ala Gly Gly Ala Asp Trp Met Asn
 70 75 80 85

atc atg tac gag gga tac gcc ccc aac gcc gtt gcc atg ctt atc gag 403
 Ile Met Tyr Glu Gly Tyr Gly Pro Asn Gly Val Ala Met Leu Ile Glu
 90 95 100

tgt ctg acc gac aac cgt aac cgc gca gct acc gaa gtt cgc acc gca 451
 Cys Leu Thr Asp Asn Arg Asn Arg Ala Ala Thr Glu Val Arg Thr Ala
 105 110 115

atg acc aaa aac ggt gcc aac ttg gcc gag tcc ggt tcc gtg tcc tac 499
 Met Thr Lys Asn Gly Gly Asn Leu Gly Glu Ser Gly Ser Val Ser Tyr
 120 125 130

atg ttc acc cgc acc ggt gtc gtc acc gta caa aag gcc gat ctt agt 547
 Met Phe Thr Arg Thr Gly Val Val Thr Val Gln Lys Gly Asp Leu Ser

135	140	145	
gaa gat gac gtg ctc atg gct gtt ctt gaa gct ggt gct gaa gaa gtc			595
Glu Asp Asp Val Leu Met Ala Val Leu Glu Ala Gly Ala Glu Glu Val			
150	155	160	165
aac gac aac ggc gat ctg ttc gag gtt acc tgc gca cca act gac att			643
Asn Asp Asn Gly Asp Leu Phe Glu Val Thr Thr Cys Ala Pro Thr Asp Ile			
	170	175	180
cag gct gtt cgc gac gca ctc gtg gaa gct ggc att gaa gta gaa gat			691
Gln Ala Val Arg Asp Ala Leu Val Glu Ala Gly Ile Glu Val Glu Asp			
	185	190	195
tct gaa tca gac ttc cgg gca tct gtt cag gtc ccc ctg gac gct gac			739
Ser Glu Ser Asp Phe Arg Ala Ser Val Gln Val Pro Leu Asp Ala Asp			
	200	205	210
ggc gca cgc aag atc ttc aag ctt gtg gac gcg ttg gaa gat tcc gac			787
Gly Ala Arg Lys Ile Phe Lys Leu Val Asp Ala Leu Glu Asp Ser Asp			
	215	220	225
gat gtg caa aac gtc tac acc aac atc gac ttg agc gat gag gtt ttg			835
Asp Val Gln Asn Val Tyr Thr Asn Ile Asp Leu Ser Asp Glu Val Leu			
	230	235	240
aca gag ctg gaa aac gac tagttcgat tttccgcaact ccg			876
Thr Glu Leu Glu Asn Asp			
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<211> 251			
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Glu Val Ala Ala Arg Thr Gly Gly Gly Asp Pro Ser Ala Asn Pro Thr			
	35	40	45
Leu Asp Asp Met Ile Lys Lys Ala Lys Lys Ala Ser Val Pro Asn Asp			
	50	55	60
Asn Ile Glu Arg Ala Arg Lys Arg Gly Ser Gly Glu Glu Ala Gly Gly			
	65	70	75
Ala Asp Trp Met Asn Ile Met Tyr Glu Gly Tyr Gly Pro Asn Gly Val			
	85	90	95
Ala Met Leu Ile Glu Cys Leu Thr Asp Asn Arg Asn Arg Ala Ala Thr			
	100	105	110
Glu Val Arg Thr Ala Met Thr Lys Asn Gly Gly Asn Leu Gly Glu Ser			
	115	120	125

Gly Ser Val Ser Tyr Met Phe Thr Arg Thr Gly Val Val Thr Val Gln
130 135 140

Lys Gly Asp Leu Ser Glu Asp Asp Val Leu Met Ala Val Leu Glu Ala
145 150 155 160

Gly Ala Glu Glu Val Asn Asp Asn Gly Asp Leu Phe Glu Val Thr Cys
165 170 175

Ala Pro Thr Asp Ile Gln Ala Val Arg Asp Ala Leu Val Glu Ala Gly
180 185 190

Ile Glu Val Glu Asp Ser Glu Ser Asp Phe Arg Ala Ser Val Gln Val
195 200 205

Pro Leu Asp Ala Asp Gly Ala Arg Lys Ile Phe Lys Leu Val Asp Ala
210 215 220

Leu Glu Asp Ser Asp Asp Val Gln Asn Val Tyr Thr Asn Ile Asp Leu
225 230 235 240

Ser Asp Glu Val Leu Thr Glu Leu Glu Asn Asp
245 250

<210> 1985

<211> 597

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(574)

<223> RXA00932

<400> 1985

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aataagggtga tgtttcaacg attaggttac ggtaggggcc atg acg cca cag aaa 115
Met Thr Pro Gln Lys
1 5

ctt cac cgt ttt gca gcc ctt tta gaa atg ggt acc tgg acc ctg ctg 163
Leu His Arg Phe Ala Ala Leu Leu Glu Met Gly Thr Trp Thr Leu Leu
10 15 20

atc atc ggc atg atc tta aaa tac agt gga gtg aca gac gcc gta acc 211
Ile Ile Gly Met Ile Leu Lys Tyr Ser Gly Val Thr Asp Ala Val Thr
25 30 35

cct att gcc ggc ggt atc cac ggc ttt ggc ttc ctc tgt ttt gca gcc 259
Pro Ile Ala Gly Gly Ile His Gly Phe Gly Phe Leu Cys Phe Ala Ala
40 45 50

atc acc atc acc gtg tgg atc aat aat aag tgg aca ttc ccg cag ggt 307
Ile Thr Ile Thr Val Trp Ile Asn Asn Lys Trp Thr Phe Pro Gln Gly
55 60 65

atc gca ggt ttg atc gtc tct gtt atc ccg tgg gct gca ttg cca ttt 355
Ile Ala Gly Leu Ile Val Ser Val Ile Pro Trp Ala Ala Leu Pro Phe
70 75 80 85

gca ttg tgg gca gac aag aag ggc ctc gtt gcc ggc gga tgg cgc ttt 403
 Ala Leu Trp Ala Asp Lys Lys Gly Leu Val Ala Gly Gly Trp Arg Phe
 90 95 100

tca gat ccg tcc gaa aag cca cac act ttc ttt gac aag atc ttg gct 451
 Ser Asp Pro Ser Glu Lys Pro His Thr Phe Phe Asp Lys Ile Leu Ala
 105 110 115

caa ttg gtc agg cac cca atc cga tcc att tta att ctg ctg gtg att 499
 Gln Leu Val Arg His Pro Ile Arg Ser Ile Leu Ile Leu Leu Val Ile
 120 125 130

atc gcc gtc gtc ttc tct atc ttg ctg gcg atg gga cca cct tat gat 547
 Ile Ala Val Val Phe Ser Ile Leu Leu Ala Met Gly Pro Pro Tyr Asp
 135 140 145

cca gat gcc atc gca aac act gtg gat taaacaacag cctccttcac 594
 Pro Asp Ala Ile Ala Asn Thr Val Asp
 150 155

atg 597

<210> 1986
 <211> 158
 <212> PRF
 <213> *Corynebacterium glutamicum*

<400> 1986
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 Thr Asp Ala Val Thr Pro Ile Ala Gly Gly Ile His Gly Phe Gly Phe
 35 40 45
 Leu Cys Phe Ala Ala Ile Thr Ile Thr Val Trp Ile Asn Asn Lys Trp
 50 55 60
 Thr Phe Pro Gln Gly Ile Ala Gly Leu Ile Val Ser Val Ile Pro Trp
 65 70 75 80
 Ala Ala Leu Pro Phe Ala Leu Trp Ala Asp Lys Lys Gly Leu Val Ala
 85 90 95
 Gly Gly Trp Arg Phe Ser Asp Pro Ser Glu Lys Pro His Thr Phe Phe
 100 105 110
 Asp Lys Ile Leu Ala Gln Leu Val Arg His Pro Ile Arg Ser Ile Leu
 115 120 125
 Ile Leu Leu Val Ile Ile Ala Val Val Phe Ser Ile Leu Leu Ala Met
 130 135 140
 Gly Pro Pro Tyr Asp Pro Asp Ala Ile Ala Asn Thr Val Asp
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<210> 1987
<211> 585
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101) .. (562)  
<223> RXA00933
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				Met	Thr	Leu	Val	Tyr	5							
ctc	ctc	atc	gct	gtc	gtt	gtc	acc	gca	act	ggt	ctg	tgg	gcg	tat	ttc	163
Leu	Leu	Ile	Ala	Val	Val	Val	Thr	Ala	Thr	Val	Leu	Trp	Ala	Tyr	Phe	
				10					15					20		
aca	gca	caa	cgc	ctc	aac	cgg	ctc	cac	atc	cgc	acc	gac	tca	gca	aga	211
Thr	Ala	Gln	Arg	Leu	Asn	Arg	Leu	His	Ile	Arg	Thr	Asp	Ser	Ala	Arg	
				25				30					35			
caa	gcc	ctg	caa	gca	gca	ctg	gat	cgc	cga	gca	gca	cta	gta	ggg	gcg	259
Gln	Ala	Leu	Gln	Ala	Ala	Leu	Asp	Arg	Arg	Ala	Ala	Leu	Val	Gly	Ala	
				40				45				50				
ttg	ttg	ccc	gat	gca	gca	gaa	gcc	tca	aaa	cgc	gct	gag	gca	att	ccc	307
Leu	Leu	Pro	Asp	Ala	Ala	Glu	Ala	Ser	Lys	Arg	Ala	Glu	Ala	Ile	Pro	
				55			60				65					
ctg	gaa	tac	tcc	cgc	ttc	tcc	caa	cgc	gcc	cgc	gcc	gaa	cga	gaa	atc	355
Leu	Glu	Tyr	Ser	Arg	Phe	Ser	Gln	Arg	Ala	Arg	Ala	Glu	Arg	Glu	Ile	
				70			75				80				85	
tct	gaa	ctc	atc	ttg	aaa	cag	ggg	aag	acc	ctt	cca	gat	tcc	atc	gtg	403
Ser	Glu	Leu	Ile	Leu	Lys	Gln	Gly	Lys	Thr	Leu	Pro	Asp	Ser	Ile	Val	
				90					95					100		
gac	gct	gcc	acc	cgc	gtg	gaa	tta	gcc	cac	cgc	ttc	tac	aac	gaa	gcc	451
Asp	Ala	Ala	Thr	Arg	Val	Glu	Leu	Ala	His	Arg	Phe	Tyr	Asn	Glu	Ala	
				105				110					115			
gtc	agt	gac	acc	cgc	gat	ctt	cga	acc	cga	ttg	atg	gtc	aga	tcc	ttc	499
Val	Ser	Asp	Thr	Arg	Asp	Leu	Arg	Thr	Arg	Leu	Met	Val	Arg	Ser	Phe	
				120			125					130				
cga	ctc	ggc	ggc	acc	gca	ccc	ttg	ccg	gag	tac	ttc	gaa	cta	ctc	gat	547
Arg	Leu	Gly	Gly	Thr	Ala	Pro	Leu	Pro	Glu	Tyr	Phe	Glu	Leu	Leu	Asp	
				135			140				145					
aca	gat	ctg	ctg	act	taa	atg	taaa	aaagc	ctc	tca						585
Thr	Asp	Leu	Leu	Thr												
150																

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<210> 1988
<211> 154
<212> PRT
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<213> *Corynebacterium glutamicum*

<400> 1988

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Met Thr Leu Val Tyr  Leu Leu Ile Ala Val Val Val Thr Ala Thr Val
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Leu Trp Ala Tyr Phe Thr Ala Gln Arg Leu Asn Arg Leu His Ile Arg
          20          25          30

Thr Asp Ser Ala Arg Gln Ala Leu Gln Ala Ala Leu Asp Arg Arg Ala
          35          40          45

Ala Leu Val Gly Ala Leu Leu Pro Asp Ala Ala Glu Ala Ser Lys Arg
 50          55          60

Ala Glu Ala Ile Pro Leu Glu Tyr Ser Arg Phe Ser Gln Arg Ala Arg
 65          70          75          80

Ala Glu Arg Glu Ile Ser Glu Leu Ile Leu Lys Gln Gly Lys Thr Leu
          85          90          95

Pro Asp Ser Ile Val Asp Ala Ala Thr Arg Val Glu Leu Ala His Arg
100          105          110

Phe Tyr Asn Glu Ala Val Ser Asp Thr Arg Asp Leu Arg Thr Arg Leu
115          120          125

Met Val Arg Ser Phe Arg Leu Gly Gly Thr Ala Pro Leu Pro Glu Tyr
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Phe Glu Leu Leu Asp Thr Asp Leu Leu Thr
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<210> 1989

<211> 519

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(496)

<223> RXA00940

<400> 1989

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                               Val Ile Leu Val Leu
                               1          5

ctg gaa gct gag tca atg cgc ggc tac cag atc atc acc acc atc agt 163
Leu Glu Ala Glu Ser Met Arg Gly Tyr Gln Ile Ile Thr Thr Ile Ser
          10          15          20

gag caa aca gaa ggt aac tgg act cca agc cca gga acc atc tat cca 211
Glu Gln Thr Glu Gly Asn Trp Thr Pro Ser Pro Gly Thr Ile Tyr Pro
          25          30          35

acc ttg tcc atg ctt gaa gat gaa ggc ctg att tcc atc tcc cat gaa 259
Thr Leu Ser Met Leu Glu Asp Glu Gly Leu Ile Ser Ile Ser His Glu

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atg ggc aga aaa atg gcg cgc ctt aca gaa gaa ggc gcg cag gaa gtg 307
Met Gly Arg Lys Met Ala Arg Leu Thr Glu Glu Gly Ala Gln Glu Val
    55          60          65

gca aag aac aag gat gcg tgg gga tca att ctg gag gct tat cgc aat 355
Ala Lys Asn Lys Asp Ala Trp Gly Ser Ile Leu Glu Ala Tyr Arg Asn
    70          75          80          85

cca gaa tcc cga gag gtg cgg gtg ttt aac att cgc tct gag ttt cac 403
Pro Glu Ser Arg Glu Val Arg Val Phe Asn Ile Arg Ser Glu Phe His
          90          95          100

aag gtc agg gaa gca gcg aaa gct gct ccc gac gat aaa gca gag caa 451
Lys Val Arg Glu Ala Ala Lys Ala Ala Pro Asp Asp Lys Ala Glu Gln
          105          110          115

ata atc gag att tta agg aga gca gca gat gac atc aag aga cta 496
Ile Ile Glu Ile Leu Arg Arg Ala Ala Asp Asp Ile Lys Arg Leu
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<210> 1990
<211> 132
<212> PRT
<213> Corynebacterium glutamicum

<400> 1990
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Gly Thr Ile Tyr Pro Thr Leu Ser Met Leu Glu Asp Glu Gly Leu Ile
          35          40          45

Ser Ile Ser His Glu Met Gly Arg Lys Met Ala Arg Leu Thr Glu Glu
          50          55          60

Gly Ala Gln Glu Val Ala Lys Asn Lys Asp Ala Trp Gly Ser Ile Leu
          65          70          75          80

Glu Ala Tyr Arg Asn Pro Glu Ser Arg Glu Val Arg Val Phe Asn Ile
          85          90          95

Arg Ser Glu Phe His Lys Val Arg Glu Ala Ala Lys Ala Ala Pro Asp
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Asp Lys Ala Glu Gln Ile Ile Glu Ile Leu Arg Arg Ala Ala Asp Asp
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Ile Lys Arg Leu
          130

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<210> 1991

<211> 771

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

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<222> (101)..(748)

<223> RXA00949

<400> 1991

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					Met	Lys	Val	Phe	Ile	
					1				5	

atc	ggc	gct	gcg	ggg	ggc	atc	ggc	aat	cga	ctt	tcc	agc	ctg	ctt	cac	163
Ile	Gly	Ala	Ala	Gly	Ile	Gly	Asn	Arg	Leu	Ser	Ser	Ser	Leu	Leu	His	
			10					15						20		

gcc	agg	gga	gat	gca	gtt	agc	ggc	atg	cac	cgc	aat	ctt	gag	cag	gcc	211
Ala	Arg	Gly	Asp	Ala	Val	Ser	Gly	Met	His	Arg	Asn	Leu	Glu	Gln	Ala	
			25					30					35			

tca	aaa	atc	aca	gac	act	ggg	gca	act	gcc	gta	ctc	ggg	gat	ctc	atc	259
Ser	Lys	Ile	Thr	Asp	Thr	Gly	Ala	Thr	Ala	Val	Leu	Gly	Asp	Leu	Ile	
		40				45						50				

cac	aac	agc	acg	gag	gag	ctt	gcg	gag	ctt	ttc	cgc	ggg	cac	gat	gcc	307
His	Asn	Ser	Thr	Glu	Glu	Leu	Ala	Glu	Leu	Phe	Arg	Gly	His	Asp	Ala	
	55					60					65					

atc	gta	ttt	tct	gca	ggc	gcc	cac	gga	aca	ggg	caa	gaa	aat	acc	acg	355
Ile	Val	Phe	Ser	Ala	Gly	Ala	His	Gly	Thr	Gly	Gln	Glu	Asn	Thr	Thr	
	70				75					80					85	

ctt	atc	gac	ggc	gcc	ggc	ctc	cgt	aaa	gcc	gcc	gac	gct	gcc	agc	gcg	403
Leu	Ile	Asp	Gly	Ala	Gly	Leu	Arg	Lys	Ala	Ala	Asp	Ala	Ala	Ser	Ala	
			90						95					100		

gcc	aac	gtt	tca	cgc	ttc	atc	ttg	gtc	tct	gcg	ttt	ccg	gaa	tcc	tcc	451
Ala	Asn	Val	Ser	Arg	Phe	Ile	Leu	Val	Ser	Ala	Phe	Pro	Glu	Ser	Ser	
		105					110						115			

cgc	ggg	gag	aac	acc	acc	gag	aac	ttt	gag	cac	tat	atg	aag	gtg	aag	499
Arg	Gly	Glu	Asn	Thr	Thr	Glu	Asn	Phe	Glu	His	Tyr	Met	Lys	Val	Lys	
		120					125					130				

aag	tcc	gcc	gat	gtc	tac	ctc	agt	cac	act	gac	cta	gac	tgg	gtt	att	547
Lys	Ser	Ala	Asp	Val	Tyr	Leu	Ser	His	Thr	Asp	Leu	Asp	Trp	Val	Ile	
	135					140					145					

gtc	cga	cca	ggc	gtg	ctt	caa	gat	gag	gca	ggg	gat	ggg	tta	gtc	act	595
Val	Arg	Pro	Gly	Val	Leu	Gln	Asp	Glu	Ala	Gly	Asp	Gly	Leu	Val	Thr	
	150				155				160					165		

gct	ggc	tta	gcg	att	aat	tac	ggc	aat	gtt	gct	cgc	gat	aat	gtc	gca	643
Ala	Gly	Leu	Ala	Ile	Asn	Tyr	Gly	Asn	Val	Ala	Arg	Asp	Asn	Val	Ala	
			170					175						180		

gcg	ttc	att	gat	gaa	gct	ctg	cat	caa	ccg	cag	ttg	tca	aag	atc	att	691
Ala	Phe	Ile	Asp	Glu	Ala	Leu	His	Gln	Pro	Gln	Leu	Ser	Lys	Ile	Ile	

185	190	195	
gtt gaa ctc acc gac ggt tca act ccg gtg gcg gaa gcc gta gaa cgc			739
Val Glu Leu Thr Asp Gly Ser Thr Pro Val Ala Glu Ala Val Glu Arg			
200	205	210	
ctc atc aag taaagacgaa aagagggaga atg			771
Leu Ile Lys			
215			
<210> 1992			
<211> 216			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 1992			
Met Lys Val Phe Ile Ile Gly Ala Ala Gly Gly Ile Gly Asn Arg Leu			
1	5	10	15
Ser Ser Leu Leu His Ala Arg Gly Asp Ala Val Ser Gly Met His Arg			
20	25	30	
Asn Leu Glu Gln Ala Ser Lys Ile Thr Asp Thr Gly Ala Thr Ala Val			
35	40	45	
Leu Gly Asp Leu Ile His Asn Ser Thr Glu Glu Leu Ala Glu Leu Phe			
50	55	60	
Arg Gly His Asp Ala Ile Val Phe Ser Ala Gly Ala His Gly Thr Gly			
65	70	75	80
Gln Glu Asn Thr Thr Leu Ile Asp Gly Ala Gly Leu Arg Lys Ala Ala			
85	90	95	
Asp Ala Ala Ser Ala Ala Asn Val Ser Arg Phe Ile Leu Val Ser Ala			
100	105	110	
Phe Pro Glu Ser Ser Arg Gly Glu Asn Thr Thr Glu Asn Phe Glu His			
115	120	125	
Tyr Met Lys Val Lys Lys Ser Ala Asp Val Tyr Leu Ser His Thr Asp			
130	135	140	
Leu Asp Trp Val Ile Val Arg Pro Gly Val Leu Gln Asp Glu Ala Gly			
145	150	155	160
Asp Gly Leu Val Thr Ala Gly Leu Ala Ile Asn Tyr Gly Asn Val Ala			
165	170	175	
Arg Asp Asn Val Ala Ala Phe Ile Asp Glu Ala Leu His Gln Pro Gln			
180	185	190	
Leu Ser Lys Ile Ile Val Glu Leu Thr Asp Gly Ser Thr Pro Val Ala			
195	200	205	
Glu Ala Val Glu Arg Leu Ile Lys			
210	215		

<210> 1993

<211> 170
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (1)..(147)
 <223> RXA00969

<400> 1993
 atc cga cag gaa gag cgc gat gat gat gca cgt ctg atc gtg gtc acc 48
 ile arg gln glu glu arg asp asp asp ala arg leu ile val val thr
 1 5 10 15
 cac tct gcg ctg gaa tct gat ctt tcc cgc acc gtt gaa ctg ctg aag 96
 his ser ala leu glu ser asp leu ser arg thr val glu leu leu lys
 20 25 30
 gct aag cct gtt gtt aag gca atc aac agt gtg atc cgc ctg gaa agg 144
 ala lys pro val val lys ala ile asn ser val ile arg leu glu arg
 35 40 45

gac taattttact gacatggcaa ttg 170
 asp

<210> 1994
 <211> 49
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 1994
 ile arg gln glu glu arg asp asp asp ala arg leu ile val val thr
 1 5 10 15
 his ser ala leu glu ser asp leu ser arg thr val glu leu leu lys
 20 25 30
 ala lys pro val val lys ala ile asn ser val ile arg leu glu arg
 35 40 45

asp

<210> 1995
 <211> 726
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(703)
 <223> RXA00973

<400> 1995
 ttgttggtgc aggccttaca gccattgcac tgagtccat gctgtcgcag ccagtagcagg 60
 ccttcacat gaccattgag atgggtgagtg tattttttcac atg aac cac tct gac 115
 met asn his ser asp

1

5

gac gat cgc atg caa aag tgg ttc cag atc cgc cgc gaa ctg ggc aaa 163
 Asp Asp Arg Met Gln Lys Trp Phe Gln Ile Arg Arg Glu Leu Gly Lys
 10 15 20

gaa att gtg aaa cag ctt caa aag gat ctg ccc gca gtc gcc tct gac 211
 Glu Ile Val Lys Gln Leu Gln Lys Asp Leu Pro Ala Val Ala Ser Asp
 25 30 35

atc ggc tcc atg gtg tat tcc tct gat caa gtt ccc ctc gga aac gcc 259
 Ile Gly Ser Met Val Tyr Ser Ser Asp Gln Val Pro Leu Gly Asn Ala
 40 45 50

acg ctc act gca tac gga gac atc ggc aac cga gtc gct tcc gct gca 307
 Thr Leu Thr Ala Tyr Gly Asp Ile Gly Asn Arg Val Ala Ser Ala Ala
 55 60 65

aca agt gcg aga tac aac gta gag gaa ctc ctg gac gca atc gaa aac 355
 Thr Ser Ala Arg Tyr Asn Val Glu Glu Leu Leu Asp Ala Ile Glu Asn
 70 75 80 85

gca cga ttt gcc atc tgg gtt cca aat tac gac aac tcc tac tac ctc 403
 Ala Arg Phe Ala Ile Trp Val Pro Asn Tyr Asp Asn Ser Tyr Tyr Leu
 90 95 100

tcc ggc gag gaa ggt gcc gac gaa ttc caa aca tac ctc atc aaa gat 451
 Ser Gly Glu Glu Gly Ala Asp Glu Phe Gln Thr Tyr Leu Ile Lys Asp
 105 110 115

gcg tca aga ttt ctt gaa tcc tcc ggg aat act cca ccc gag aac ccg 499
 Ala Ser Arg Phe Leu Glu Ser Ser Gly Asn Thr Pro Pro Glu Asn Pro
 120 125 130

cag tac agc gac tcc aaa tta acc ttt gct agc gaa cta ctc ccc ttc 547
 Gln Tyr Ser Asp Ser Lys Leu Thr Phe Ala Ser Glu Leu Leu Pro Phe
 135 140 145

tac acc gca ttt aac aac tcg acc tac cca cta ctt cat gct tgt gtg 595
 Tyr Thr Ala Phe Asn Asn Ser Ser Thr Tyr Pro Leu Leu His Ala Cys Val
 150 155 160 165

caa ggt gaa cca act gaa gta gac ctc tac ttc tac gag ctc gag cag 643
 Gln Gly Glu Pro Thr Glu Val Asp Leu Tyr Phe Tyr Glu Leu Glu Gln
 170 175 180

gca gaa ttg aag gaa aaa gag act gca cag ctc tcg agt gga tca agt 691
 Ala Glu Leu Lys Glu Lys Glu Thr Ala Gln Leu Ser Ser Gly Ser Ser
 185 190 195

ttt ggc tcc agt tagtcagaat tctcctaaag ggc 726
 Phe Gly Ser Ser
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<210> 1996

<211> 201

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1996

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Met Asn His Ser Asp Asp Asp Arg Met Gln Lys Trp Phe Gln Ile Arg
 1          5          10          15

Arg Glu Leu Gly Lys Glu Ile Val Lys Gln Leu Gln Lys Asp Leu Pro
          20          25          30

Ala Val Ala Ser Asp Ile Gly Ser Met Val Tyr Ser Ser Asp Gln Val
          35          40          45

Pro Leu Gly Asn Ala Thr Leu Thr Ala Tyr Gly Asp Ile Gly Asn Arg
          50          55          60

Val Ala Ser Ala Ala Thr Ser Ala Arg Tyr Asn Val Glu Glu Leu Leu
          65          70          75          80

Asp Ala Ile Glu Asn Ala Arg Phe Ala Ile Trp Val Pro Asn Tyr Asp
          85          90          95

Asn Ser Tyr Tyr Leu Ser Gly Glu Glu Gly Ala Asp Glu Phe Gln Thr
          100          105          110

Tyr Leu Ile Lys Asp Ala Ser Arg Phe Leu Glu Ser Ser Gly Asn Thr
          115          120          125

Pro Pro Glu Asn Pro Gln Tyr Ser Asp Ser Lys Leu Thr Phe Ala Ser
          130          135          140

Glu Leu Leu Pro Phe Tyr Thr Ala Phe Asn Asn Ser Thr Tyr Pro Leu
          145          150          155          160

Leu His Ala Cys Val Gln Gly Glu Pro Thr Glu Val Asp Leu Tyr Phe
          165          170          175

Tyr Glu Leu Glu Gln Ala Glu Leu Lys Lys Glu Thr Ala Gln Leu
          180          185          190

Ser Ser Gly Ser Ser Phe Gly Ser Ser
          195          200

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<210> 1997

<211> 738

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(715)

<223> RXA00978

<400> 1997

tcctgggtag catgggctta tgagcactga tagccaaaac cctgtaagaa aatcctgcgc 60

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acagccacat tcttgttccc aagaggtgcg attgaaagcg atg tcc agg tca ccg 115
                Met Ser Arg Ser Pro
                        1          5

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ctt act aaa ggt cta aat caa ctt gaa cac ctc gag tta gat aag tca 163
Leu Thr Lys Gly Leu Asn Gln Leu Glu His Leu Glu Leu Asp Lys Ser
                10          15          20

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cta act gcg tgg tgc tgg gca gaa gat gat cct ttg tac ctc gca ggt 211
 Leu Thr Ala Trp Ser Trp Ala Glu Asp Asp Pro Leu Tyr Leu Ala Gly
 25 30 35
 gag aac tta aac ggc agt tac ctc att gtc gca gga cga gtg cgg gtc 259
 Glu Asn Leu Asn Gly Ser Tyr Leu Ile Val Ala Gly Arg Val Arg Val
 40 45 50
 tct cgc gac acc atc gac ggg aaa gaa ctc acc gtt gat att gca acg 307
 Ser Arg Asp Thr Ile Asp Gly Lys Glu Leu Thr Val Asp Ile Ala Thr
 55 60 65
 ccc ggc gat gtt att ggt gcg ata gat aca gaa cct cag ccg gca gta 355
 Pro Gly Asp Val Ile Gly Ala Ile Asp Thr Cys Glu Pro Gln Pro Ala Val
 70 75 80 85
 gat tcc gct tgg gca ata gaa acc acc tgt gcg ctg ttt ctt cca gca 403
 Asp Ser Ala Trp Ala Ile Glu Thr Thr Cys Ala Leu Phe Leu Pro Ala
 90 95 100
 acc gcg ttg gca act gtg att gaa cag cat cca agt ttt gct ttg gcg 451
 Thr Ala Leu Ala Thr Val Ile Glu Gln His Pro Ser Phe Ala Leu Ala
 105 110 115
 atg att cgg atg cag cag caa cgt ttg gct aca gcc aga gat cat gaa 499
 Met Ile Arg Met Gln Gln Gln Arg Leu Ala Thr Ala Arg Asp His Glu
 120 125 130
 att aac ctg act acg acc aca gtt gag caa cga gta gct att gca gtg 547
 Ile Asn Leu Thr Thr Thr Val Glu Gln Arg Val Ala Ile Ala Val
 135 140 145
 aga act ctg gga cga aaa atc ggg caa cga cga ccc gat gga atc ttg 595
 Arg Thr Leu Gly Arg Lys Ile Gly Gln Arg Arg Pro Asp Gly Ile Leu
 150 155 160 165
 ctc att caa gtt cga atc cgg cgg gaa gat gtt gcg ggt tta gca ggc 643
 Leu Ile Gln Val Arg Ile Arg Arg Glu Asp Val Ala Gly Leu Ala Gly
 170 175 180
 acc acc gtg gaa tct act tct aga gtt ttg gcg cga tta cgt aaa gaa 691
 Thr Thr Val Glu Ser Thr Ser Arg Val Leu Ala Arg Leu Arg Lys Glu
 185 190 195
 ggg gtc att gat agc ggt agg gaa tgattgccgt ggtcgatgaa cgg 738
 Gly Val Ile Asp Ser Gly Arg Glu
 200 205

<210> 1998

<211> 205

<212> PRT

<213> Corynebacterium glutamicum

<400> 1998

Met Ser Arg Ser Pro Leu Thr Lys Gly Leu Asn Gln Leu Glu His Leu
 1 5 10 15

Glu Leu Asp Lys Ser Leu Thr Ala Trp Ser Trp Ala Glu Asp Asp Pro
 20 25 30

[illegible]

<213> *Corynebacterium glutamicum*

<223> RXA00986

ctacttttgat aacaccgcca cccaagccaa gccggagtga tctccgtatc ctttaaggcatg 62
Met
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act tta aaa gat aag tac gac act gaa gta gct gtt tct aat aat cag 110
Thr Leu Lys Asp Lys Tyr Asp Thr Glu Val Ala Val Ser Asn Asn Gln
5 10 15

gac aag cac caa ttt gag gtc agt tac cct gaa gat gcc gtg act gct 158
Asp Lys His Gln Phe Glu Val Ser Tyr Pro Glu Asp Ala Val Thr Ala
20 25 30

ggc ttt gct gca tac ctt gat aaa ggt gat tcg cgg atc ttc tat cac 206
Gly Phe Ala Ala Tyr Leu Asp Lys Gly Asp Ser Arg Ile Phe Tyr His
35 40 45

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acc gtt gtt ggc gat gaa ttc ggt ggc aag gga ctt gcg tca att ctt 254
Thr Val Val Gly Asp Glu Phe Gly Gly Lys Gly Leu Ala Ser Ile Leu
50 55 60 65

gtt tca gag gcg tta aaa gcc aca aaa gaa gct ggt ctt acc gtg gtt 302
Val Ser Glu Ala Leu Lys Ala Thr Lys Glu Ala Gly Leu Thr Val Val
70 75 80

ccg gta tgt ccc ttt gtt aaa gga ttc gtg gaa aag aac gca ttc gag 350
Pro Val Cys Pro Phe Val Lys Gly Phe Val Glu Lys Asn Ala Phe Glu
85 90 95

ggg tac cgc aaa cca aac cat gag gat atg gag ctg gtg aag agc cag 398
Gly Tyr Arg Lys Pro Asn His Glu Asp Met Glu Leu Val Lys Ser Gln
100 105 110

atg tagaaactac tcaacttcca gaa 424
Met

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<210> 2000
<211> 114
<212> PRT
<213> Corynebacterium glutamicum

<400> 2000
Met Thr Leu Lys Asp Lys Tyr Asp Thr Glu Val Ala Val Ser Asn Asn
1 5 10 15

Gln Asp Lys His Gln Phe Glu Val Ser Tyr Pro Glu Asp Ala Val Thr
20 25 30

Ala Gly Phe Ala Ala Tyr Leu Asp Lys Gly Asp Ser Arg Ile Phe Tyr
35 40 45

His Thr Val Val Gly Asp Glu Phe Gly Gly Lys Gly Leu Ala Ser Ile
50 55 60

Leu Val Ser Glu Ala Leu Lys Ala Thr Lys Glu Ala Gly Leu Thr Val
65 70 75 80

Val Pro Val Cys Pro Phe Val Lys Gly Phe Val Glu Lys Asn Ala Phe
85 90 95

Glu Gly Tyr Arg Lys Pro Asn His Glu Asp Met Glu Leu Val Lys Ser
100 105 110

Gln Met

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<210> 2001
<211> 588
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(565)
<223> RXA00987

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<400> 2001

cgcgggctgc ttaccacgca gcacagctaa gctttaaggc cctccggggc ettttttgc 60

tttcgacgcc tacctctctc ggaggcgat tctgtcgctc atg cct aaa tct ctg 115
Met Pro Lys Ser Leu
1 5

acc ttt gaa gac agc att aac atc gca gcg ccc atc aat cag gtc tac 163
Thr Phe Glu Asp Ser Ile Asn Ile Ala Ala Pro Ile Asn Gln Val Tyr
10 15 20

gca cta gtt tct gac atc act cga act gga gaa tgg tcg ccc gtg tgt 211
Ala Leu Val Ser Asp Ile Thr Arg Thr Gly Glu Trp Ser Pro Val Cys
25 30 35

gag aaa tgc tgg tgg gat gaa gac gaa ggc ccc gtc gtg ggt gcg cac 259
Glu Lys Cys Trp Trp Asp Glu Asp Glu Gly Pro Val Val Gly Ala His
40 45 50

ttt act ggc cga aac gtc aca cct gag cgc acc tgg gag aca cgg agc 307
Phe Thr Gly Arg Asn Val Thr Pro Glu Arg Thr Trp Glu Thr Arg Ser
55 60 65

gag gtt atc gtc gca gag cca aat cgt tgc ttt ggt tgg agc gtg act 355
Glu Val Ile Val Ala Glu Pro Asn Arg Cys Phe Gly Trp Ser Val Thr
70 75 80 85

gat gga aac gtc aag tgg att tat tcc atg gaa ccg tta gaa gaa ggc 403
Asp Gly Asn Val Lys Trp Ile Tyr Ser Met Glu Pro Leu Glu Glu Gly
90 95 100

aca gta ttg act gaa tca tgg gaa ttt acc ccc aaa ggt caa cga ttc 451
Thr Val Leu Thr Glu Ser Trp Glu Phe Thr Pro Lys Gly Gln Arg Phe
105 110 115

ttc cac gac aaa ttc ggc gac aaa tca att gaa gaa att gaa aag cga 499
Phe His Asp Lys Phe Gly Asp Lys Ser Ile Glu Glu Ile Glu Lys Arg
120 125 130

cgc ttg gca gct ata acc gga att cca gaa aca ctg gtt gcc att cag 547
Arg Leu Ala Ala Ile Thr Gly Ile Pro Glu Thr Leu Val Ala Ile Gln
135 140 145

cgc att ctg gaa gtt gag tagttctac atctggctct tca 588
Arg Ile Leu Glu Val Glu
150 155

<210> 2002

<211> 155

<212> PRT

<213> Corynebacterium glutamicum

<400> 2002

Met Pro Lys Ser Leu Thr Phe Glu Asp Ser Ile Asn Ile Ala Ala Pro
1 5 10 15

Ile Asn Gln Val Tyr Ala Leu Val Ser Asp Ile Thr Arg Thr Gly Glu
20 25 30

Trp Ser Pro Val Cys Glu Lys Cys Trp Trp Asp Glu Asp Glu Gly Pro
 35 40 45
 Val Val Gly Ala His Phe Thr Gly Arg Asn Val Thr Pro Glu Arg Thr
 50 55 60
 Trp Glu Thr Arg Ser Glu Val Ile Val Ala Glu Pro Asn Arg Cys Phe
 65 70 75 80
 Gly Trp Ser Val Thr Asp Gly Asn Val Lys Trp Ile Tyr Ser Met Glu
 85 90 95
 Pro Leu Glu Glu Gly Thr Val Leu Thr Glu Ser Trp Glu Phe Thr Pro
 100 105 110
 Lys Gly Gln Arg Phe Phe His Asp Lys Phe Gly Asp Lys Ser Ile Glu
 115 120 125
 Glu Ile Glu Lys Arg Arg Leu Ala Ala Ile Thr Gly Ile Pro Glu Thr
 130 135 140
 Leu Val Ala Ile Gln Arg Ile Leu Glu Val Glu
 145 150 155

<210> 2003

<211> 546

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(523)

<223> RXA00988

<400> 2003

tagcagaaga cacgatgta cagtcggat caggtgtgtg gatcaccggt tcaatcgtga 60

ccgccgcga tgcgcgcacg ctgtttggaa aggaacctgc atg agc aag cgt gaa 115
 Met Ser Lys Arg Glu
 1 5

gaa tca att gag tac gga cca tta ggc aaa ggc cac gat cca tta aag 163
 Glu Ser Ile Glu Tyr Gly Pro Leu Gly Lys Gly His Asp Pro Leu Lys
 10 15 20

gat ccc atg aag ggt atc cga ggt gtc atg gcc gcc acc tta gtg atg 211
 Asp Pro Met Lys Gly Ile Arg Gly Val Met Ala Gly Thr Leu Val Met
 25 30 35

gaa gca atc acc tta ggt ctt gtt ctc acc gtg att ctg cgc gtg gac 259
 Glu Ala Ile Thr Leu Gly Leu Val Leu Thr Val Ile Leu Arg Val Asp
 40 45 50

gac ggc atc tac tgg acc acc ttc aac tgg gtc tat gta tca gca gtc 307
 Asp Gly Ile Tyr Trp Thr Phe Asn Trp Val Tyr Val Ser Ala Val
 55 60 65

gcg atc gca cac ttt gtt gct gca ttt ctg caa agg ttt agt tgg tcc 355
 Ala Ile Ala His Phe Val Ala Ala Phe Leu Gln Arg Phe Ser Trp Ser
 70 75 80 85

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atc cgc atg aac atc gtg ctg cag gtt ctt gca ctt gcc ggt ttc ttt 403
Ile Pro Met Asn Ile Val Leu Gln Val Leu Ala Leu Ala Gly Phe Phe
          90                      95                      100

gtt cac ccc gcg atg ggc ttc gcc gcc atc atc ttc atc atc gcg tgg 451
Val His Pro Ala Met Gly Phe Ala Ala Ile Ile Phe Ile Ile Ala Trp
          105                      110                      115

gcg tac ctg ttc tac ctg cgc tct aat ctg att gat cgc atg aaa cgc 499
Ala Tyr Leu Phe Tyr Leu Arg Ser Asn Leu Ile Asp Arg Met Lys Arg
          120                      125                      130

ggg ctg ctt acc acg cag cac agc taagctttaa ggccctccgg ggc 546
Gly Leu Leu Thr Thr Gln His Ser
          135                      140

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<210> 2004

<211> 141

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2004

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Met Ser Lys Arg Glu Glu Ser Ile Glu Tyr Gly Pro Leu Gly Lys Gly
1          5                      10                      15

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His Asp Pro Leu Lys Asp Pro Met Lys Gly Ile Arg Gly Val Met Ala
          20                      25                      30

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Gly Thr Leu Val Met Glu Ala Ile Thr Leu Gly Leu Val Leu Thr Val
          35                      40                      45

```

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Ile Leu Arg Val Asp Asp Gly Ile Tyr Trp Thr Thr Phe Asn Trp Val
          50                      55                      60

```

```

Tyr Val Ser Ala Val Ala Ile Ala His Phe Val Ala Ala Phe Leu Gln
          65                      70                      75                      80

```

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Arg Phe Ser Trp Ser Ile Pro Met Asn Ile Val Leu Gln Val Leu Ala
          85                      90                      95

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Leu Ala Gly Phe Phe Val His Pro Ala Met Gly Phe Ala Ala Ile Ile
          100                      105                      110

```

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Phe Ile Ile Ala Trp Ala Tyr Leu Phe Tyr Leu Arg Ser Asn Leu Ile
          115                      120                      125

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Asp Arg Met Lys Arg Gly Leu Leu Thr Thr Gln His Ser
          130                      135                      140

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<210> 2005

<211> 969

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(946)

<223> RXA01005

tgggcaccgct	caacgattgg	actcacgaaa	gtctccgacga	ctagaaatag	taactgtgtt	60										
ggacactttt	cacctccgcg	tattgagcga	ggatgagtgg	atg Met	gaa Glu	cta Leu	gcc Ala	cgc Arg	115							
gcc Ala	cac His	cac His	gcg Ala	cgg Arg	gct Ala	gat Asp	tca Ser	ttc Phe	acc Thr	aaa Lys	gac Asp	cac His	ttg Leu	aag Lys	cgt Arg	163
cga Arg	caa Gln	gcg Ala	cat His	atc Ile	aag Lys	cac His	ccc Pro	gtc Val	ttc Phe	gac Asp	ttc Phe	ctc Leu	ttc Phe	gag Glu	tac Tyr	211
tac Tyr	ccc Pro	gtg Val	gcg Arg	gtc Val	gcg Ala	cac His	cta Leu	aaa Lys	acc Thr	tgg Trp	cac His	ccc Pro	ggc Gly	atc Ile	ggc Gly	259
gtg Val	ttt Phe	cta Leu	gaa Glu	ggc Gly	aca Thr	cgc Pro	cgc Pro	cat His	gcc Ala	acc Thr	atg Met	gcg Arg	gat Asp	ttt Phe	ttg Leu	307
ctt Leu	gtc Val	gac Asp	gcc Ala	tcc Ser	ctc Leu	cat His	cac His	gca Ala	gcc Ala	ggc Gly	gtc Val	cag Gln	ctt Leu	gac Asp	ctg Leu	355
gcc Ala	tcc Ser	tat Tyr	atg Met	caa Gln	cgc Arg	cgt Arg	ggg Gly	tcc Ser	tct Ser	gtg Val	cgc Arg	tac Tyr	atc Ile	cac His	gaa Glu	403
ctg Leu	ttg Leu	tcc Ser	gcc Ala	acc Thr	cgc Arg	gac Asp	aac Asn	cac Ala	gcc Ala	caa Gln	ttt Phe	gat Asp	tgt Cys	ttt Phe	ggt Gly	451
ctg Leu	cac His	gaa Glu	tgg Trp	gca Ala	atg Met	gtg Val	tac Tyr	aaa Lys	tca Ser	aac Asn	gat Asp	ctc Leu	cgc Arg	cat His	gac Asp	499
ctt Leu	ccc Pro	ctg Leu	cgc Arg	ctt Leu	acc Thr	cca Pro	tgc Ser	gaa Glu	acc Thr	gac Asp	cgt Arg	gtg Val	gtg Val	gaa Glu	agc Ser	547
cac His	aac Asn	atc Ile	aaa Lys	tgc Cys	acc Thr	cac His	ttt Phe	gat Asp	gcc Ala	tac Tyr	cga Arg	ttc Phe	ttc Phe	acc Thr	aca Thr	595
cca Pro	gcc Ala	atc Ile	ccg Pro	ttg Leu	aac Asn	ctc Leu	acg Thr	gtg Val	tta Val	acc Thr	cgc Glu	gaa Glu	gat Asp	cag Gln	cca Pro	643
cgc Arg	aac Asn	gat Asp	caa Gln	tgt Cys	ggc Gly	tgt Cys	ctg Leu	cat His	gcc Ala	acg Thr	atg Met	gat Asp	cta Leu	tac Tyr	aaa Lys	691
tgg Trp	tcc Ser	gca Ala	aag Lys	ctt Leu	ggc Gly	cct Pro	ctt Val	gtg Val	cca Pro	ggc Gly	gat Asp	ctt Leu	ttc Phe	ttg Leu	gac Asp	739
gcg Gly	ttt Leu	gaa Ala	cta Leu	gcc Gly	cgc Gly	gac Gly	acc Gly	cgc Ala	atc Thr	ttg Gly	gac Gly	atg Gly	gag Gly	gct Gly	tcg Gly	787

Ala Phe Glu Leu Ala Arg Asp Thr Arg Ile Leu Asp Met Glu Ala Ser
 215 220 225

cct tac gac gtc cgc gga tac ggc ttt ggc tac gtc ccc att gag acc 835
 Pro Tyr Asp Val Arg Gly Tyr Gly Phe Gly Tyr Val Pro Ile Glu Thr
 230 235 240 245

gcc gag ggc aaa gcc gaa tat gtc agt aga caa cgc gag ctg tct gaa 883
 Ala Glu Gly Lys Ala Glu Tyr Val Ser Arg Gln Arg Glu Leu Ser Glu
 250 255 260

cga gca aaa ccc atc cgt gac cgg ctt gtc tcc att act aaa caa gct 931
 Arg Ala Lys Pro Ile Arg Asp Arg Leu Val Ser Ile Thr Lys Gln Ala
 265 270 275

cta cag gct agt att tagaaaatta gacttgtaa tgt 969
 Leu Gln Ala Ser Ile
 280

<210> 2006

<211> 282

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2006

Met Glu Leu Ala Arg Ala His His Ala Arg Ala Asp Ser Phe Thr Lys
 1 5 10 15

Asp His Leu Lys Arg Arg Gln Ala His Ile Lys His Pro Val Phe Asp
 20 25 30

Phe Leu Phe Glu Tyr Tyr Pro Val Arg Val Ala His Leu Lys Thr Trp
 35 40 45

His Pro Gly Ile Gly Val Phe Leu Glu Gly Thr Pro Pro His Ala Thr
 50 55 60

Met Arg Asp Phe Leu Leu Val Asp Ala Ser Leu His His Ala Ala Gly
 65 70 75 80

Val Gln Leu Asp Leu Ala Ser Tyr Met Gln Arg Arg Gly Ser Ser Val
 85 90 95

Arg Tyr Ile His Glu Leu Leu Ser Ala Thr Arg Asp Asn His Ala Gln
 100 105 110

Phe Asp Cys Phe Gly Leu His Glu Trp Ala Met Val Tyr Lys Ser Asn
 115 120 125

Asp Leu Arg His Asp Leu Pro Leu Arg Leu Thr Pro Ser Glu Thr Asp
 130 135 140

Arg Val Val Glu Ser His Asn Ile Lys Cys Thr His Phe Asp Ala Tyr
 145 150 155 160

Arg Phe Phe Thr Thr Pro Ala Ile Pro Leu Asn Leu Thr Val Leu Thr
 165 170 175

Arg Glu Asp Gln Pro Arg Asn Asp Gln Cys Gly Cys Leu His Ala Thr
 180 185 190

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Met Asp Leu Tyr Lys Trp Ser Ala Lys Leu Gly Pro Leu Val Pro Gly
    195                200                205
Asp Leu Phe Leu Asp Ala Phe Glu Leu Ala Arg Asp Thr Arg Ile Leu
    210                215                220
Asp Met Glu Ala Ser Pro Tyr Asp Val Arg Gly Tyr Gly Phe Gly Tyr
    225                230                235                240
Val Pro Ile Glu Thr Ala Glu Gly Lys Ala Glu Tyr Val Ser Arg Gln
    245                250                255
Arg Glu Leu Ser Glu Arg Ala Lys Pro Ile Arg Asp Arg Leu Val Ser
    260                265                270
Ile Thr Lys Gln Ala Leu Gln Ala Ser Ile
    275                280

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<210> 2007

<211> 1830

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1807)

<223> RXA01007

<400> 2007

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tctgaaccaa tataccgcatc agtctaaaag tgtgttaagt tctggaacat aaattagctg 60
acacgtaaag taacttaaag attcactgga ggtaagccta gtg ttt aaa aag cac 115
                                Val Phe Lys Lys His
                                1                    5
aga cac ggt ctc ggc tcc ccc gaa acc aaa cca cgc tca ata acc cgc 163
Arg His Gly Leu Gly Ser Pro Glu Thr Lys Pro Arg Ser Ile Thr Arg
                                10                15                20
cgg ttt ttc acc gcg gcc gcc gct acg ctg gca gga ttg gca gtc ctg 211
Arg Phe Phe Thr Ala Ala Ala Ala Thr Leu Ala Gly Leu Ala Val Leu
                                25                30                35
tcc ggc tgc aca gca caa ccc tca caa gca gaa gac aac acg ctc act 259
Ser Gly Cys Thr Ala Gln Pro Ser Gln Ala Glu Asp Asn Thr Leu Thr
                                40                45                50
tac tta gag cca cag ttc ttc cgc acc ctg tac cca cca tca gcg ggc 307
Tyr Leu Glu Pro Gln Phe Phe Arg Thr Leu Tyr Pro Pro Ser Ala Gly
                                55                60                65
ttt tac ccc aac ggc agt gtg gtg aac aac att gca gac cgc ttg etc 355
Phe Tyr Pro Asn Gly Ser Val Val Asn Asn Ile Ala Asp Arg Leu Leu
                                70                75                80                85
tac cag gat cct gaa acc ttg gaa ctc aag ccg tgg atc gcc acc gaa 403
Tyr Gln Asp Pro Glu Thr Leu Glu Leu Lys Pro Trp Ile Ala Thr Glu
                                90                95                100

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ctc cca gaa gta aac gaa gac gcc acg gaa ttt acc ttc aac atc cgc 451
 Leu Pro Glu Val Asn Glu Asp Ala Thr Glu Phe Thr Phe Asn Ile Arg
 105 110 115

acc gat gtc acc tac tcc gat ggc acc ccg ctg acg gct gaa aac gtg 499
 Thr Asp Val Thr Tyr Ser Asp Gly Thr Pro Leu Thr Ala Glu Asn Val
 120 125 130

gtg aaa aac ttc gat ctc tat ggc ctc ggc gat caa gat cga cgc ctc 547
 Val Lys Asn Phe Asp Leu Tyr Gly Leu Gly Asp Gln Asp Arg Arg Leu
 135 140 145

acc atc tct gag cag atc acc aac tac gac cac ggc gaa gta gta gat 595
 Thr Ile Ser Glu Gln Ile Thr Asn Tyr Asp His Gly Glu Val Val Asp
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gag gac acc gtc cga ttc cac ttc tct gag cct gca cct ggt ttt gct 643
 Glu Asp Thr Val Arg Phe His Phe Ser Glu Pro Ala Pro Gly Phe Ala
 170 175 180

cag gcc acc agc tcc ttc aac gct ggc ctt tat gcc gat tcc acc ttg 691
 Gln Ala Thr Ser Ser Phe Asn Ala Gly Leu Tyr Ala Asp Ser Thr Leu
 185 190 195

gag ttc gcc aat gag gat ttc gcg cca ggc aac gcc caa aac gtc atc 739
 Glu Phe Ala Asn Glu Asp Phe Ala Pro Gly Asn Ala Gln Asn Val Ile
 200 205 210

ggc tcc ggt cct ttc gtg atc acc gat gaa acc cta ggc acc aac ctc 787
 Gly Ser Gly Pro Phe Val Ile Thr Asp Glu Thr Leu Gly Thr Asn Leu
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acc ttg act gcg cgt gag gat tac gat tgg gca cca cca tca cgc gaa 835
 Thr Leu Thr Ala Arg Glu Asp Tyr Asp Trp Ala Pro Pro Ser Arg Glu
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cat caa ggt cgc gcg aag ctt gac gcc gtc aat tat gtc ctc gcg ggt 883
 His Gln Gly Arg Ala Lys Leu Asp Ala Val Asn Tyr Val Leu Ala Gly
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 Glu Glu Ser Val Arg Ile Gly Ala Ile Val Ala Gly Gln Gly Asp Ile
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 Ala Arg Gln Ile Glu Ala Pro Val Glu Ala His Leu Lys Asp Ala Gly
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atc ccg atc atc tcc gca gcc acc aac ggt gtg aac aac agc ttc aac 1027
 Ile Pro Ile Ile Ser Ala Ala Thr Asn Gly Val Asn Asn Ser Phe Asn
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ttc cgc ttc aaa aac gag ctg ctc tca gac atc cgt gtt cgc caa gct 1075
 Phe Arg Phe Lys Asn Glu Leu Leu Ser Asp Ile Arg Val Arg Gln Ala
 310 315 320 325

ctg atc cac gcg atc gac cgc gaa aag atc atg cgt gtg ctg ttt agt 1123
 Leu Ile His Ala Ile Asp Arg Glu Lys Ile Met Arg Val Leu Phe Ser
 330 335 340

gat tcc tat ccg ctg gca act tct gtg ctt gcg caa aat gca ctg ggc 1171

Asp Ser Tyr Pro Leu Ala Thr Ser Val Leu Ala Gln Asn Ala Leu Gly
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 tac aaa gaa caa gta gat gcc tat gtc tac gac cta gac aaa gca aca 1219
 Tyr Lys Glu Gln Val Asp Ala Tyr Val Tyr Asp Leu Asp Lys Ala Thr
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 gct ctg ctt gac gaa gcc gcc tgg acc ctt gat agc gac gcc atg cgt 1267
 Ala Leu Leu Asp Glu Ala Gly Trp Thr Leu Asp Ser Asp Gly Met Arg
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 cgc aag gac ggt gaa ctt cta gag ctc acc ttc aac gaa gcc ctc cca 1315
 Arg Lys Asp Gly Glu Leu Leu Glu Leu Thr Phe Asn Glu Ala Leu Pro
 390 395 400 405
 cag cct cgt tca cgc gaa gtt gtc acc atg gtc caa gaa cag ctc ggt 1363
 Gln Pro Arg Ser Arg Glu Val Val Thr Met Val Gln Glu Gln Leu Gly
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 Asp Leu Gly Ile Lys Val Asn Leu Asn Pro Gly Asp Gln Ala Ala Gln
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 gac gct gac tcc aag gat ctc aac aag atc cag gtt cgc cac acc atg 1459
 Asp Ala Asp Ser Lys Asp Leu Asn Lys Ile Gln Val Arg His Thr Met
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 Val Gly Arg Ala Asp Tyr Asp Val Leu Lys Ser Gln Leu Tyr Ser Thr
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 Ile Gly Asp Pro His Leu Glu Glu Leu Leu Met Ala Ile Ala Ser Ser
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 Pro Arg Glu Glu Asp Arg Ala Ala Ala Ser Ala Ala Ala Gln Asp Tyr
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 Ile Thr Glu Gln Ala Tyr Val Leu Pro Leu Phe Glu Glu Pro Val Val
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 Tyr Gly Val Gln Pro Tyr Val Lys Gly Phe Ser Pro Glu Val Ile Gly
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 Ser Glu Glu Asp

<211> 569

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2008

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Gly	Leu	Ala	Val	Leu	Ser	Gly	Cys	Thr	Ala	Gln	Pro	Ser	Gln	Ala	Glu
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Asp	Asn	Thr	Leu	Thr	Tyr	Leu	Glu	Pro	Gln	Phe	Phe	Arg	Thr	Leu	Tyr
	50				55					60					
Pro	Pro	Ser	Ala	Gly	Phe	Tyr	Pro	Asn	Gly	Ser	Val	Val	Asn	Asn	Ile
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Ala	Asp	Arg	Leu	Leu	Tyr	Gln	Asp	Pro	Glu	Thr	Leu	Glu	Leu	Lys	Pro
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Trp	Ile	Ala	Thr	Glu	Leu	Pro	Glu	Val	Asn	Glu	Asp	Ala	Thr	Glu	Phe
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Thr	Phe	Asn	Ile	Arg	Thr	Asp	Val	Thr	Tyr	Ser	Asp	Gly	Thr	Pro	Leu
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Thr	Ala	Glu	Asn	Val	Val	Lys	Asn	Phe	Asp	Leu	Tyr	Gly	Leu	Gly	Asp
	130					135					140				
Gln	Asp	Arg	Arg	Leu	Thr	Ile	Ser	Glu	Gln	Ile	Thr	Asn	Tyr	Asp	His
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Gly	Glu	Val	Val	Asp	Glu	Asp	Thr	Val	Arg	Phe	His	Phe	Ser	Glu	Pro
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Ala	Pro	Gly	Phe	Ala	Gln	Ala	Thr	Ser	Ser	Phe	Asn	Ala	Gly	Leu	Tyr
			180					185					190		
Ala	Asp	Ser	Thr	Leu	Glu	Phe	Ala	Asn	Glu	Asp	Phe	Ala	Pro	Gly	Asn
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Pro	Pro	Ser	Arg	Glu	His	Gln	Gly	Arg	Ala	Lys	Leu	Asp	Ala	Val	Asn
			245					250					255		
Tyr	Val	Leu	Ala	Gly	Glu	Glu	Ser	Val	Arg	Ile	Gly	Ala	Ile	Val	Ala
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Gly	Gln	Gly	Asp	Ile	Ala	Arg	Gln	Ile	Glu	Ala	Pro	Val	Glu	Ala	His
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Asn Asn Ser Phe Asn Phe Arg Phe Lys Asn Glu Leu Leu Ser Asp Ile
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Arg Val Arg Gln Ala Leu Ile His Ala Ile Asp Arg Glu Lys Ile Met
                      325                      330                      335

Arg Val Leu Phe Ser Asp Ser Tyr Pro Leu Ala Thr Ser Val Leu Ala
                      340                      345                      350

Gln Asn Ala Leu Gly Tyr Lys Glu Gln Val Asp Ala Tyr Val Tyr Asp
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Leu Asp Lys Ala Thr Ala Leu Leu Asp Glu Ala Gly Trp Thr Leu Asp
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Ser Asp Gly Met Arg Arg Lys Asp Gly Glu Leu Leu Glu Leu Thr Phe
385                      390                      395                      400

Asn Glu Ala Leu Pro Gln Pro Arg Ser Arg Glu Val Val Thr Met Val
                      405                      410                      415

Gln Glu Gln Leu Gly Asp Leu Gly Ile Lys Val Asn Leu Asn Pro Gly
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Asp Gln Ala Ala Gln Asp Ala Asp Ser Lys Asp Leu Asn Lys Ile Gln
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Val Arg His Thr Met Val Gly Arg Ala Asp Tyr Asp Val Leu Lys Ser
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Gln Leu Tyr Ser Thr Asn Arg Asn Glu Leu Leu Asn Met Thr Val Glu
465                      470                      475                      480

Gly Glu Thr Ala Asp Ile Gly Asp Pro His Leu Glu Glu Leu Leu Met
                      485                      490                      495

Ala Ile Ala Ser Ser Pro Arg Glu Glu Asp Arg Ala Ala Ala Ser Ala
500                      505                      510

Ala Ala Gln Asp Tyr Ile Thr Glu Gln Ala Tyr Val Leu Pro Leu Phe
515                      520                      525

Glu Glu Pro Val Val Tyr Gly Val Gln Pro Tyr Val Lys Gly Phe Ser
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<210> 2009

<211> 2064

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(2041)

<400> 2009

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215 220 225	
gtc aag ccc ggc aac cct gtc gag cag gat gcc agc ctc att ccc gct	835
Val Lys Pro Gly Asn Pro Val Glu Gln Asp Ala Ser Leu Ile Pro Ala	
230 235 240 245	
ggc gaa cag gtg ctt gtc cgc ggg ctg ggc atg gga ttt ttc gat atc	883
Gly Glu Gln Val Leu Val Arg Gly Leu Gly Met Gly Phe Phe Asp Ile	
250 255 260	
atg gcg ctg acc acc atc gat cgt ggc ggc atc ttc cac gag gat ccc	931
Met Ala Leu Thr Thr Ile Asp Arg Gly Gly Ile Phe His Asp Pro	
265 270 275	
agc acc cgt tcc ggt ttg cgc tac gag gca tct ggt gag gaa cca cac	979
Ser Thr Arg Ser Gly Leu Arg Tyr Glu Ala Ser Gly Glu Glu Pro His	
280 285 290	
ttt gtt att tcc tcc ggg cgc ggc tac ccc tac ctg cct aaa tcc gat	1027
Phe Val Ile Ser Ser Gly Arg Gly Tyr Pro Tyr Leu Pro Lys Ser Asp	
295 300 305	
tac aaa tcg ctg cca cca ggg gca aag cta gcg cga ctc aag gct gtt	1075
Tyr Lys Ser Leu Pro Pro Gly Ala Lys Leu Ala Arg Leu Lys Ala Val	
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Ile Ala Ala Ile Asn Ala Gln Asn Arg Gly Val Ala Ser Ile Asn Tyr	
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gat gcg gaa gtg tgg cca gct gtt gct cgc gac gcc tac gaa gcc tat	1171
Asp Ala Glu Val Trp Pro Ala Val Ala Arg Asp Ala Tyr Glu Ala Tyr	
345 350 355	
tac gaa acc ctt gat cgc gta agc cca gaa tct atc cgg acc ggt ctg	1219
Tyr Glu Thr Leu Asp Arg Val Ser Pro Glu Ser Ile Arg Thr Gly Leu	
360 365 370	
gat aaa att gtg gaa att att gat gag gtg gac gtc gat aag ctt cct	1267
Asp Lys Ile Val Glu Ile Ile Asp Glu Val Asp Val Asp Lys Leu Pro	
375 380 385	
aaa gca ctc gcc gcg cac acc gat gac gtc ttt gac ctg cat gct tgg	1315
Lys Ala Leu Ala Ala His Thr Asp Asp Val Phe Asp Leu His Ala Trp	
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gaa ttt ccg ctc gcg gga att aat gaa agc gtc gag gcg ctg acc gca	1363
Glu Phe Pro Leu Ala Gly Ile Asn Glu Ser Val Glu Ala Leu Thr Ala	
410 415 420	
cgc atc gcg gac ggc atg gcc cgc gat att cgc cat gca gta acg gcc	1411
Arg Ile Ala Asp Gly Met Ala Arg Asp Ile Arg His Ala Val Thr Ala	
425 430 435	
tgg gac agc ccg ctg aaa tcc gcg ctg tgg tcc att tcc gcc gcg cgc	1459
Trp Asp Ser Pro Leu Lys Ser Ala Leu Trp Ser Ile Ser Ala Ala Arg	
440 445 450	
aaa ccc agc tcc atc ctg ggc gcg gaa ggc cgc ctg acc ttc gaa tcg	1507

Lys Pro Ser Ser Ile Leu Gly Ala Glu Gly Arg Leu Thr Phe Glu Ser
 455 460 465
 cgc cgc aac cgc ttc gcc gcc gtc atg cgc atc gcc cag atg gtc gcc 1555
 Arg Arg Asn Arg Phe Ala Ala Val Met Ala Ile Gly Gln Met Val Gly
 470 475 480 485
 tcc gcc cca ccg ctt ttc cgc acc cgc gaa ctt ctt gcg ctt gtc gac 1603
 Ser Gly Pro Pro Leu Phe Arg Thr Arg Glu Leu Leu Ala Leu Val Asp
 490 495 500
 gcc gcc ctc gct cac ttc gcc gcc gcc cgc ccc cgc ctc agc gtg agc 1651
 Ala Gly Leu Ala His Phe Ala Gly Ala Arg Pro Arg Leu Ser Val Ser
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 gac ggt caa tgg cag atc tcc tcg ccc acc acc gcc gat acg ccg ctg 1699
 Asp Gly Gln Trp Gln Ile Ser Ser Pro Thr Thr Asp Thr Pro Leu
 520 525 530
 aga tcg aaa gtg ctt gtc gac gcg tgg atg cac aac cca gat gtg cgt 1747
 Arg Ser Lys Val Leu Val Asp Ala Trp Met His Asn Pro Asp Val Arg
 535 540 545
 cgc aac gcc gac ccg cta gca ctg tct ttg gaa gat gcc gac cgg gta 1795
 Arg Asn Ala Asp Pro Leu Ala Leu Ser Leu Glu Asp Ala Asp Arg Val
 550 555 560 565
 cgc ccc ttc aac gac tat tcc gtc gac gga acc gct gcc ccc aca gcc 1843
 Arg Pro Phe Asn Asp Tyr Ser Val Asp Gly Thr Ala Ala Pro Thr Gly
 570 575 580
 tcc ccc gaa gtt gat ccg gca acc cga ctt ttg gtt cac ccc aac gcc 1891
 Ser Pro Glu Val Asp Pro Ala Thr Arg Leu Leu Val His Pro Asn Gly
 585 590 595
 aac ctc gat ccg cgc gtg cac ctg att gcc atc cca acc tat ggg cag 1939
 Asn Leu Asp Pro Arg Val His Leu Ile Gly Ile Pro Thr Tyr Gly Gln
 600 605 610
 ctg gcc gac acc acc atc tcg ccg atg cct gga acc aac ccg ctc atg 1987
 Leu Ala Asp Thr Thr Ile Ser Pro Met Pro Gly Thr Asn Pro Leu Met
 615 620 625
 ctg caa gaa acc gac aaa aca gcc gtt cac gtg cta aag cag ctc gcc 2035
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<210> 2010

<211> 647

<212> PRT

<213> Corynebacterium glutamicum

<400> 2010

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 Gly Ala Gly Asn Val Trp Arg Thr Asp Gln Thr Arg Thr Leu Cys Met
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 Asn Thr Leu Ala Gly Ala Val Thr Leu Phe Thr Glu Pro Gly Ser Thr
 65 70 75 80
 Val Ser Ala Pro Val Val Glu Gly Pro Leu Gln Phe Asp Trp Ile Arg
 85 90 95
 Leu Leu Arg Gly Asp Glu Asp Leu Ser Gly Ile Pro Thr Lys Ala Ile
 100 105 110
 Glu Leu Phe Arg Thr Tyr Pro Pro Ala Ala Ser Val Ala Glu Asp Phe
 115 120 125
 Lys Glu Glu Leu Ala Ala Thr Val Ile Gln Ser Asn Pro Ser Arg Ala
 130 135 140
 Leu Tyr Gly Ala Tyr Leu Arg Trp Ala Phe Asp Val Ala Leu Gln Leu
 145 150 155 160
 Leu Pro Gln Trp Val Lys Val Glu Gln His His Ala Arg Ala Ile Gly
 165 170 175
 Ile Arg Glu Asp Gly Asp Arg Asp Val Ile Thr Leu Asp Asn Ser Glu
 180 185 190
 Met Ile Ser Ala Asp Ser Thr Val Leu Ala Val Gly Trp Gln Thr Pro
 195 200 205
 Ala Pro Asn Ala Glu Glu Leu Ser Ile Ala Ala Ala Leu Glu Glu Asn
 210 215 220
 Pro Asp Leu Val Trp Val Lys Pro Gly Asn Pro Val Glu Gln Asp Ala
 225 230 235 240
 Ser Leu Ile Pro Ala Gly Glu Gln Val Leu Val Arg Gly Leu Gly Met
 245 250 255
 Gly Phe Phe Asp Ile Met Ala Leu Thr Thr Ile Asp Arg Gly Gly Ile
 260 265 270
 Phe His Glu Asp Pro Ser Thr Arg Ser Gly Leu Arg Tyr Glu Ala Ser
 275 280 285
 Gly Glu Glu Pro His Phe Val Ile Ser Ser Gly Arg Gly Tyr Pro Tyr
 290 295 300
 Leu Pro Lys Ser Asp Tyr Lys Ser Leu Pro Pro Gly Ala Lys Leu Ala
 305 310 315 320
 Arg Leu Lys Ala Val Ile Ala Ala Ile Asn Ala Gln Asn Arg Gly Val
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 Ala Ser Ile Asn Tyr Asp Ala Glu Val Trp Pro Ala Val Ala Arg Asp

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Gly	Gln	Met	Val	Gly	Ser	Gly	Pro	Pro	Leu	Phe	Arg	Thr	Arg	Glu	Leu
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<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1333)

<223> RXA01011

<400> 2011

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Asp	Met	Leu	Val	Gly	Glu	Asp	Leu	Pro	Gln	Leu	Arg	Asp	Asn	Arg	Pro	
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caa	gct	cgc	gac	aat	gca	caa	aag	agc	ttc	gaa	gct	ctg	ctc	gaa	ccg	211
Gln	Ala	Arg	Asp	Asn	Ala	Gln	Lys	Ser	Phe	Glu	Ala	Leu	Leu	Glu	Pro	
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gtc	aac	cca	gga	acc	ttc	agc	ttc	ggc	gag	cgt	tac	gcc	gtg	gcc	acc	259
Val	Asn	Pro	Gly	Thr	Phe	Ser	Phe	Gly	Glu	Arg	Tyr	Ala	Val	Ala	Thr	
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tat	gtt	gca	ggg	ttg	cac	caa	ttc	gcg	cca	gct	gta	gat	ctc	tac	caa	307
Tyr	Val	Ala	Gly	Leu	His	Gln	Phe	Ala	Pro	Ala	Val	Asp	Leu	Tyr	Gln	
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gat	ttg	ctt	ctc	gac	gac	gcc	cca	acc	acc	ctg	gca	aac	gcc	gtc	ttc	355
Asp	Leu	Leu	Leu	Asp	Asp	Ala	Pro	Thr	Thr	Leu	Ala	Asn	Ala	Val	Ser	
	70				75				80					85		

gat	gcc	atc	gac	gag	ggc	cta	tcc	gca	ggc	cca	tac	ggc	acc	tac	cgt	403
Asp	Ala	Ile	Asp	Glu	Gly	Leu	Ser	Ala	Gly	Pro	Tyr	Gly	Thr	Tyr	Arg	
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Glu	Pro	Gly	Leu	Glu	Ser	Glu	Ser	Glu	Pro	Gly	Gly	Ser	Val	Arg	Asn	
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cac	cta	cta	gtt	ttc	cac	ccc	cgt	gat	tcc	cgc	ccc	gag	gtc	ctt	ggt	547
His	Leu	Leu	Val	Phe	His	Pro	Arg	Asp	Ser	Arg	Pro	Glu	Val	Leu	Gly	
		135				140					145					

cga	ctc	tcc	ggc	gct	ggc	tgg	agc	gcg	gat	gac	acc	gtg	aca	ttg	gct	595
Arg	Leu	Ser	Gly	Ala	Gly	Trp	Ser	Ala	Asp	Asp	Thr	Val	Thr	Leu	Ala	
	150			155					160					165		

cag	ctg	gtg	tcg	ttc	ctg	gca	ttc	cag	ctg	cgt	gtt	gcc	tac	ggc	ctg	643
Gln	Leu	Val	Ser	Phe	Leu	Ala	Phe	Gln	Leu	Arg	Val	Ala	Tyr	Gly	Leu	
			170					175					180			

cgc	acc	ctc	aaa	ggg	gaa	gac	att	cag	gtg	aaa	gct	cct	cgc	ctg	agt	691
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Arg	Thr	Leu	Lys	Gly	Glu	Asp	Ile	Gln	Val	Lys	Ala	Pro	Arg	Leu	Ser	
			185					190					195			
att	cct	gaa	gcg	aag	tgg	gaa	ctg	tcc	aac	aac	ggc	ttt	gag	atc	tcc	739
Ile	Pro	Glu	Ala	Lys	Trp	Glu	Leu	Ser	Asn	Asn	Gly	Phe	Glu	Ile	Ser	
		200					205				210					
acc	tat	gaa	gaa	ctc	aac	cgc	cct	gaa	gcg	ttt	gtg	aac	cac	tct	ttg	787
Thr	Tyr	Glu	Glu	Leu	Asn	Arg	Pro	Glu	Ala	Phe	Val	Asn	His	Ser	Leu	
	215					220					225					
ggc	tgg	aag	cca	tgg	gta	cca	cca	gta	gca	aag	gca	gat	ctc	acc	gaa	835
Gly	Trp	Lys	Pro	Trp	Val	Pro	Pro	Val	Ala	Lys	Ala	Asp	Leu	Thr	Glu	
	230			235						240					245	
gaa	cag	ctg	gat	tct	ttg	atc	cag	cct	gag	cgc	gct	gat	atg	cca	tac	883
Glu	Gln	Leu	Asp	Ser	Leu	Ile	Gln	Pro	Glu	Arg	Ala	Asp	Met	Pro	Tyr	
			250					255						260		
ttc	cgt	ctc	ttg	gca	cgc	gat	cct	gca	gca	ttg	aag	gcg	cgt	acc	ctg	931
Phe	Arg	Leu	Leu	Ala	Arg	Asp	Pro	Ala	Ala	Leu	Lys	Ala	Arg	Thr	Leu	
			265					270					275			
acc	gat	ctg	gat	atc	ttc	ttc	aac	act	gac	ggc	gaa	ggc	cta	gga	cgt	979
Thr	Asp	Leu	Asp	Ile	Phe	Phe	Asn	Thr	Asp	Gly	Glu	Gly	Leu	Gly	Arg	
		280					285					290				
gca	gag	cgt	gaa	ctc	ggc	gcc	acc	gtt	act	tcc	cgc	tac	aac	ggc	tgc	1027
Ala	Glu	Arg	Glu	Leu	Gly	Ala	Thr	Val	Thr	Ser	Arg	Tyr	Asn	Gly	Cys	
	295					300					305					
gtg	tac	tgc	gca	tcc	gtg	cac	gca	gga	cgt	gct	cag	gaa	gaa	tcc	ggc	1075
Val	Tyr	Cys	Ala	Ser	Val	His	Ala	Gly	Arg	Ala	Gln	Glu	Glu	Ser	Gly	
	310			315					320						325	
cga	gct	gat	gat	gtc	aac	gca	ctg	ttg	gca	agc	atc	gac	tcc	gat	ctg	1123
Arg	Ala	Asp	Asp	Val	Asn	Ala	Leu	Leu	Ala	Ser	Ile	Asp	Ser	Asp	Leu	
				330					335					340		
ggc	tct	gac	cag	tgg	aat	gtc	atc	cgt	gac	gct	gct	cgc	gca	ctg	agc	1171
Gly	Ser	Asp	Gln	Trp	Asn	Val	Ile	Arg	Asp	Ala	Ala	Arg	Ala	Leu	Ser	
			345					350					355			
tcc	acc	cct	gct	gct	ttc	aac	cag	gga	tgc	atc	acc	aag	ctg	cgt	ggc	1219
Ser	Thr	Pro	Ala	Ala	Phe	Asn	Gln	Gly	Cys	Ile	Thr	Lys	Leu	Arg	Gly	
		360					365					370				
gtt	gga	ttc	agc	gac	ctg	cag	atc	gtg	gac	ttg	atc	aac	tct	gtg	gcg	1267
Val	Gly	Phe	Ser	Asp	Leu	Gln	Ile	Val	Asp	Leu	Ile	Asn	Ser	Val	Ala	
		375				380						385				
ttc	ttc	aac	tgg	gcg	aac	cgc	ctg	atg	ttg	tca	ctg	ggc	gaa	ccc	gaa	1315
Phe	Phe	Asn	Trp	Ala	Asn	Arg	Leu	Met	Leu	Ser	Leu	Gly	Glu	Pro	Glu	
	390				395					400					405	
gtg	cca	aag	cgt	ttc	ctg	taaaacgcat	aaccccgaaat	acc								1356
Val	Pro	Lys	Arg	Phe	Leu											
				410												

<211> 411

<212> PRT

<213> Corynebacterium glutamicum

<400> 2012

Met Ser Asp Leu Ile Asp Met Leu Val Gly Glu Asp Leu Pro Gln Leu
 1 5 10 15

Arg Asp Asn Arg Pro Gln Ala Arg Asp Asn Ala Gln Lys Ser Phe Glu
 20 25 30

Ala Leu Leu Glu Pro Val Asn Pro Gly Thr Phe Ser Phe Gly Glu Arg
 35 40 45

Tyr Ala Val Ala Thr Tyr Val Ala Gly Leu His Gln Phe Ala Pro Ala
 50 55 60

Val Asp Leu Tyr Gln Asp Leu Leu Leu Asp Asp Ala Pro Thr Thr Leu
 65 70 75 80

Ala Asn Ala Val Ser Asp Ala Ile Asp Glu Gly Leu Ser Ala Gly Pro
 85 90 95

Tyr Gly Thr Tyr Arg Glu Pro Gly Leu Glu Ser Glu Ser Glu Pro Gly
 100 105 110

Gly Ser Val Arg Asn Asp Ala Ala Lys Leu Gly Glu Arg Leu Ala Ala
 115 120 125

Ala Phe Asp Tyr Ala His Leu Leu Val Phe His Pro Arg Asp Ser Arg
 130 135 140

Pro Glu Val Leu Gly Arg Leu Ser Gly Ala Gly Trp Ser Ala Asp Asp
 145 150 155 160

Thr Val Thr Leu Ala Gln Leu Val Ser Phe Leu Ala Phe Gln Leu Arg
 165 170 175

Val Ala Tyr Gly Leu Arg Thr Leu Lys Gly Glu Asp Ile Gln Val Lys
 180 185 190

Ala Pro Arg Leu Ser Ile Pro Glu Ala Lys Trp Glu Leu Ser Asn Asn
 195 200 205

Gly Phe Glu Ile Ser Thr Tyr Glu Glu Leu Asn Arg Pro Glu Ala Phe
 210 215 220

Val Asn His Ser Leu Gly Trp Lys Pro Trp Val Pro Pro Val Ala Lys
 225 230 235 240

Ala Asp Leu Thr Glu Glu Gln Leu Asp Ser Leu Ile Gln Pro Glu Arg
 245 250 255

Ala Asp Met Pro Tyr Phe Arg Leu Leu Ala Arg Asp Pro Ala Ala Leu
 260 265 270

Lys Ala Arg Thr Leu Thr Asp Leu Asp Ile Phe Phe Asn Thr Asp Gly
 275 280 285

Glu Gly Leu Gly Arg Ala Glu Arg Glu Leu Gly Ala Thr Val Thr Ser
 290 295 300

Arg Tyr Asn Gly Cys Val Tyr Cys Ala Ser Val His Ala Gly Arg Ala
 305 310 315 320

Gln Glu Glu Ser Gly Arg Ala Asp Asp Val Asn Ala Leu Leu Ala Ser
 325 330 335

Ile Asp Ser Asp Leu Gly Ser Asp Gln Trp Asn Val Ile Arg Asp Ala
 340 345 350

Ala Arg Ala Leu Ser Ser Thr Pro Ala Ala Phe Asn Gln Gly Cys Ile
 355 360 365

Thr Lys Leu Arg Gly Val Gly Phe Ser Asp Leu Gln Ile Val Asp Leu
 370 375 380

Ile Asn Ser Val Ala Phe Phe Asn Trp Ala Asn Arg Leu Met Leu Ser
 385 390 395 400

Leu Gly Glu Pro Glu Val Pro Lys Arg Phe Leu
 405 410

<210> 2013

<211> 732

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(709)

<223> RXA01017

<400> 2013

gaaatttgag ggggcgctac ccttagaagg tgcgcaatga caccacgata gttcgcgcct 60

agtggtggatt gctagaaaac tttaagaaag aggaaataat atg gct caa aaa gta 115
 Met Ala Gln Lys Val
 1 5

acc ttc tgg ttc gat acc acc tgc cca ttc tgc tgg gtc acc tcc cgc 163
 Thr Phe Trp Phe Asp Thr Thr Cys Pro Phe Cys Trp Val Thr Ser Arg
 10 15 20

tgg att aag gaa gtc gaa caa gtc cgc gat att gaa atc cag tgg gtt 211
 Trp Ile Lys Glu Val Glu Gln Val Arg Asp Ile Glu Ile Gln Trp Val
 25 30 35

cca atg agc ctc gct gtc cta aac gaa ggc cgt gat ctc cca gag gat 259
 Pro Met Ser Leu Ala Val Leu Asn Glu Gly Arg Asp Leu Pro Glu Asp
 40 45 50

tac aag gag cgc atg aag gct gca tgg gga cca gca cgc gtt ttc gca 307
 Tyr Lys Glu Arg Met Lys Ala Ala Trp Gly Pro Ala Arg Val Phe Ala
 55 60 65

gct gtc gcc acc gac cat gct gac aag ctc ggc gac ctg tac acc gca 355
 Ala Val Ala Thr Asp His Ala Asp Lys Leu Gly Asp Leu Tyr Thr Ala
 70 75 80 85

atg ggt acc cgc atc cac aac gac ggt cgc gga cca atc gaa ggt tcc 403

Met Gly Thr Arg Ile His Asn Asp Gly Arg Gly Pro Ile Glu Gly Ser
 90 95 100

ttc aat gat gtc atc gca gag gca ctt gaa gag gtc ggc cta gac gct 451
 Phe Asn Asp Val Ile Ala Glu Ala Leu Glu Glu Val Gly Leu Asp Ala
 105 110 115

gca ctt ggt gaa gtt gca gac acc acc gaa tgg gac gac gca ctt cgc 499
 Ala Leu Gly Glu Val Ala Asp Thr Thr Glu Trp Asp Ala Leu Arg
 120 125 130

gca ttc cac cag acc gca atg gac gag gtc ggc aac gat gtc gga acc 547
 Ala Phe His Gln Thr Ala Met Asp Glu Val Gly Asn Asp Val Gly Thr
 135 140 145

cca gtg gtc aag etc ggc gac acc gct ttc ttc ggc cca gtg etc acc 595
 Pro Val Val Lys Leu Gly Asp Thr Ala Phe Phe Gly Pro Val Leu Thr
 150 155 160 165

cgc atc cca cgc ggc gag gaa gca gga gag atc ttc gac gct tcc ttc 643
 Arg Ile Pro Arg Gly Glu Glu Ala Gly Glu Ile Phe Asp Ala Ser Phe
 170 175 180

aag etc gca agc tat ccc cac ttc ttt gaa atc aag cgc agc cgc act 691
 Lys Leu Ala Ser Tyr Pro His Phe Phe Glu Ile Lys Arg Ser Arg Thr
 185 190 195

gag aac cca cag ttc gac taattaacgc tgtctctgct tat 732
 Glu Asn Pro Gln Phe Asp
 200

<210> 2014
 <211> 203
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 2014

Met Ala Gln Lys Val Thr Phe Trp Phe Asp Thr Thr Cys Pro Phe Cys
 1 5 10 15

Trp Val Thr Ser Arg Trp Ile Lys Glu Val Glu Gln Val Arg Asp Ile
 20 25 30

Glu Ile Gln Trp Val Pro Met Ser Leu Ala Val Leu Asn Glu Gly Arg
 35 40 45

Asp Leu Pro Glu Asp Tyr Lys Glu Arg Met Lys Ala Ala Trp Gly Pro
 50 55 60

Ala Arg Val Phe Ala Ala Val Ala Thr Asp His Ala Asp Lys Leu Gly
 65 70 75 80

Asp Leu Tyr Thr Ala Met Gly Thr Arg Ile His Asn Asp Gly Arg Gly
 85 90 95

Pro Ile Glu Gly Ser Phe Asn Asp Val Ile Ala Glu Ala Leu Glu Glu
 100 105 110

Val Gly Leu Asp Ala Ala Leu Gly Glu Val Ala Asp Thr Thr Glu Trp
 115 120 125

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Asp Asp Ala Leu Arg Ala Phe His Gln Thr Ala Met Asp Glu Val Gly
130                      135                      140

Asn Asp Val Gly Thr Pro Val Val Lys Leu Gly Asp Thr Ala Phe Phe
145                      150                      155                      160

Gly Pro Val Leu Thr Arg Ile Pro Arg Gly Glu Glu Ala Gly Glu Ile
165                      170                      175

Phe Asp Ala Ser Phe Lys Leu Ala Ser Tyr Pro His Phe Phe Glu Ile
180                      185                      190

Lys Arg Ser Arg Thr Glu Asn Pro Gln Phe Asp
195                      200

```

<210> 2015

<211> 622

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(622)

<223> RXA01021

<400> 2015

cgagaggctt ttttggctct aagcctttta gtcgtgcgaa cgaaatctta agcagcctcg 60

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gtgccaccga gatcgattgg tcgctgtaag gtatctgatt atg tcc agt tcc gaa 115
                               Met Ser Ser Ser Glu
                               1                      5

```

```

agc tcg cgt tcc gaa ggc tcg cag cca gca cgg tct gta cag cct gaa 163
Ser Ser Arg Ser Glu Gly Ser Gln Pro Ala Pro Ser Val Gln Pro Glu
                      10                      15                      20

```

```

cgc cgt gct gat tca acg ggg gct cct gcg gca gct tcc aag gaa gct 211
Arg Arg Ala Asp Ser Thr Gly Ala Pro Ala Ala Ala Ser Lys Glu Ala
                      25                      30                      35

```

```

tcc caa caa atg gac gct gcc gga gtt ctt gag tgg gcc agg acc gct 259
Ser Gln Gln Met Asp Ala Ala Gly Val Leu Glu Trp Ala Arg Thr Ala
                      40                      45                      50

```

```

gtc gag cag ctt tct gaa cgt cgt gca gag atc aat gca ctg aat gtc 307
Val Glu Gln Leu Ser Glu Arg Arg Ala Glu Ile Asn Ala Leu Asn Val
                      55                      60                      65

```

```

ttt cct gtt cca gat gca gac act gga tca aac atg acc tac acc atg 355
Phe Pro Val Pro Asp Ala Asp Thr Gly Ser Asn Met Thr Tyr Thr Met
                      70                      75                      80                      85

```

```

aca gct gcg ttg gat gaa gcg ctg aaa ctg ggg gag ttg ggt gat gtc 403
Thr Ala Ala Leu Asp Glu Ala Leu Lys Leu Gly Glu Leu Gly Asp Val
                      90                      95                      100

```

```

gca agg att act gag gct ttg gct gtt ggt tct gtg cgt gga gcc cga 451
Ala Arg Ile Thr Glu Ala Leu Ala Val Gly Ser Val Arg Gly Glu Ala Arg
                      105                      110                      115

```

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gga aat tct gga gta gtc ctt agt cag gtc ctt cgc gct att gct cag 499
Gly Asn Ser Gly Val Val Leu Ser Gln Val Leu Arg Ala Ile Ala Gln
    120                125                130

gca gct gct gac ggg gtt att gat ggc cac aca atc caa gaa gcg cta 547
Ala Ala Ala Asp Gly Val Ile Asp Gly His Thr Ile Gln Glu Ala Leu
    135                140                145

tcc att gct cgc tcc cta gtt gat cgc gca att aca gat cct gtg gag 595
Ser Ile Ala Arg Ser Leu Val Asp Arg Ala Ile Thr Asp Pro Val Glu
    150                155                160                165

ggc act gtt gtc act gtg ttg cgt tct 622
Gly Thr Val Val Thr Val Leu Arg Ser
    170

```

<210> 2016

<211> 174

<212> PRT

<213> Corynebacterium glutamicum

<400> 2016

```

Met Ser Ser Ser Glu Ser Ser Arg Ser Glu Gly Ser Gln Pro Ala Pro
  1                5                10                15

Ser Val Gln Pro Glu Arg Arg Ala Asp Ser Thr Gly Ala Pro Ala Ala
    20                25                30

Ala Ser Lys Glu Ala Ser Gln Gln Met Asp Ala Ala Gly Val Leu Glu
    35                40                45

Trp Ala Arg Thr Ala Val Glu Gln Leu Ser Glu Arg Arg Ala Glu Ile
    50                55                60

Asn Ala Leu Asn Val Phe Pro Val Pro Asp Ala Asp Thr Gly Ser Asn
    65                70                75                80

Met Thr Tyr Thr Met Thr Ala Ala Leu Asp Glu Ala Leu Lys Leu Gly
    85                90                95

Glu Leu Gly Asp Val Ala Arg Ile Thr Glu Ala Leu Ala Val Gly Ser
    100                105                110

Val Arg Gly Ala Arg Gly Asn Ser Gly Val Val Leu Ser Gln Val Leu
    115                120                125

Arg Ala Ile Ala Gln Ala Ala Asp Gly Val Ile Asp Gly His Thr
    130                135                140

Ile Gln Glu Ala Leu Ser Ile Ala Arg Ser Leu Val Asp Arg Ala Ile
    145                150                155                160

Thr Asp Pro Val Glu Gly Thr Val Val Thr Val Leu Arg Ser
    165                170

```

<210> 2017

<211> 612

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(589)

<223> RXA01029

<400> 2017

atgggtggtt gtcttaatta aggggtgttc gtgaacacg caaccggaga ggaggggtgaa 60

gtgtggggtt	ccttgcggcg	gtatgtccgg	gggtccttgc	atg	ctt	caa	acg	att	115
				Met	Leu	Gln	Thr	Ile	
				1				5	

tca	ttc	aag	aaa	ctt	aat	tta	tta	aca	act	ctt	aaa	aga	aaa	gga	gag	163
Ser	Phe	Lys	Lys	Leu	Asn	Leu	Leu	Thr	Thr	Leu	Lys	Arg	Lys	Gly	Glu	
				10						15				20		

ctg	gtc	atc	atg	atc	act	cgt	cac	gat	gtt	ccc	tac	atc	atc	gct	ccg	211
Leu	Val	Ile	Met	Ile	Thr	Arg	His	Asp	Val	Pro	Tyr	Ile	Ile	Ala	Pro	
			25					30					35			

cct	gtc	tac	gcg	atc	ttt	gcg	agc	ctg	atg	acc	acg	cca	cca	tgg	ttt	259
Pro	Val	Tyr	Ala	Ile	Phe	Ala	Ser	Leu	Met	Thr	Thr	Pro	Pro	Trp	Phe	
			40				45					50				

tat	cga	acc	acc	tac	acc	att	gac	ggc	ttc	gat	ttt	aag	atc	agc	tgg	307
Tyr	Arg	Thr	Thr	Tyr	Thr	Ile	Asp	Gly	Phe	Asp	Phe	Lys	Ile	Ser	Trp	
	55					60					65					

gtc	tac	acc	atc	acc	atc	tac	atc	agc	ctc	atg	atc	ctc	att	atc	ggg	355
Val	Tyr	Thr	Ile	Thr	Ile	Tyr	Ile	Ser	Leu	Met	Ile	Leu	Ile	Ile	Gly	
	70				75				80					85		

ttc	tac	caa	gcc	aat	atg	cgc	aaa	gcg	tgc	cct	tat	gag	gaa	gat	cct	403
Phe	Tyr	Gln	Ala	Asn	Met	Arg	Lys	Ala	Cys	Pro	Tyr	Glu	Glu	Asp	Pro	
			90					95						100		

ttg	gtc	gat	att	tgg	cac	aag	gtg	tgg	agc	act	gca	ctc	ttt	atc	cta	451
Leu	Val	Asp	Ile	Trp	His	Lys	Val	Trp	Ser	Thr	Ala	Leu	Phe	Ile	Leu	
			105					110					115			

cct	atc	gtt	tta	tcc	atc	gcg	gtg	tac	tca	ctg	atc	aca	cag	cgc	ggg	499
Pro	Ile	Val	Leu	Ser	Ile	Ala	Val	Tyr	Ser	Leu	Ile	Thr	Gln	Arg	Gly	
		120				125						130				

ttt	gac	tgg	tat	gtc	atg	gtg	ttt	att	ctc	cct	gta	ggc	ttg	atg	atc	547
Phe	Asp	Trp	Tyr	Val	Met	Val	Phe	Ile	Leu	Pro	Val	Gly	Leu	Met	Ile	
	135					140					145					

gct	tat	gga	ttc	ttc	aag	ccc	tgt	gat	tgc	gac	aaa	cac	cgt			589
Ala	Tyr	Gly	Phe	Phe	Lys	Pro	Cys	Asp	Cys	Asp	Lys	His	Arg			
	150				155				160							

taaggtatac	ttgtccaaga	ctt	612
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<210> 2018

<211> 163

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2018

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Met Leu Gln Thr Ile Ser Phe Lys Lys Leu Asn Leu Leu Thr Thr Leu
 1             5             10             15

Lys Arg Lys Gly Glu Leu Val Ile Met Ile Thr Arg His Asp Val Pro
      20             25             30

Tyr Ile Ile Ala Pro Pro Val Tyr Ala Ile Phe Ala Ser Leu Met Thr
      35             40             45

Thr Pro Pro Trp Phe Tyr Arg Thr Thr Tyr Thr Ile Asp Gly Phe Asp
      50             55             60

Phe Lys Ile Ser Trp Val Tyr Thr Ile Thr Ile Tyr Ile Ser Leu Met
      65             70             75             80

Ile Leu Ile Ile Gly Phe Tyr Gln Ala Asn Met Arg Lys Ala Cys Pro
      85             90             95

Tyr Glu Glu Asp Pro Leu Val Asp Ile Trp His Lys Val Trp Ser Thr
      100            105            110

Ala Leu Phe Ile Leu Pro Ile Val Leu Ser Ile Ala Val Tyr Ser Leu
      115            120            125

Ile Thr Gln Arg Gly Phe Asp Trp Tyr Val Met Val Phe Ile Leu Pro
      130            135            140

Val Gly Leu Met Ile Ala Tyr Gly Phe Phe Lys Pro Cys Asp Cys Asp
      145            150            155            160

Lys His Arg

```

<210> 2019

<211> 789

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(766)

<223> RXA01031

<400> 2019

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cagctgaact tgatcatttt gatgatctgc cagtacagcg ccaagaagat cttggcacct 60

tagttgttat ctctgctggt cacgcaagcg actctgcggc atg aaa ctg ctg caa 115
                               Met Lys Leu Leu Gln
                               1             5

tac gca ggt ggt gct gtc tat gtc gat cca gaa gat tct gcg cag tcc 163
Tyr Ala Gly Gly Ala Val Tyr Val Asp Pro Glu Asp Ser Ala Gln Ser
      10             15             20

caa gac ctg gat gcc agc act gca cgt gat gtt atc gac gct acc aac 211
Gln Asp Leu Asp Ala Ser Thr Ala Arg Asp Val Ile Asp Ala Thr Asn
      25             30             35

```

acc gcc atg acc act att acc tct cgc ccc acc atg att gtg cac ctg 259
 Thr Ala Met Thr Thr Ile Thr Ser Arg Pro Thr Met Ile Val His Leu
 40 45 50

cac aag gtg cga aaa gtc att gag att tta tgc aac cct gca ctc ggc 307
 His Lys Val Arg Lys Val Ile Glu Ile Leu Cys Asn Pro Ala Leu Gly
 55 60 65

ggg gaa cct gtc aat atc gac cag gac gag acc gga aaa cag gtg tac 355
 Gly Glu Pro Val Asn Ile Asp Gln Asp Glu Thr Gly Lys Gln Val Tyr
 70 75 80 85

aca ccc acc cca acg ctt gtc gcc tat cgc ttt atc tct gac aaa gaa 403
 Thr Pro Thr Pro Thr Leu Val Ala Tyr Arg Phe Ile Ser Asp Lys Glu
 90 95 100

atc ctg ett cat tac ctg gcg cag gcg ggt gtg cag ggt gtg gag gtt 451
 Ile Leu Leu His Thr Leu Ala Gln Ala Gly Val Gln Gly Val Glu Val
 105 110 115

ttt gac ggg tcg cct gac atg ctg agc cgt tgg aat gcg gga cgc att 499
 Phe Asp Gly Ser Pro Asp Met Leu Ser Arg Trp Asn Ala Gly Arg Ile
 120 125 130

ccg gtc tta ctt ttg cag cct gcg tct gct ggt cac ggc ttg aat ttc 547
 Pro Val Leu Leu Leu Gln Pro Ala Ser Ala Gly His Gly Leu Asn Phe
 135 140 145

cag cac ggc ggg cat cgc ttg gtg tgg tac aac ctg ccc gat aat aac 595
 Gln His Gly Gly His Arg Leu Val Trp Tyr Asn Leu Pro Asp Asn Asn
 150 155 160 165

gag cat tat atg caa gcg aat gct cgt cta cat cgc att ggt caa aag 643
 Glu His Tyr Met Gln Ala Asn Ala Arg Leu His Arg Ile Gly Gln Lys
 170 175 180

aat ccc gtg acc att cac cgc att att acc gct gat act tat gat gcg 691
 Asn Pro Val Thr Ile His Arg Ile Ile Thr Ala Asp Thr Tyr Asp Ala
 185 190 195

aat atg ccg gcg att ctg gcc ggt aaa gca aat aga cag caa cgt ctc 739
 Asn Met Pro Ala Ile Leu Ala Gly Lys Ala Asn Arg Gln Gln Arg Leu
 200 205 210

atc gac gcc gtg cgc cgt gat cca gtc taagaccggc acgatcgcac 786
 Ile Asp Ala Val Arg Arg Asp Pro Val
 215 220

cgt 789

<210> 2020

<211> 222

<212> PRT

<213> Corynebacterium glutamicum

<400> 2020

Met Lys Leu Leu Gln Tyr Ala Gly Gly Ala Val Tyr Val Asp Pro Glu
 1 5 10 15

Asp Ser Ala Gln Ser Gln Asp Leu Asp Ala Ser Thr Ala Arg Asp Val

20

25

30

Ile Asp Ala Thr Asn Thr Ala Met Thr Thr Ile Thr Ser Arg Pro Thr
35 40 45

Met Ile Val His Leu His Lys Val Arg Lys Val Ile Glu Ile Leu Cys
50 55 60

Asn Pro Ala Leu Gly Gly Glu Pro Val Asn Ile Asp Gln Asp Glu Thr
65 70 75 80

Gly Lys Gln Val Tyr Thr Pro Thr Pro Thr Leu Val Ala Tyr Arg Phe
85 90 95

Ile Ser Asp Lys Glu Ile Leu Leu His Tyr Leu Ala Gln Ala Gly Val
100 105 110

Gln Gly Val Glu Val Phe Asp Gly Ser Pro Asp Met Leu Ser Arg Trp
115 120 125

Asn Ala Gly Arg Ile Pro Val Leu Leu Leu Gln Pro Ala Ser Ala Gly
130 135 140

His Gly Leu Asn Phe Gln His Gly Gly His Arg Leu Val Trp Tyr Asn
145 150 155 160

Leu Pro Asp Asn Asn Glu His Tyr Met Gln Ala Asn Ala Arg Leu His
165 170 175

Arg Ile Gly Gln Lys Asn Pro Val Thr Ile His Arg Ile Ile Thr Ala
180 185 190

Asp Thr Tyr Asp Ala Asn Met Pro Ala Ile Leu Ala Gly Lys Ala Asn
195 200 205

Arg Gln Gln Arg Leu Ile Asp Ala Val Arg Arg Asp Pro Val
210 215 220

<210> 2021

<211> 498

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(475)

<223> RXA01032

<400> 2021

agctaatacag caccacctac aacaccacaa acacacccca atcagcatga tegtgcgcgt 60

tggtgtgtgtgt cttatccctt aagaaagtga cacctttacc atg tca gac cac gac 115
Met Ser Asp His Asp
1 5

gcc cca caa aca ccg atc ccc aag ggg ttt tgg cag cag atc gac cac 163
Ala Pro Gln Thr Pro Ile Pro Lys Gly Phe Trp Gln Gln Ile Asp His
10 15 20

caa ctc gat cgc ctc ggc acg cag cgc cca gag acc ttc gca gca ctg 211

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Gln Leu Asp Arg Leu Gly Thr Gln Arg Pro Glu Thr Phe Ala Ala Leu
      25                      30                      35

cgt gac att ttg ctt gat cct gcc tac acc gcc att gtt cat gac cgt 259
Arg Asp Ile Leu Leu Asp Pro Ala Tyr Thr Ala Ile Val His Asp Arg
      40                      45                      50

aat cgc tac ggc gtt gtc acc ttt gac acc aac tca gcc ttc ttc tca 307
Asn Arg Tyr Gly Val Val Thr Phe Asp Thr Asn Ser Ala Phe Phe Ser
      55                      60                      65

ggc tct ggc gga gac aac ggc tta gcc gac gta ctc att aac tgt gat 355
Gly Ser Gly Gly Asp Asn Gly Leu Ala Asp Val Leu Ile Asn Cys Asp
      70                      75                      80                      85

tgg cgc atg act gac tac cgc gcc gag tac tac gtc atg aca cat 403
Trp Arg Met Thr Asp Tyr Arg Ala Glu Tyr Tyr Val Met Thr His
      90                      95                      100

aaa tac acc aag gaa tcg ttt acc tat atc gag gcc gac gtg aaa cgc 451
Lys Tyr Thr Lys Glu Ser Phe Thr Tyr Ile Glu Gly Asp Val Lys Arg
      105                      110                      115

ggc gac ctc atc ccg cct aat aat taaggacaac cgccatgact cag 498
Gly Asp Leu Ile Pro Pro Asn Asn
      120                      125

<210> 2022
<211> 125
<212> PRT
<213> Corynebacterium glutamicum

<400> 2022
Met Ser Asp His Asp Ala Pro Gln Thr Pro Ile Pro Lys Gly Phe Trp
  1                      5                      10                      15

Gln Gln Ile Asp His Gln Leu Asp Arg Leu Gly Thr Gln Arg Pro Glu
  20                      25                      30

Thr Phe Ala Ala Leu Arg Asp Ile Leu Leu Asp Pro Ala Tyr Thr Ala
  35                      40                      45

Ile Val His Asp Arg Asn Arg Tyr Gly Val Val Thr Phe Asp Thr Asn
  50                      55                      60

Ser Ala Phe Phe Ser Gly Ser Gly Gly Asp Asn Gly Leu Ala Asp Val
  65                      70                      75                      80

Leu Ile Asn Cys Asp Trp Arg Met Thr Asp Tyr Arg Ala Glu Tyr Tyr
  85                      90                      95

Tyr Val Met Thr His Lys Tyr Thr Lys Glu Ser Phe Thr Tyr Ile Glu
  100                      105                      110

Gly Asp Val Lys Arg Gly Asp Leu Ile Pro Pro Asn Asn
  115                      120                      125

<210> 2023
<211> 459

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<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(436)

<223> RXA01033

<400> 2023

acgtcatgac acataaatat accaaggaat cggttaccta tatcgagggc gacgtgaaac 60

gcggcgacct catccgcct aataattaag gacaaccgcc atg act cag atc gcc 115
 Met Thr Gln Ile Ala
 1 5

atg tat ctc gca gga ccc atg aca ggt atc cct gaa tac aac tac ccc 163
 Met Tyr Leu Ala Gly Pro Met Thr Gly Ile Pro Glu Tyr Asn Tyr Pro
 10 15 20

acc ttc cat gca gcg gct aat aag ttc cgt gca gct ggc tac acc gta 211
 Thr Phe His Ala Ala Ala Asn Lys Phe Arg Ala Ala Gly Tyr Thr Val
 25 30 35

ctc tcc ccc gct gaa gac gaa tat gaa tcc cag ctc act gca cca ttg 259
 Leu Ser Pro Ala Glu Asp Glu Tyr Glu Ser Gln Leu Thr Ala Pro Leu
 40 45 50

cct gag aac gct gag cac aaa tac gac cac tac ttg cgt ctc ggt atc 307
 Pro Glu Asn Ala Glu His Lys Tyr Asp His Tyr Leu Arg Leu Gly Ile
 55 60 65

gaa aag ctg ctc aag gct gat gct gtc cac atg ctt cag gga tgg cag 355
 Glu Lys Leu Leu Lys Ala Asp Ala Val His Met Leu Gln Gly Trp Gln
 70 75 80 85

agt agc gcc ggt gcc act ctt gag cac gat att gca cag aaa ttg agg 403
 Ser Ser Ala Gly Ala Thr Leu Glu His Asp Ile Ala Gln Lys Leu Arg
 90 95 100

ctt gcc att acc tat gaa gaa cca cca gca tcc taaggcgcc cggcatagc 456
 Leu Ala Ile Thr Tyr Glu Glu Pro Pro Ala Ser
 105 110

gta 459

<210> 2024

<211> 112

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2024

Met Thr Gln Ile Ala Met Tyr Leu Ala Gly Pro Met Thr Gly Ile Pro
 1 5 10 15

Glu Tyr Asn Tyr Pro Thr Phe His Ala Ala Asn Lys Phe Arg Ala
 20 25 30

Ala Gly Tyr Thr Val Leu Ser Pro Ala Glu Asp Glu Tyr Glu Ser Gln
 35 40 45

```

Leu Thr Ala Pro Leu Pro Glu Asn Ala Glu His Lys Tyr Asp His Tyr
  50                      55                      60

Leu Arg Leu Gly Ile Glu Lys Leu Leu Lys Ala Asp Ala Val His Met
  65                      70                      75                      80

Leu Gln Gly Trp Gln Ser Ser Ala Gly Ala Thr Leu Glu His Asp Ile
                      85                      90                      95

Ala Gln Lys Leu Arg Leu Ala Ile Thr Tyr Glu Glu Pro Pro Ala Ser
  100                      105                      110

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<210> 2025

<211> 477

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(454)

<223> RXA01034

<400> 2025

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agaaagtatg tcaataactt tgacataacc taaacacaaat aaattatgta gtattatgtg 60

```

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acactaagtt attacattta ttacatgatt ggtaggact atg gac atg gcc att 115
                      Met Asp Met Ala Ile
                      1                      5

```

```

att cag tgc gtc gaa tac aca tct gat gtc tca cat gag cgc atc acc 163
Ile Gln Ser Val Glu Tyr Thr Ser Asp Val Ser His Glu Arg Ile Thr
                      10                      15                      20

```

```

aat gtc gtc tct gta ggc gtg gtc tac gag ggt aaa cag tat gta gtg 211
Asn Val Val Ser Val Gly Val Val Tyr Glu Gly Lys Gln Tyr Val Val
                      25                      30                      35

```

```

gac ctt aat ggt gac gac att gat act gag ctc gat atg atc acg ctc 259
Asp Leu Asn Gly Asp Asp Ile Asp Thr Glu Leu Asp Met Ile Thr Leu
                      40                      45                      50

```

```

aaa gaa gtc atc aag att ggt cgt gag gaa tct gca cgc cag atc cgt 307
Lys Glu Val Ile Lys Ile Gly Arg Glu Glu Ser Ala Arg Gln Ile Arg
                      55                      60                      65

```

```

cgt gga tct gta gat gca gag ctg cac cgt aag gcg cgt ttg tgg gct 355
Arg Gly Ser Val Asp Ala Glu Leu His Arg Lys Ala Arg Leu Trp Ala
  70                      75                      80                      85

```

```

att gac aat gac atg gcc gtt ggt caa cgt ggt atc gtg cca cag gaa 403
Ile Asp Asn Asp Met Ala Val Gly Gln Arg Gly Ile Val Pro Gln Glu
                      90                      95                      100

```

```

atc atc gac gcg tac aaa gag tac tgc gaa aaa gaa ggc att cct ttc 451
Ile Ile Asp Ala Tyr Lys Glu Tyr Cys Glu Lys Glu Gly Ile Pro Phe
                      105                      110                      115

```

gaa taagagccct gtggagaatt gtt
Glu

477

<210> 2026
<211> 118
<212> PRT
<213> Corynebacterium glutamicum

<400> 2026
Met Asp Met Ala Ile Ile Gln Ser Val Glu Tyr Thr Ser Asp Val Ser
1 5 10 15
His Glu Arg Ile Thr Asn Val Val Ser Val Gly Val Val Tyr Glu Gly
20 25 30
Lys Gln Tyr Val Val Asp Leu Asn Gly Asp Asp Ile Asp Thr Glu Leu
35 40 45
Asp Met Ile Thr Leu Lys Glu Val Ile Lys Ile Gly Arg Glu Glu Ser
50 55 60
Ala Arg Gln Ile Arg Arg Gly Ser Val Asp Ala Glu Leu His Arg Lys
65 70 75 80
Ala Arg Leu Trp Ala Ile Asp Asn Asp Met Ala Val Gly Gln Arg Gly
85 90 95
Ile Val Pro Gln Glu Ile Ile Asp Ala Tyr Lys Glu Tyr Cys Glu Lys
100 105 110
Glu Gly Ile Pro Phe Glu
115

<210> 2027
<211> 729
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(706)
<223> RXA01035

<400> 2027
ggcagtgatg caccgcactt gagaaaaata aatcatctca agaaacaaac taatacgtta 60
ttattgtaat ttaattagag aaaagaaagt gactttttaa gtg ctt att cgc atc 115
Val Leu Ile Arg Ile
1 5
gcc gag cat caa gcc cgg ctc cat gtc cat agc ccc tac tca aag gct 163
Ala Glu His Gln Gly Arg Leu His Val His Ser Pro Tyr Ser Lys Ala
10 15 20
ttt gcc gcc cgc gct cga aag ctc aac ggt ctc tgg tca ccc gaa acg 211
Phe Ala Ala Arg Ala Arg Lys Leu Asn Gly Leu Trp Ser Pro Glu Thr
25 30 35

aag acc tgg cat ttc agc ccc gat aaa gaa caa ccg gtg aga cgc gca 259
Lys Thr Trp His Phe Ser Pro Asp Lys Glu Gln Pro Val Arg Arg Ala
40 45 50
ctc aag gat gtc tac gcc tgg gat gaa ttc acc aca ccc gag cta tgc 307
Leu Lys Asp Val Tyr Gly Trp Asp Glu Phe Thr Thr Pro Glu Leu Cys
55 60 65
acg gtg cag ctc act gtg acc cca gag gca gtg ctc aac aaa cac aca 355
Thr Val Gln Leu Thr Val Thr Pro Glu Ala Val Leu Asn Lys His Thr
70 75 80 85
ctc acc atc gct ggt gtt aca ctt ctg agc cgt tta cgc aga aat tac 403
Leu Thr Ile Ala Gly Val Thr Leu Leu Ser Arg Leu Arg Arg Asn Tyr
90 95 100
tcg gtg tgg ttg ggt gat aat gtc cgc atc atc agt ggc aat ttc cca 451
Ser Val Trp Leu Gly Asp Asn Val Arg Ile Ile Ser Gly Asn Phe Pro
105 110 115
gaa gca gca gga tca ccc cag tac ccc ctc atc atg ggt gtg aag gct 499
Glu Ala Ala Gly Ser Pro Gln Tyr Pro Leu Ile Met Gly Val Lys Ala
120 125 130
caa ccc gtt gtt atc cat gtg cag gaa ttc cct gta gat gct gtt tcg 547
Gln Pro Val Val Ile His Val Gln Glu Phe Pro Val Asp Ala Val Ser
135 140 145
act att ccc ccg cga ttt aat cct att gtt atc act gca ccg ccg agc 595
Thr Ile Pro Pro Arg Phe Asn Pro Ile Val Ile Thr Ala Pro Pro Ser
150 155 160 165
att gat att gct gct ctt cga gct gaa cgc gaa cag ctc acc cga cgc 643
Ile Asp Ile Ala Ala Leu Arg Ala Glu Arg Glu Gln Leu Thr Arg Arg
170 175 180
atc agc gaa att gac aag aaa atc gca cgt gct gtg cat cca acc att 691
Ile Ser Glu Ile Asp Lys Lys Ile Ala Arg Ala Val His Pro Thr Ile
185 190 195
cag act gag gct gcc taataatgat gcagactctc aag 729
Gln Thr Glu Ala Ala
200

<210> 2028

<211> 202

<212> PRT

<213> Corynebacterium glutamicum

<400> 2028

Val Leu Ile Arg Ile Ala Glu His Gln Gly Arg Leu His Val His Ser
1 5 10
Pro Tyr Ser Lys Ala Phe Ala Ala Arg Ala Arg Lys Leu Asn Gly Leu
20 25 30
Trp Ser Pro Glu Thr Lys Thr Trp His Phe Ser Pro Asp Lys Glu Gln
35 40 45
Pro Val Arg Arg Ala Leu Lys Asp Val Tyr Gly Trp Asp Glu Phe Thr

50 55 60
 Thr Pro Glu Leu Cys Thr Val Gln Leu Thr Val Thr Pro Glu Ala Val
 65 70 75 80
 Leu Asn Lys His Thr Leu Thr Ile Ala Gly Val Thr Leu Leu Ser Arg
 85 90 95
 Leu Arg Arg Asn Tyr Ser Val Trp Leu Gly Asp Asn Val Arg Ile Ile
 100 105 110
 Ser Gly Asn Phe Pro Glu Ala Ala Gly Ser Pro Gln Tyr Pro Leu Ile
 115 120 125
 Met Gly Val Lys Ala Gln Pro Val Val Ile His Val Gln Glu Phe Pro
 130 135 140
 Val Asp Ala Val Ser Thr Ile Pro Pro Arg Phe Asn Pro Ile Val Ile
 145 150 155 160
 Thr Ala Pro Pro Ser Ile Asp Ile Ala Ala Leu Arg Ala Glu Arg Glu
 165 170 175
 Gln Leu Thr Arg Arg Ile Ser Glu Ile Asp Lys Lys Ile Ala Arg Ala
 180 185 190
 Val His Pro Thr Ile Gln Thr Glu Ala Ala
 195 200
 <210> 2029
 <211> 576
 <212> DNA
 <213> Corynebacterium glutamicum
 <220>
 <221> CDS
 <222> (101)..(553)
 <223> RXA01036
 <400> 2029
 ctgaggctgc ctaataatga tgcagactct caagcgga aa attccgctca tctcatgcaa 60
 tgacctcaaa gaagtgcagt tactttttct taaaggtcag atg cac aca gtc ggc 115
 Met His Thr Val Gly
 1 5
 tac aag cta gat acc gat ctt cgc aag ctc act aat acc gat gtg ctt 163
 Tyr Lys Leu Asp Thr Asp Leu Arg Lys Leu Thr Asn Thr Asp Val Leu
 10 15 20
 gat ctt att aac gcg ctc ttc ggc acc act gtg acc agc gca gat gac 211
 Asp Leu Ile Asn Ala Leu Phe Gly Thr Thr Val Thr Ser Ala Asp Asp
 25 30 35
 gaa gca gca gat ttc att gac tct gat cct cag ttt gca gtg ctc gtt 259
 Glu Ala Ala Asp Phe Ile Asp Ser Asp Pro Gln Phe Ala Val Leu Val
 40 45 50
 gag ctg gcc tac cac gac tgt gca cgc cgc gct gcc atg ggt cta tcc 307
 Glu Leu Ala Tyr His Asp Cys Ala Arg Arg Ala Ala Met Gly Leu Ser

55 60 65
 agg gta cag cag ctc atc tat gac aat gcg gct aaa tca acc tac tac 355
 Arg Val Gln Gln Leu Ile Tyr Asp Asn Ala Ala Lys Ser Thr Tyr Tyr
 70 75 80
 cgc agc gtc gca gct aga cat cgc aaa cac atc cgt gaa ctc cac gag 403
 Arg Ser Val Ala Ala Arg His Arg Lys His Ile Arg Glu Leu His Glu
 90 95 100
 caa aca cag cga gat ggt att cac ttc gac aac cgg ttg tct cgt gca 451
 Gln Thr Gln Arg Asp Gly Ile His Phe Asp Asn Pro Leu Ser Arg Ala
 105 110 115
 gtc atc aac gat ctc agc atg tcc atg aac cgt gct cga cta aac cgc 499
 Val Ile Asn Asp Leu Ser Met Ser Met Asn Arg Ala Arg Leu Asn Arg
 120 125 130
 atc gct tca tgg aaa tca gcc ggc gta cag cgc tat ctc aac ccc act 547
 Ile Ala Ser Trp Lys Ser Ala Gly Val Gln Arg Tyr Leu Asn Pro Thr
 135 140 145
 atc tct tagaaccaca cacaaccaag aaa 576
 Ile Ser
 150
 <210> 2030
 <211> 151
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 2030
 Met His Thr Val Gly Tyr Lys Leu Asp Thr Asp Leu Arg Lys Leu Thr
 1 5 10 15
 Asn Thr Asp Val Leu Asp Leu Ile Asn Ala Leu Phe Gly Thr Thr Val
 20 25 30
 Thr Ser Ala Asp Asp Glu Ala Ala Asp Phe Ile Asp Ser Asp Pro Gln
 35 40 45
 Phe Ala Val Leu Val Glu Leu Ala Tyr His Asp Cys Ala Arg Arg Ala
 50 55 60
 Ala Met Gly Leu Ser Arg Val Gln Gln Leu Ile Tyr Asp Asn Ala Ala
 65 70 75 80
 Lys Ser Thr Tyr Tyr Arg Ser Val Ala Ala Arg His Arg Lys His Ile
 85 90 95
 Arg Glu Leu His Glu Gln Thr Gln Arg Asp Gly Ile His Phe Asp Asn
 100 105 110
 Pro Leu Ser Arg Ala Val Ile Asn Asp Leu Ser Met Ser Met Asn Arg
 115 120 125
 Ala Arg Leu Asn Arg Ile Ala Ser Trp Lys Ser Ala Gly Val Gln Arg
 130 135 140
 Tyr Leu Asn Pro Thr Ile Ser

145

150

<210> 2031
 <211> 651
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(628)
 <223> RXA01037

<400> 2031
 cgactaaacc gcacgccttc atggaaatca gccgcgctac agcgcctatct caacccccact 60
 atctctttaga accacacaca accaagaagaag cagtcactac atg acc acc tca tca 115
 Met Thr Thr Ser Ser
 1 5
 ccc ctt aag tcc aaa aat tcc ctt aac ggc gcg cag acc aca ttt gtc 163
 Pro Leu Lys Ser Lys Asn Ser Leu Asn Gly Ala Gln Thr Thr Phe Val
 10 15 20
 cgc aat tgt gtt gca gac ggc cca acc gag gta aaa gcc acc att gat 211
 Arg Asn Cys Val Ala Asp Gly Pro Thr Glu Val Lys Ala Thr Ile Asp
 25 30 35
 gca cgt ggc ggt atc gaa cag ctc cgt gac aat gag att tca cag ctc 259
 Ala Arg Gly Ile Glu Gln Leu Arg Asp Asn Glu Ile Ser Gln Leu
 40 45 50
 ccc gac aag ctg tgg ttc aat agc gca acc tcc gca tcc aat gac gag 307
 Pro Asp Lys Leu Trp Phe Asn Ser Ala Thr Ser Ala Ser Asn Asp Glu
 55 60 65
 ttc acc acc gat aac atc cga ctt ggg ttg ctc tac aac atg gca ctg 355
 Phe Thr Thr Asp Asn Ile Arg Leu Gly Leu Tyr Asn Met Ala Leu
 70 75 80 85
 aat aag gca tcg gct cat cgc tat gag ctt gct gcc cgc tgg tac gcc 403
 Asn Lys Ala Ser Ala His Arg Tyr Glu Leu Ala Ala Arg Trp Tyr Ala
 90 95 100
 att gtt agc cct cag cca tcg caa gaa gct agc cac aag cgc atc gcg 451
 Ile Val Ser Pro Gln Pro Ser Gln Glu Ala Ser His Lys Arg Ile Ala
 105 110 115
 tcc tgg cac ctt acc cag ctg cac gca ctg gtg acc cta tct cgc acc 499
 Ser Trp His Leu Thr Gln Leu His Ala Leu Val Thr Leu Ser Arg Thr
 120 125 130
 cta ggg gtc atc att cct ggt gat gag atc gac gct cta gcg cag tct 547
 Leu Gly Val Ile Ile Pro Gly Asp Glu Ile Asp Ala Leu Ala Gln Ser
 135 140 145
 atg gag aat gct cgt caa gtt ggc acc gag aat tgg tcc act gtc acc 595
 Met Glu Asn Ala Arg Gln Val Gly Thr Glu Asn Trp Ser Thr Val Thr
 150 155 160 165
 atg cgc acc tac gtg acc aac cgc aag gca tcc taatgaactcg cgatatatttc 648

Met Arg Thr Tyr Val Thr Asn Arg Lys Ala Ser
170 175

cac

651

<210> 2032

<211> 176

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2032

Met Thr Thr Ser Ser Pro Leu Lys Ser Lys Asn Ser Leu Asn Gly Ala
1 5 10 15

Gln Thr Thr Phe Val Arg Asn Cys Val Ala Asp Gly Pro Thr Glu Val
20 25 30

Lys Ala Thr Ile Asp Ala Arg Gly Gly Ile Glu Gln Leu Arg Asp Asn
35 40 45

Glu Ile Ser Gln Leu Pro Asp Lys Leu Trp Phe Asn Ser Ala Thr Ser
50 55 60

Ala Ser Asn Asp Glu Phe Thr Thr Asp Asn Ile Arg Leu Gly Leu Leu
65 70 75 80

Tyr Asn Met Ala Leu Asn Lys Ala Ser Ala His Arg Tyr Glu Leu Ala
85 90 95

Ala Arg Trp Tyr Ala Ile Val Ser Pro Gln Pro Ser Gln Glu Ala Ser
100 105 110

His Lys Arg Ile Ala Ser Trp His Leu Thr Gln Leu His Ala Leu Val
115 120 125

Thr Leu Ser Arg Thr Leu Gly Val Ile Ile Pro Gly Asp Glu Ile Asp
130 135 140

Ala Leu Ala Gln Ser Met Glu Asn Ala Arg Gln Val Gly Thr Glu Asn
145 150 155 160

Trp Ser Thr Val Thr Met Arg Thr Tyr Val Thr Asn Arg Lys Ala Ser
165 170 175

<210> 2033

<211> 870

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(847)

<223> RXA01038

<400> 2033

acgctctagc gcagtcctatg gagaatgctc gtcaagttgg caccgagaat tgggtccactg 60

tcaccatgcg cacctacgtg accaaccgca aggcataccta atg act cgc gat att	115
Met Thr Arg Asp Ile	
1 5	
ttc cac gag gct gca aaa ctc atc gca cac ctg ggg tgg agg gac gct	163
Phe His Glu Ala Ala Lys Leu Ile Ala His Leu Gly Trp Arg Asp Ala	
10 15 20	
ttt cca gca cta cag cgc act gac cca gcg cca aca cat gct gtg ccg	211
Phe Pro Ala Leu Gln Arg Thr Asp Pro Ala Pro Thr His Ala Val Pro	
25 30 35	
atc agg gcc ttt gat ctc aag gcg ggc gcc gtc atc acc gat gaa aat	259
Ile Arg Ala Phe Asp Leu Lys Ala Gly Ala Val Ile Thr Asp Glu Asn	
40 45 50	
cga agc aat gct tat atc tat gac acc ctt gtc atc acg cag cca tat	307
Arg Ser Asn Ala Tyr Ile Tyr Asp Thr Leu Val Ile Thr Gln Pro Tyr	
55 60 65	
aag cac gag tta cct cat caa aac acc cac cct ttt gag tgg gcc ctg	355
Lys His Glu Leu Pro His Gln Asn Thr His Pro Phe Glu Trp Ala Leu	
70 75 80 85	
gaa caa att gcc acg ctt gat ccg gcg ttc tcg atc aag ctc gat cgc	403
Glu Gln Ile Ala Thr Leu Asp Pro Ala Phe Ser Ile Lys Leu Asp Arg	
90 95 100	
tca gtg acc gtc cct gaa att gga ctc tac gcc cgc aca ctg cat gac	451
Ser Val Thr Val Pro Glu Ile Gly Leu Tyr Ala Arg Thr Leu His Asp	
105 110 115	
ctt aat act cgg cat caa gac ttc ttg gca cag cgc aac gcc atg ttg	499
Leu Asn Thr Arg His Gln Asp Phe Leu Ala Gln Arg Asn Ala Met Leu	
120 125 130	
ctt gtt gtt gcc cgt cgt ggt gtt gat cca aaa aat atc gca gac gta	547
Leu Val Val Ala Arg Arg Gly Val Asp Pro Lys Asn Ile Ala Asp Val	
135 140 145	
ctt ggt tta acc acc aat cag ata cat cgg att ctc agt gct act ccg	595
Leu Gly Leu Thr Thr Asn Gln Ile His Arg Ile Leu Ser Ala Thr Pro	
150 155 160 165	
gct gat tcc cct act gat tta ggc gtt aac ccc gcc aca aca atg ggt	643
Ala Asp Ser Pro Thr Asp Leu Gly Val Asn Pro Ala Thr Thr Met Gly	
170 175 180	
gat gta gtg agg ttt atc aag aaa cgt cgc acc act atg caa cta cgc	691
Asp Val Val Arg Phe Ile Lys Lys Arg Arg Thr Thr Met Gln Leu Arg	
185 190 195	
ggc acc gct gtc cgt gca ctg ctc tat cac ggc ctt acg ccg gca gtc	739
Gly Thr Ala Val Arg Ala Leu Leu Tyr His Gly Leu Thr Pro Ala Val	
200 205 210	
atc tcc cga cta agc ggc atg tcg cgt gcg ggt gtc atc aac gca gcc	787
Ile Ser Arg Leu Ser Gly Met Ser Arg Ala Gly Val Ile Asn Ala Ala	
215 220 225	

aag gca ttc ccc acc acc atc aac cac aag gtc aag aaa aga aag cag 835
 Lys Ala Phe Pro Thr Thr Ile Asn His Lys Val Lys Lys Arg Lys Gln
 230 235 240 245

cac ttc cat gtc taatctcggc acatactatg cag 870
 His Phe His Val

<210> 2034

<211> 249

<212> PRT

<213> Corynebacterium glutamicum

<400> 2034

Met Thr Arg Asp Ile Phe His Glu Ala Ala Lys Leu Ile Ala His Leu
 1 5 10 15

Gly Trp Arg Asp Ala Phe Pro Ala Leu Gln Arg Thr Asp Pro Ala Pro
 20 25 30

Thr His Ala Val Pro Ile Arg Ala Phe Asp Leu Lys Ala Gly Ala Val
 35 40 45

Ile Thr Asp Glu Asn Arg Ser Asn Ala Tyr Ile Tyr Asp Thr Leu Val
 50 55 60

Ile Thr Gln Pro Tyr Lys His Glu Leu Pro His Gln Asn Thr His Pro
 65 70 75 80

Phe Glu Trp Ala Leu Glu Gln Ile Ala Thr Leu Asp Pro Ala Phe Ser
 85 90 95

Ile Lys Leu Asp Arg Ser Val Thr Val Pro Glu Ile Gly Leu Tyr Ala
 100 105 110

Arg Thr Leu His Asp Leu Asn Thr Arg His Gln Asp Phe Leu Ala Gln
 115 120 125

Arg Asn Ala Met Leu Leu Val Val Ala Arg Arg Gly Val Asp Pro Lys
 130 135 140

Asn Ile Ala Asp Val Leu Gly Leu Thr Thr Asn Gln Ile His Arg Ile
 145 150 155 160

Leu Ser Ala Thr Pro Ala Asp Ser Pro Thr Asp Leu Gly Val Asn Pro
 165 170 175

Ala Thr Thr Met Gly Asp Val Val Arg Phe Ile Lys Lys Arg Thr Thr
 180 185 190

Thr Met Gln Leu Arg Gly Thr Ala Val Arg Ala Leu Leu Tyr His Gly
 195 200 205

Leu Thr Pro Ala Val Ile Ser Arg Leu Ser Gly Met Ser Arg Ala Gly
 210 215 220

Val Ile Asn Ala Ala Lys Ala Phe Pro Thr Thr Ile Asn His Lys Val
 225 230 235 240

Lys Lys Arg Lys Gln His Phe His Val

245

<210> 2035

<211> 699

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(676)

<223> RXA01039

<400> 2035

aaacctatat gttaatagta acagaaatta ataagatact agagttaaatt ttgtagtatc 60

cagggaacat taaacgggta aaggtaaagg acaaacgaac atg gcg att aaa ggc 115
 Met Ala Ile Lys Gly
 1 5

gca atg ccg aaa aat cga gta cca ggt gtg gca gca ggt gcg ttt att 163
 Ala Met Pro Lys Asn Arg Val Pro Gly Val Ala Ala Gly Ala Phe Ile
 10 15 20

gct gct gcc gtt att gca ggt gga tca gcc gtg acc ttt ctc gcc caa 211
 Ala Ala Ala Val Ile Ala Gly Gly Ser Gly Val Thr Phe Leu Ala Gln
 25 30 35

ggc ggt ggt gat gtc aat aca gtg gcc gtc gtc gag cca cag gac gag 259
 Gly Gly Gly Asp Val Asn Thr Val Ala Val Val Glu Pro Gln Asp Glu
 40 45 50

gta aaa aat cag gtc gtg aca gaa acc gaa att gtc acg aag gtt cac 307
 Val Lys Asn Gln Val Val Thr Glu Thr Glu Ile Val Thr Lys Val His
 55 60 65

gat cct tct tca tct gac gcc agt gat gct gac agc aac aca ggc acc 355
 Asp Pro Ser Ser Ser Asp Ala Ser Asp Ala Ser Asn Thr Gly Thr
 70 75 80 85

gcc gaa ggc gca gac tca gat cac aaa gaa ccc cgt gag cac gac agt 403
 Ala Glu Gly Ala Asp Ser Asp His Lys Glu Pro Arg Glu His Asp Ser
 90 95 100

gct caa gag cca acg gct ccg acc gac ccc acc ttg acc att acc ggc 451
 Ala Gln Glu Pro Thr Ala Pro Thr Asp Pro Thr Leu Thr Ile Thr Gly
 105 110 115

aac ggt gac aca cca gta tca gca ctt gat gct gtc gca gga cct gcc 499
 Asn Gly Asp Thr Pro Val Ser Ala Leu Asp Ala Val Ala Gly Pro Ala
 120 125 130

cgt cca ggt acg gtg cac gtc att gag aat ggc gaa acc ttg tcc tct 547
 Arg Pro Gly Thr Val His Val Ile Glu Asn Gly Glu Thr Leu Ser Ser
 135 140 145

att tct cag gac agt ggt gtg ccg gtt ggg ttg atc att gat cgc aac 595
 Ile Ser Gln Asp Ser Gly Val Pro Val Gly Leu Ile Ile Asp Arg Asn
 150 155 160 165

aag ctt gtt gat cca gac ctg atc tat gca ggc acg cca ttg gcg att 643

Lys Leu Val Asp Pro Asp Leu Ile Tyr Ala Gly Thr Pro Leu Ala Ile
 170 175 180

ccg act gag cag gaa ctt gct gct gcg ata cag taatgtagtg gtagagggtt 696
 Pro Thr Glu Gln Glu Leu Ala Ala Ala Ile Gln
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aaa

699

<210> 2036

<211> 192

<212> PRT

<213> Corynebacterium glutamicum

<400> 2036

Met Ala Ile Lys Gly Ala Met Pro Lys Asn Arg Val Pro Gly Val Ala
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 20 25 30

Thr Phe Leu Ala Gln Gly Gly Gly Asp Val Asn Thr Val Ala Val Val
 35 40 45

Glu Pro Gln Asp Glu Val Lys Asn Gln Val Val Thr Glu Thr Glu Ile
 50 55 60

Val Thr Lys Val His Asp Pro Ser Ser Ser Asp Ala Ser Asp Ala Asp
 65 70 75 80

Ser Asn Thr Gly Thr Ala Glu Gly Ala Asp Ser Asp His Lys Glu Pro
 85 90 95

Arg Glu His Asp Ser Ala Gln Glu Pro Thr Ala Pro Thr Asp Pro Thr
 100 105 110

Leu Thr Ile Thr Gly Asn Gly Asp Thr Pro Val Ser Ala Leu Asp Ala
 115 120 125

Val Ala Gly Pro Ala Arg Pro Gly Thr Val His Val Ile Glu Asn Gly
 130 135 140

Glu Thr Leu Ser Ser Ile Ser Gln Asp Ser Gly Val Pro Val Gly Leu
 145 150 155 160

Ile Ile Asp Arg Asn Lys Leu Val Asp Pro Asp Leu Ile Tyr Ala Gly
 165 170 175

Thr Pro Leu Ala Ile Pro Thr Glu Gln Glu Leu Ala Ala Ala Ile Gln
 180 185 190

<210> 2037

<211> 1026

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1003)

<223> RXA01040

<400> 2037

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agaaatcact acaccagttt ctcgaaaggg tttttctctc atg acc tac cca gtt 115
 Met Thr Tyr Pro Val
 1 5

acc cct caa cct gtg cag cca gca cca gtc gcc gaa aag atc aag gca 163
 Thr Pro Gln Pro Val Gln Pro Ala Pro Val Ala Glu Lys Ile Lys Ala
 10 15 20

tca agc ctc aaa gaa ggc act cag gta ttt atc aaa ggt cgg gtt aat 211
 Ser Ser Leu Lys Glu Gly Thr Gln Val Phe Ile Lys Gly Arg Val Asn
 25 30 35

tac tcc cgc atc gca agc ttt att act ggt acc gag cgc gaa aac cgt 259
 Tyr Ser Arg Ile Ala Ser Phe Ile Thr Gly Thr Glu Arg Glu Asn Arg
 40 45 50

aat cgc gac agg ctt cac cca atc gaa ttc gac tac acc tcc ctg act 307
 Asn Arg Asp Arg Leu His Pro Ile Glu Phe Asp Tyr Thr Ser Leu Thr
 55 60 65

ttg agc cac cct gaa atc atc tac ggc aac ccg caa caa aag acc aat 355
 Leu Ser His Pro Glu Ile Ile Tyr Gly Asn Pro Gln Gln Lys Thr Asn
 70 75 80 85

gaa gaa ctc ttc ctt gag cag cga atc ttt gtc ggc aag aag cgt cct 403
 Glu Glu Leu Phe Leu Glu Gln Arg Ile Phe Val Gly Lys Lys Arg Pro
 90 95 100

gaa gag ggt cca aaa ttc tcc att gac aac aag agc aac cgt cta cca 451
 Glu Glu Gly Pro Lys Phe Ser Ile Asp Asn Lys Ser Asn Arg Leu Pro
 105 110 115

cag gtt tgg gtg cca tcc acc aat gct gat ggt act tat gag cag ctt 499
 Gln Val Trp Val Pro Ser Thr Asn Ala Asp Gly Thr Tyr Glu Gln Leu
 120 125 130

gaa ggt ctc gaa ggt gag ctc gac gca ggg ctc aac gtc att att ctc 547
 Glu Gly Leu Glu Gly Leu Asp Ala Gly Leu Asn Val Ile Ile Leu
 135 140 145

atc gag ttc tat aag cca cgt aca cag gtt aat cgc ggc tcc cgc ctc 595
 Ile Glu Phe Tyr Lys Pro Arg Thr Gln Val Asn Arg Gly Ser Arg Leu
 150 155 160 165

aac gcc gtg ttc ctg cag gag ccc att cgt tac tac acc cct ggt tac 643
 Asn Ala Val Phe Leu Gln Glu Pro Ile Arg Tyr Thr Pro Gly Tyr
 170 175 180

aat gca gat aag ctc gct gcc ctc gga atc gta ctt aac gca ccg cca 691
 Asn Ala Asp Lys Leu Ala Ala Leu Gly Ile Val Leu Asn Ala Pro Pro
 185 190 195

aag gac act att cag ctc gtt cct aat gag gtc gct gca gga caa gac 739

Lys Asp Thr Ile Gln Leu Val Pro Asn Glu Val Ala Ala Gly Gln Asp
 200 205 210
 cag tcc acc acc gat gca tcc ggt ctc ccg ctt cca ggc cag gga tat 787
 Gln Ser Thr Thr Asp Ala Ser Gly Leu Pro Leu Pro Gly Gln Gly Tyr
 215 220 225
 agc gca cct gat cag cca tat cag gcg cag cct cag tat cag cag gca 835
 Ser Ala Pro Asp Gln Pro Tyr Gln Ala Gln Pro Gln Tyr Gln Gln Ala
 230 235 240 245
 acc cca gcg gct gca cct cag cag tac cag gcc cca cag ccc cag tac 883
 Thr Pro Ala Ala Ala Pro Gln Gln Tyr Gln Ala Pro Gln Pro Gln Tyr
 250 255 260
 cag cag tca gct cca cag gca caa cct gca ccg gca cca gtt gcg cag 931
 Gln Gln Ser Ala Pro Gln Ala Gln Pro Ala Pro Ala Pro Val Ala Gln
 265 270 275
 ttc cag cag gca agc gcc tca ggc acc tgc tca gcc agc aca gca gca 979
 Phe Gln Gln Ala Ser Ala Ser Gly Thr Cys Ser Ala Ser Thr Ala Ala
 280 285 290
 gta tca ggc acc act tcc tgc cgg taatcctctt gcagcaggtc agc 1026
 Val Ser Gly Thr Thr Ser Cys Arg
 295 300
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 <211> 301
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 2038
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 20 25 30
 Lys Gly Arg Val Asn Tyr Ser Arg Ile Ala Ser Phe Ile Thr Gly Thr
 35 40 45
 Glu Arg Glu Asn Arg Asn Arg Asp Arg Leu His Pro Ile Glu Phe Asp
 50 55 60
 Tyr Thr Ser Leu Thr Leu Ser His Pro Glu Ile Ile Tyr Gly Asn Pro
 65 70 75 80
 Gln Gln Lys Thr Asn Glu Glu Leu Phe Leu Glu Gln Arg Ile Phe Val
 85 90 95
 Gly Lys Lys Arg Pro Glu Glu Gly Pro Lys Phe Ser Ile Asp Asn Lys
 100 105 110
 Ser Asn Arg Leu Pro Gln Val Trp Val Pro Ser Thr Asn Ala Asp Gly
 115 120 125
 Thr Tyr Glu Gln Leu Glu Gly Leu Glu Gly Glu Leu Asp Ala Gly Leu
 130 135 140

Asn Val Ile Ile Leu Ile Glu Phe Tyr Lys Pro Arg Thr Gln Val Asn
145 150 155 160

Arg Gly Ser Arg Leu Asn Ala Val Phe Leu Gln Glu Pro Ile Arg Tyr
165 170 175

Tyr Thr Pro Gly Tyr Asn Ala Asp Lys Leu Ala Ala Leu Gly Ile Val
180 185 190

Leu Asn Ala Pro Pro Lys Asp Thr Ile Gln Leu Val Pro Asn Glu Val
195 200 205

Ala Ala Gly Gln Asp Gln Ser Thr Thr Asp Ala Ser Gly Leu Pro Leu
210 215 220

Pro Gly Gln Gly Tyr Ser Ala Pro Asp Gln Pro Tyr Gln Ala Gln Pro
225 230 235 240

Gln Tyr Gln Gln Ala Thr Pro Ala Ala Ala Pro Gln Gln Tyr Gln Ala
245 250 255

Pro Gln Pro Gln Tyr Gln Gln Ser Ala Pro Gln Ala Gln Pro Ala Pro
260 265 270

Ala Pro Val Ala Gln Phe Gln Gln Ala Ser Ala Ser Gly Thr Cys Ser
275 280 285

Ala Ser Thr Ala Ala Val Ser Gly Thr Thr Ser Cys Arg
290 295 300

<210> 2039

<211> 276

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(253)

<223> RXA01041

<400> 2039

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accacaagcc ggttctgcac ttaccgatgc tccgggtgct gtg cca cag gca cca 115
Val Pro Gln Ala Pro
1 5

gca gtt cag gct gct ccc gct gta gct cag gcg cct gtc gcg cca gta 163
Ala Val Gln Ala Ala Pro Ala Val Ala Gln Ala Pro Val Ala Pro Val
10 15 20

gtt gat atg acc gag cca gca tcc cca tgg gat ctt cca gct gca cct 211
Val Asp Met Thr Glu Pro Ala Ser Pro Trp Asp Leu Pro Ala Ala Pro
25 30 35

agt cag cca gcg cag cca gct cag ggc atc acc tac ccg gca 253
Ser Gln Pro Ala Gln Pro Ala Gln Gly Ile Thr Tyr Pro Ala
40 45 50

taacaaccag cacaaccctt aga 276

<210> 2040
 <211> 51
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 2040
 Val Pro Gln Ala Pro Ala Val Gln Ala Ala Pro Ala Val Ala Gln Ala
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 Pro Val Ala Pro Val Val Asp Met Thr Glu Pro Ala Ser Pro Trp Asp
 20 25 30
 Leu Pro Ala Ala Pro Ser Gln Pro Ala Gln Pro Ala Gln Gly Ile Thr
 35 40 45
 Tyr Pro Ala
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<210> 2041
 <211> 1401
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1378)
 <223> RXA01042

<400> 2041
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 Met Val Asn Pro Phe
 1 5
 cac acg ctt gat aac tca cgg ttt gat cgg gtg gca cag ttt cct gcg 163
 His Thr Leu Asp Asn Ser Pro Phe Asp Pro Val Ala Gln Phe Pro Ala
 10 15 20
 ttt tat cac aac cgg ctt atc aat cac ttg ggc cgc cgt cgc gcc tgg 211
 Phe Tyr His Asn Pro Leu Ile Asn His Leu Gly Arg Arg Arg Ala Trp
 25 30 35
 aca atc tca gac atc aac aaa cgc ccc atc aat gtc caa cag atg ctg 259
 Thr Ile Ser Asp Ile Asn Lys Arg Pro Ile Asn Val Gln Met Leu
 40 45 50
 acc acg gcc acc tac ggt agc ccc gtt att cat ggt gcc cgc att gaa 307
 Thr Thr Ala Thr Tyr Gly Ser Pro Val Ile His Gly Ala Arg Ile Glu
 55 60 65
 gac gca gca acc tcc cta ctt acc ctg gat gaa ctg cgt aca cag att 355
 Asp Ala Ala Thr Ser Leu Leu Thr Leu Asp Glu Leu Arg Thr Gln Ile
 70 75 80 85
 ccc acc gct gcc aac aat gcg ttt tat ctc gat gct gtc caa gat ggc 403
 Pro Thr Ala Ala Asn Asn Ala Phe Tyr Leu Asp Ala Val Gln Asp Gly
 90 95 100

tgt ctt att tta gat att gaa aaa acc tgt ccc ccc gag gtc gca gcc	451
Cys Leu Ile Leu Asp Ile Glu Lys Thr Cys Pro Pro Glu Val Ala Ala	
105 110 115	
aca cta ctc acg ctc tcc ccc acc gcc ttt tac aca gag gtg tcc atg	499
Thr Leu Leu Thr Leu Ser Pro Thr Ala Phe Tyr Thr Glu Val Ser Met	
120 125 130	
agt ggt cgt ggc tat cac ctc gtt atg ccg ata cca gag aat ttt gca	547
Ser Gly Arg Gly Tyr His Leu Val Met Pro Ile Pro Glu Asn Phe Ala	
135 140 145	
gcg ttt cct gcc gta cac aac aaa ccc agt atc aaa cac ccc aag cgc	595
Ala Phe Pro Ala Val His Asn Lys Pro Ser Ile Lys His Pro Lys Arg	
150 155 160 165	
tgg ttc gaa att ctt acc tca cag tgg atc acc ttc acc cga caa cca	643
Trp Phe Glu Ile Leu Thr Ser Gln Trp Ile Thr Phe Thr Arg Gln Pro	
170 175 180	
atc cca gag cat gtt ctc cat cac agt gaa tct gct aac aca agt gct	691
Ile Pro Glu His Val Leu His His Ser Glu Ser Ala Asn Thr Ser Ala	
185 190 195	
gtg cca tgg ttg aat gat caa cca ctt aca tgg gaa aac gtc ttt gca	739
Val Pro Trp Leu Asn Asp Gln Pro Leu Thr Trp Glu Asn Val Phe Ala	
200 205 210	
gac tta gct aaa act gtt gca ccc aac tta aaa acc ggt gcc gga ctt	787
Asp Leu Ala Lys Thr Val Ala Pro Asn Leu Lys Thr Gly Ala Gly Leu	
215 220 225	
acc atc aca ccc aat gca ctg atg cca cca gat ctc agc gat gct gag	835
Thr Ile Thr Pro Asn Ala Leu Met Pro Pro Asp Leu Ser Asp Ala Glu	
230 235 240 245	
cgc att cgc gac gat gaa gtc atc gac tcg acc tgt cga tta ttt gcc	883
Arg Ile Arg Asp Asp Glu Val Ile Asp Ser Thr Cys Arg Leu Phe Ala	
250 255 260	
gaa cat tac tcg aaa aca ctt gcg gac ttc tat gat gat gca tcc cgg	931
Glu His Tyr Ser Lys Thr Leu Ala Asp Phe Tyr Asp Asp Ala Ser Arg	
265 270 275	
ttc gag ttc agc caa att ggt gtc att atc aat cta ctg ctc ccc act	979
Phe Glu Phe Ser Gln Ile Gly Val Ile Ile Asn Leu Leu Leu Pro Thr	
280 285 290	
atg agg atg cat ccc acc acg atc agt ctc gac aaa ccc atc aac tcc	1027
Met Arg Met His Pro Thr Thr Ile Ser Leu Asp Lys Pro Ile Asn Ser	
295 300 305	
gat cac atc atc aga ctt ctg ttc gct gtc gct act cgc gtg atc act	1075
Asp His Ile Ile Arg Leu Leu Phe Ala Val Ala Thr Arg Val Ile Thr	
310 315 320 325	
cac cgc agc aaa cat gat gag gag cga tct ggc gtt ccg tat ctg atg	1123
His Arg Ser Lys His Asp Glu Glu Arg Ser Gly Val Pro Tyr Leu Met	
330 335 340	

tat cag gtt att tcc tgc ctt gac atg cga gaa cac ccc gac aat ggc 1171
 Tyr Gln Val Ile Ser Cys Leu Asp Met Arg Glu His Pro Asp Asn Gly
 345 350 355

gac tac cgt gtc gta ccc tcc cgg cat aat aga gac caa cac agc aac 1219
 Asp Tyr Arg Val Val Pro Ser Arg His Asn Arg Asp Gln His Ser Asn
 360 365 370

aac ccc tca gct cat gtg gtc cac caa caa cca caa ccc cag ccc agc 1267
 Asn Pro Ser Ala His Val Val His Gln Gln Pro Gln Pro Gln Pro Ser
 375 380 385

gca gca gat tcg cca cat cac tac cgt gca cta ccc caa gaa aac acg 1315
 Ala Ala Asp Ser Pro His His Tyr Arg Ala Leu Pro Gln Glu Asn Thr
 390 395 400 405

gtg tcc gaa cac agt ttt aaa atc tat aac cca cca gcc aca ccc cct 1363
 Val Ser Glu His Ser Phe Lys Ile Tyr Asn Pro Pro Ala Thr Pro Pro
 410 415 420

cta gga ggt gaa aat tagatttatt attaaaaacac ttg 1401
 Leu Gly Gly Glu Asn
 425

<210> 2042
 <211> 426
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2042
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 Ala Gln Phe Pro Ala Phe Tyr His Asn Pro Leu Ile Asn His Leu Gly
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 Arg Arg Arg Ala Trp Thr Ile Ser Asp Ile Asn Lys Arg Pro Ile Asn
 35 40 45
 Val Gln Gln Met Leu Thr Thr Ala Thr Tyr Gly Ser Pro Val Ile His
 50 55 60
 Gly Ala Arg Ile Glu Asp Ala Ala Thr Ser Leu Leu Thr Leu Asp Glu
 65 70 75 80
 Leu Arg Thr Gln Ile Pro Thr Ala Ala Asn Asn Ala Phe Tyr Leu Asp
 85 90 95
 Ala Val Gln Asp Gly Cys Leu Ile Leu Asp Ile Glu Lys Thr Cys Pro
 100 105 110
 Pro Glu Val Ala Ala Thr Leu Leu Thr Leu Ser Pro Thr Ala Phe Tyr
 115 120 125
 Thr Glu Val Ser Met Ser Gly Arg Gly Tyr His Leu Val Met Pro Ile
 130 135 140
 Pro Glu Asn Phe Ala Ala Phe Pro Ala Val His Asn Lys Pro Ser Ile
 145 150 155 160

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Lys His Pro Lys Arg Trp Phe Glu Ile Leu Thr Ser Gln Trp Ile Thr
      165                      170                      175

Phe Thr Arg Gln Pro Ile Pro Glu His Val Leu His His Ser Glu Ser
      180                      185                      190

Ala Asn Thr Ser Ala Val Pro Trp Leu Asn Asp Gln Pro Leu Thr Trp
      195                      200                      205

Glu Asn Val Phe Ala Asp Leu Ala Lys Thr Val Ala Pro Asn Leu Lys
      210                      215                      220

Thr Gly Ala Gly Leu Thr Ile Thr Pro Asn Ala Leu Met Pro Pro Asp
      225                      230                      235                      240

Leu Ser Asp Ala Glu Arg Ile Arg Asp Asp Glu Val Ile Asp Ser Thr
      245                      250                      255

Cys Arg Leu Phe Ala Glu His Tyr Ser Lys Thr Leu Ala Asp Phe Tyr
      260                      265                      270

Asp Asp Ala Ser Arg Phe Glu Phe Ser Gln Ile Gly Val Ile Ile Asn
      275                      280                      285

Leu Leu Leu Pro Thr Met Arg Met His Pro Thr Thr Ile Ser Leu Asp
      290                      295                      300

Lys Pro Ile Asn Ser Asp His Ile Ile Arg Leu Leu Phe Ala Val Ala
      305                      310                      315                      320

Thr Arg Val Ile Thr His Arg Ser Lys His Asp Glu Glu Arg Ser Gly
      325                      330                      335

Val Pro Tyr Leu Met Tyr Gln Val Ile Ser Cys Leu Asp Met Arg Glu
      340                      345                      350

His Pro Asp Asn Gly Asp Tyr Arg Val Val Pro Ser Arg His Asn Arg
      355                      360                      365

Asp Gln His Ser Asn Asn Pro Ser Ala His Val Val His Gln Gln Pro
      370                      375                      380

Gln Pro Gln Pro Ser Ala Ala Asp Ser Pro His His Tyr Arg Ala Leu
      385                      390                      395                      400

Pro Gln Glu Asn Thr Val Ser Glu His Ser Phe Lys Ile Tyr Asn Pro
      405                      410                      415

Pro Ala Thr Pro Pro Leu Gly Gly Glu Asn
      420                      425

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<210> 2043

<211> 696

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(673)

<223> RXA01043

<400> 2043

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atcactacct attcaccact tgaacggagc gtttttcgcc atg ttg aaa ttc cgc 115
 Met Leu Lys Phe Arg
 1 5

atc atc tcc aca gtc act act gga tct cag cca act cca cga aaa agc 163
 Ile Ile Ser Thr Val Thr Thr Gly Ser Gln Pro Thr Pro Arg Lys Ser
 10 15 20

tgg agc cac ccc gac acc act ctc ctg gtc acc atg gtc act gca cca 211
 Trp Ser His 25 Thr Thr Leu Leu Val Thr Met Thr Ala Pro 35

tcg ctg tgc tca gcc atc aac gtg tgg aac gca act gag cgt att ccc 259
 Ser Leu Cys Ser Ala Ile Asn Val Trp Asn Ala Thr Glu Arg Ile Pro
 40 45 50

gct caa aaa atc ctt aat gtc gaa gaa gta cac gtt ctt ggt gag tgc 307
 Ala Gln Lys Ile Leu Asn Val Glu Glu Val His Val Leu Gly Glu Cys
 55 60 65

agc gac gcc atc atc tct acg tca cta acc aaa aag gac aat ccg cac 355
 Ser Asp Ala Ile Ile Ser Thr Ser Leu Thr Lys Lys Asp Asn Pro His
 70 75 80 85

gca ctt gtg ccc gat gat ttc gac caa atc ggc gat gtg ttt ggc tat 403
 Ala Leu Val Pro Asp Asp Phe Asp Gln Ile Gly Asp Val Phe Gly Tyr
 90 95 100

gcg caa gac aat gta gct gtt ttt gat gtc att gtc gca gca ctg ggc 451
 Ala Gln Asp Asn Val Ala Val Phe Asp Val Ile Val Ala Ala Leu Gly
 105 110 115

ggc gct ggt tat ggc ctg cta ccc gga ctg gtc atg cac cac att gat 499
 Gly Ala Gly Tyr Gly Leu Leu Pro Gly Leu Val Met His His Ile Asp
 120 125 130

gag cac acc gtt gca ctt gtc ttt gat act gat tcc cct act ggg acg 547
 Glu His Thr Val Ala Leu Val Phe Asp Thr Asp Ser Pro Thr Gly Thr
 135 140 145

cat atc ctc ggt gag cgc tgc gtg tac tcc gac atc att cac atg act 595
 His Ile Leu Gly Glu Arg Cys Val Tyr Ser Asp Ile Ile His Met Thr
 150 155 160 165

gac gat aag tct gcc cgt ggc tgg ggt gca gtc att gcc ata gca cga 643
 Asp Asp Lys Ser Ala Arg Gly Trp Gly Ala Val Ile Ala Arg
 170 175 180

gcc atc atc ctc aaa gtc gaa cag atc atg tagtacccca ccatgactca 693
 Ala Ile Ile Leu Lys Val Glu Gln Ile Met
 185 190

ctt 696

<210> 2044

<211> 191

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2044

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Thr Pro Arg Lys Ser Trp Ser His Pro Asp Thr Thr Leu Leu Val Thr
 20 25 30

Met Val Thr Ala Pro Ser Leu Cys Ser Ala Ile Asn Val Trp Asn Ala
 35 40 45

Thr Glu Arg Ile Pro Ala Gln Lys Ile Leu Asn Val Glu Glu Val His
 50 55 60

Val Leu Gly Glu Cys Ser Asp Ala Ile Ile Ser Thr Ser Leu Thr Lys
 65 70 75 80

Lys Asp Asn Pro His Ala Leu Val Pro Asp Phe Asp Gln Ile Gly
 85 90 95

Asp Val Phe Gly Tyr Ala Gln Asp Asn Val Ala Val Phe Asp Val Ile
 100 105 110

Val Ala Ala Leu Gly Gly Ala Gly Tyr Gly Leu Leu Pro Gly Leu Val
 115 120 125

Met His His Ile Asp Glu His Thr Val Ala Leu Val Phe Asp Thr Asp
 130 135 140

Ser Pro Thr Gly Thr His Ile Leu Gly Glu Arg Cys Val Tyr Ser Asp
 145 150 155 160

Ile Ile His Met Thr Asp Asp Lys Ser Ala Arg Gly Trp Gly Ala Val
 165 170 175

Ile Ala Ile Ala Arg Ala Ile Ile Leu Lys Val Glu Gln Ile Met
 180 185 190

<210> 2045

<211> 1380

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1357)

<223> RXA01044

<400> 2045

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 Met Ser Leu Tyr Leu
 1 5

gac gac act ttg tct cgc atc gtt gaa ctt gat ctc aaa gac acc cgc 163
 Asp Asp Thr Leu Ser Arg Ile Val Glu Leu Asp Leu Lys Asp Thr Arg
 10 15 20

att gtc ccg ttt ctt gct ggt gaa cca ggt atc ggt aaa acc tca ttc	211
Ile Val Pro Phe Leu Ala Gly Glu Pro Gly Ile Gly Lys Thr Ser Phe	
25 30 35	
atc tac ggc atc ggc gaa cgt gca ggc tac aaa gtc ttc agt atc tcg	259
Ile Tyr Gly Ile Gly Glu Arg Ala Gly Tyr Lys Val Phe Ser Ile Ser	
40 45 50	
gtt aac acc ctt gcc gat aag ggt gac ctc acg ggc gct cgc acc ctg	307
Val Asn Thr Leu Ala Asp Lys Gly Asp Leu Thr Gly Ala Arg Thr Leu	
55 60 65	
cag gac cct gcc gat ggc aag tgg aag cag atg ttt ttc ccg cac gcg	355
Gln Asp Pro Ala Asp Gly Lys Trp Lys Gln Met Phe Phe Pro His Ala	
70 75 80 85	
acc ttc gtc gaa gca aat gac tat gca cta gca aac cca aac gaa acg	403
Thr Phe Val Glu Ala Asn Asp Tyr Ala Leu Ala Asn Pro Asn Glu Thr	
90 95 100	
gtc gtc att ctt ctc gat gag att aac cga act gat tcg gat gtc acc	451
Val Val Ile Leu Leu Asp Glu Ile Asn Arg Thr Asp Ser Asp Val Thr	
105 110 115	
tct gcc tcg atg act atc tct act gag cgt cgc gtt ggt acc acc gat	499
Ser Ala Ser Met Thr Ile Ser Thr Glu Arg Arg Val Gly Thr Thr Asp	
120 125 130	
cta gca ccc aat gtc cgc ctt gct gtc acc gga aac ctc acc ggt aat	547
Leu Ala Pro Asn Val Arg Leu Ala Val Thr Gly Asn Leu Thr Gly Asn	
135 140 145	
gtc acc cac ctt gat tca gca tct ctg acc agg ttc tcc ctc tat gag	595
Val Thr His Leu Asp Ser Ala Ser Leu Thr Arg Phe Ser Leu Tyr Glu	
150 155 160 165	
gtc aag cca tcc gca gag acc ttc atg aac atc atg ggc ggc cgc ctc	643
Val Lys Pro Ser Ala Glu Thr Phe Met Asn Ile Met Gly Gly Arg Leu	
170 175 180	
aac aag tac atc cgt acc gtg ctg acc aaa tac ccg gaa tac atc ttc	691
Asn Lys Tyr Ile Arg Thr Val Leu Thr Lys Tyr Pro Glu Tyr Ile Phe	
185 190 195	
atg aag cca act act gct act gct ctt att acc act ggc gat gat gat	739
Met Lys Pro Thr Thr Ala Thr Ala Leu Ile Thr Thr Gly Asp Asp Asp	
200 205 210	
gac gac cat aca acc aat gcg aag caa atg atg gac ttc aac gct gtg	787
Asp Asp His Thr Thr Asn Ala Lys Gln Met Met Asp Phe Asn Ala Val	
215 220 225	
ctc ggt tca gac caa gac atg gtt caa ttt acc gca cct aga act atc	835
Leu Gly Ser Asp Gln Asp Met Val Gln Phe Thr Ala Pro Arg Thr Ile	
230 235 240 245	
gaa ggt ttg tcc gtc tgg ctc aac aac gcc gat gat gac ttt ctt cgt	883
Glu Gly Leu Ser Val Trp Leu Asn Asn Ala Asp Asp Asp Phe Leu Arg	
250 255 260	

cta ctt cta caa gaa aag gtg gat ggt ctt gct cga tcc atg agc ttg 931
 Leu Leu Leu Glu Lys Val Asp Gly Leu Ala Arg Ser Met Ser Leu
 265 270 275

ctg cag gct acg ctc gaa tct cac acc ggc gat acc gct ttt acc gca 979
 Leu Gln Ala Thr Leu Glu Ser His Thr Gly Asp Thr Ala Phe Thr Ala
 280 285 290

gaa gtc ctc agc gaa atg acc aat gat ctg ctg agc tcc gca tgc caa 1027
 Glu Val Leu Ser Glu Met Thr Asn Asp Leu Ser Ser Ala Ser Gln
 295 300 305

gct cct agt ggt cca atc aaa cca ttt gtc tac gac cga ctc gct gct 1075
 Ala Pro Ser Gly Pro Ile Lys Pro Phe Val Tyr Asp Arg Leu Ala Ala
 310 315 320 325

gca cca agc aat act gta ctg gaa caa gag gtt cac aca ctc agt ctc 1123
 Ala Pro Ser Asn Thr Val Leu Glu Gln Glu Val His Thr Leu Ser Leu
 330 335 340

aat gac cgc gcc gat gtc ttg ttg ttt gcc ctc cat gac act gta aac 1171
 Asn Asp Arg Ala Asp Val Leu Leu Phe Ala Leu His Asp Thr Val Asn
 345 350 355

aac gct gca cca agc atc atc gct cac ctt gca tct gaa ggc gta ctt 1219
 Asn Ala Ala Pro Ser Ile Ile Ala His Leu Ala Ser Glu Gly Val Leu
 360 365 370

gat gaa ctg ccc aaa gac aga atc agc aaa att gtt tca ctc ggt cct 1267
 Asp Glu Leu Pro Lys Asp Arg Ile Ser Lys Ile Val Ser Leu Gly Pro
 375 380 385

gta cca acg gca aac tat cac gcc ttg acc aga cag gat aca acg ttg 1315
 Val Pro Thr Ala Asn Tyr His Ala Leu Thr Arg Gln Asp Thr Thr Leu
 390 395 400 405

act cga aat ctc ggt ccc gct gtc ttg ggc ttc ttg gaa agt 1357
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 35 40 45
 Val Phe Ser Ile Ser Val Asn Thr Leu Ala Asp Lys Gly Asp Leu Thr
 50 55 60

Gly Ala Arg Thr Leu Gln Asp Pro Ala Asp Gly Lys Trp Lys Gln Met
 65 70 75 80
 Phe Phe Pro His Ala Thr Phe Val Glu Ala Asn Asp Tyr Ala Leu Ala
 85 90 95
 Asn Pro Asn Glu Thr Val Val Ile Leu Leu Asp Glu Ile Asn Arg Thr
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 Asp Ser Asp Val Thr Ser Ala Ser Met Thr Ile Ser Thr Glu Arg Arg
 115 120 125
 Val Gly Thr Thr Asp Leu Ala Pro Asn Val Arg Leu Ala Val Thr Gly
 130 135 140
 Asn Leu Thr Gly Asn Val Thr His Leu Asp Ser Ala Ser Leu Thr Arg
 145 150 155 160
 Phe Ser Leu Tyr Glu Val Lys Pro Ser Ala Glu Thr Phe Met Asn Ile
 165 170 175
 Met Gly Gly Arg Leu Asn Lys Tyr Ile Arg Thr Val Leu Thr Lys Tyr
 180 185 190
 Pro Glu Tyr Ile Phe Met Lys Pro Thr Thr Ala Thr Ala Leu Ile Thr
 195 200 205
 Thr Gly Asp Asp Asp Asp Asp His Thr Thr Asn Ala Lys Gln Met Met
 210 215 220
 Asp Phe Asn Ala Val Leu Gly Ser Asp Gln Asp Met Val Gln Phe Thr
 225 230 235 240
 Ala Pro Arg Thr Ile Glu Gly Leu Ser Val Trp Leu Asn Asn Ala Asp
 245 250 255
 Asp Asp Phe Leu Arg Leu Leu Leu Gln Glu Lys Val Asp Gly Leu Ala
 260 265 270
 Arg Ser Met Ser Leu Leu Gln Ala Thr Leu Glu Ser His Thr Gly Asp
 275 280 285
 Thr Ala Phe Thr Ala Glu Val Leu Ser Glu Met Thr Asn Asp Leu Leu
 290 295 300
 Ser Ser Ala Ser Gln Ala Pro Ser Gly Pro Ile Lys Pro Phe Val Tyr
 305 310 315 320
 Asp Arg Leu Ala Ala Pro Ser Asn Thr Val Leu Glu Gln Glu Val
 325 330 335
 His Thr Leu Ser Leu Asn Asp Arg Ala Asp Val Leu Leu Phe Ala Leu
 340 345 350
 His Asp Thr Val Asn Asn Ala Ala Pro Ser Ile Ile Ala His Leu Ala
 355 360 365
 Ser Glu Gly Val Leu Asp Glu Leu Pro Lys Asp Arg Ile Ser Lys Ile
 370 375 380
 Val Ser Leu Gly Pro Val Pro Thr Ala Asn Tyr His Ala Leu Thr Arg

385 390 395 400

Gln Asp Thr Thr Leu Thr Arg Asn Leu Gly Pro Ala Val Leu Gly Phe
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Leu Glu Ser

<210> 2047
 <211> 1947
 <212> DNA
 <213> *Corynebacterium glutamicum*

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 <222> (101)..(1924)
 <223> RXA01045

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 Met Val Thr Phe Ser
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gtc gca aat cac gcg cct cat act ttt agc cca ttc gat att gaa cca 163
 Val Ala Asn His Ala Pro His Thr Phe Ser Pro Phe Asp Ile Glu Pro
 10 15 20

cca ctc acc ggt aac gcc acc acc gac gaa cat ggt tac gaa cac acc 211
 Pro Leu Thr Gly Asn Ala Thr Thr Asp Glu His Gly Tyr Glu His Thr
 25 30 35

tca gtg cta gaa aaa cta gcc tcc aac cac ctg ttc aat cca atc aat 259
 Ser Val Leu Glu Lys Leu Ala Ser Asn His Leu Phe Asn Pro Ile Asn
 40 45 50

ccg caa cac cca gtc act atc aca gcc acc gaa aac gga tca acc gtt 307
 Pro Gln His Pro Val Thr Ile Thr Ala Thr Glu Asn Gly Ser Thr Val
 55 60 65

gat ctt gat gca gca gca cta gca caa cat ctt gct cta gcg att acc 355
 Asp Leu Asp Ala Ala Leu Ala Gln His Leu Ala Leu Ala Ile Thr
 70 75 80 85

cca gac tca atg ctg gca aat cat caa ggc tac aac cgt gac atg atg 403
 Pro Asp Ser Met Leu Ala Asn His Gln Gly Tyr Asn Arg Asp Met Met
 90 95 100

ggt cta ctt tcg cag ctt act aac cat gtt ggc ttt gat cgc cga ttc 451
 Gly Leu Leu Ser Gln Leu Thr Asn His Val Gly Phe Asp Arg Arg Phe
 105 110 115

att gtt gac caa ctc ttt atc tcc caa gtg ctc aaa gcg aat cgt cta 499
 Ile Val Asp Gln Leu Phe Ile Ser Gln Val Leu Lys Ala Asn Arg Leu
 120 125 130

cca gca ccg gca aac aac gtt att tac acc gtg ccc aat gac gtt atc 547
 Pro Ala Pro Ala Asn Asn Val Ile Tyr Thr Val Pro Asn Asp Val Ile
 135 140 145

cca tct gct aaa gac atc ttg tcc acc act gca aaa atg aac aat cca	595
Pro Ser Ala Lys Asp Ile Leu Ser Thr Thr Ala Lys Met Asn Asn Pro	
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ctg aca gtt act gca agt gcc cca att act gtt gac gac att cac aca	643
Leu Thr Val Thr Ala Ser Ala Pro Ile Thr Val Asp Asp Ile His Thr	
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Ala Tyr Glu Val Phe Phe Ala Ser Leu Ala Ser Val Phe Phe Pro Tyr	
185 190 195	
acc tac ggt gcg gta ttc ctt aac aac gca gaa ttc gtt gag ttt gtt	739
Thr Tyr Gly Ala Val Phe Leu Asn Asn Ala Glu Phe Val Glu Phe Val	
200 205 210	
gat tac ctt att aac gaa gca aca aca ctg cac tcg gca tca ctc atc	787
Asp Tyr Leu Ile Asn Glu Ala Thr Thr Leu His Ser Ala Ser Leu Ile	
215 220 225	
tcc aac aac acc ttt aat agg ttc caa tca atg cgt aac atc tcc att	835
Ser Asn Asn Thr Phe Asn Arg Phe Gln Ser Met Arg Asn Ile Ser Ile	
230 235 240 245	
gat aat ctc acc gcc gag ttt ctc tta cgc aaa aat gaa gca gag aca	883
Asp Asn Leu Thr Ala Glu Phe Leu Leu Arg Lys Asn Glu Ala Glu Thr	
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act gat gat tat tca ttc ccc cgc gta ctt gtt tcc ctg ctg cat tct	931
Thr Asp Asp Tyr Ser Phe Pro Arg Val Leu Val Ser Leu Leu His Ser	
265 270 275	
tgg gtg aaa ctc aat cac gat gat gct cgt gct aac aat gat gca ccc	979
Trp Val Lys Leu Asn His Asp Asp Ala Arg Ala Asn Asn Asp Ala Pro	
280 285 290	
acc tgt gca cta gca ccg ttt agt gtg gct caa tgg atc atg ccg gag	1027
Thr Cys Ala Leu Ala Pro Phe Ser Val Ala Gln Trp Ile Met Pro Glu	
295 300 305	
acc att gtg ttt att aat gct gaa gct cat gct cat gca tcc tcc cag	1075
Thr Ile Val Phe Ile Asn Ala Glu Ala His Ala His Ala Ser Ser Gln	
310 315 320 325	
gac att gag aag aaa tgg aag gaa att aat gcg gcg tta aca ggg tct	1123
Asp Ile Glu Lys Lys Trp Lys Glu Ile Asn Ala Ala Leu Thr Gly Ser	
330 335 340	
att cgt att atg tcg cca aat gca att tcc aag ctg caa tct gct cag	1171
Ile Arg Ile Met Ser Pro Asn Ala Ile Ser Lys Leu Gln Ser Ala Gln	
345 350 355	
cat ctc ggg atg caa gca caa atg cag gcc atg cgt gct cga aaa gat	1219
His Leu Gly Met Gln Ala Gln Met Gln Ala Met Arg Ala Arg Lys Asp	
360 365 370	
cac cac aac atg cag aag cgt tcc tca caa gaa aac gac ttt tcc aag	1267
His His Asn Met Gln Lys Arg Ser Ser Gln Glu Asn Asp Phe Ser Lys	
375 380 385	

gca ctc ccc tca cca cag act atc gtg ctt tct gtc gca gag gtt ctg 1315
Ala Leu Pro Ser Pro Gln Thr Ile Val Leu Ser Val Ala Glu Val Leu
390 395 400 405

cgc aaa ctc act cac gta cgc caa tcg cac aac cct cag aaa tac cag 1363
Arg Lys Leu Thr His Val Arg Gln Ser His Asn Pro Gln Lys Tyr Gln
410 415 420

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Lys Lys Ser Leu Thr Arg Ala Ser Arg Arg His Pro Asp Asn Pro Asn
425 430 435

gtc cct ggc acc att aag agc aag ctc ttc tac cct gac ctg cat gtt 1459
Val Pro Gly Thr Ile Lys Ser Lys Leu Phe Tyr Pro Asp Leu His Val
440 445 450

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Tyr Val Asp Thr Ser Gly Ser Ile Ser Glu Glu Ser Tyr Arg Asn Ser
455 460 465

gtg gtt ctg ctc atg cag ctt gcc acc aaa ctg gac atc aac ctc tat 1555
Val Val Leu Leu Met Gln Leu Ala Thr Lys Leu Asp Ile Asn Leu Tyr
470 475 480 485

ttc tcc acc ttc tct cac gtg ctc tcc gaa gaa gta cta ttg ccg acc 1603
Phe Ser Thr Phe Ser His Val Leu Ser Glu Glu Val Leu Leu Pro Thr
490 495 500

aag ggt aaa aca cca cag caa ttg gca gct ctt att tcg gcc atc cca 1651
Lys Gly Lys Thr Pro Gln Gln Leu Ala Ala Leu Ile Ser Ala Ile Pro
505 510 515

aag gtc tct ggc ggt act gac tat cac cag att tgg gat tac atc cag 1699
Lys Val Ser Gly Gly Thr Asp Tyr His Gln Ile Trp Asp Tyr Ile Gln
520 525 530

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Ile Asn Pro Gln Arg Gln Glu Arg Met Asn Leu Val Leu Thr Asp Phe
535 540 545

gga ttc atg ccg aat cgc ggc tta aac atc gac cac cca agt tct att 1795
Gly Phe Met Pro Asn Arg Gly Leu Asn Ile Asp His Pro Ser Ser Ile
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Phe Tyr Val Pro Ile Leu Pro Asp Tyr Gly Ser Trp Ser Met Val Arg
570 575 580

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Arg Asp Met Ser His Phe Ala Asn Glu Met Val Asp Phe Asp Pro Tyr
585 590 595

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gtc 1947

<210> 2048

<211> 608

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<213> *Corynebacterium glutamicum*

<400> 2048

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Gly Tyr Glu His Thr Ser Val Leu Glu Lys Leu Ala Ser Asn His Leu
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Phe Asn Pro Ile Asn Pro Gln His Pro Val Thr Ile Thr Ala Thr Glu
          50             55             60

Asn Gly Ser Thr Val Asp Leu Asp Ala Ala Ala Leu Ala Gln His Leu
          65             70             75             80

Ala Leu Ala Ile Thr Pro Asp Ser Met Leu Ala Asn His Gln Gly Tyr
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Asn Arg Asp Met Met Gly Leu Leu Ser Gln Leu Thr Asn His Val Gly
          100             105             110

Phe Asp Arg Arg Phe Ile Val Asp Gln Leu Phe Ile Ser Gln Val Leu
          115             120             125

Lys Ala Asn Arg Leu Pro Ala Pro Ala Asn Asn Val Ile Tyr Thr Val
          130             135             140

Pro Asn Asp Val Ile Pro Ser Ala Lys Asp Ile Leu Ser Thr Thr Ala
          145             150             155             160

Lys Met Asn Asn Pro Leu Thr Val Thr Ala Ser Ala Pro Ile Thr Val
          165             170             175

Asp Asp Ile His Thr Ala Tyr Glu Val Phe Phe Ala Ser Leu Ala Ser
          180             185             190

Val Phe Phe Pro Tyr Thr Tyr Gly Ala Val Phe Leu Asn Asn Ala Glu
          195             200             205

Phe Val Glu Phe Val Asp Tyr Leu Ile Asn Glu Ala Thr Thr Leu His
          210             215             220

Ser Ala Ser Leu Ile Ser Asn Asn Thr Phe Asn Arg Phe Gln Ser Met
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Arg Asn Ile Ser Ile Asp Asn Leu Thr Ala Glu Phe Leu Leu Arg Lys
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Asn Glu Ala Glu Thr Thr Asp Asp Tyr Ser Phe Pro Arg Val Leu Val
          260             265             270

Ser Leu Leu His Ser Trp Val Lys Leu Asn His Asp Asp Ala Arg Ala
          275             280             285

Asn Asn Asp Ala Pro Thr Cys Ala Leu Ala Pro Phe Ser Val Ala Gln
          290             295             300

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Trp Ile Met Pro Glu Thr Ile Val Phe Ile Asn Ala Glu Ala His Ala
 305 310 315 320
 His Ala Ser Ser Gln Asp Ile Glu Lys Lys Trp Lys Glu Ile Asn Ala
 325 330 335
 Ala Leu Thr Gly Ser Ile Arg Ile Met Ser Pro Asn Ala Ile Ser Lys
 340 345 350
 Leu Gln Ser Ala Gln His Leu Gly Met Gln Ala Gln Met Gln Ala Met
 355 360 365
 Arg Ala Arg Lys Asp His His Asn Met Gln Lys Arg Ser Ser Gln Glu
 370 375 380
 Asn Asp Phe Ser Lys Ala Leu Pro Ser Pro Gln Thr Ile Val Leu Ser
 385 390 395 400
 Val Ala Glu Val Leu Arg Lys Leu Thr His Val Arg Gln Ser His Asn
 405 410 415
 Pro Gln Lys Tyr Gln Lys Lys Ser Leu Thr Arg Ala Ser Arg Arg His
 420 425 430
 Pro Asp Asn Pro Asn Val Pro Gly Thr Ile Lys Ser Lys Leu Phe Tyr
 435 440 445
 Pro Asp Leu His Val Tyr Val Asp Thr Ser Gly Ser Ile Ser Glu Glu
 450 455 460
 Ser Tyr Arg Asn Ser Val Val Leu Leu Met Gln Leu Ala Thr Lys Leu
 465 470 475 480
 Asp Ile Asn Leu Tyr Phe Ser Thr Phe Ser His Val Leu Ser Glu Glu
 485 490 495
 Val Leu Leu Pro Thr Lys Gly Lys Thr Pro Gln Gln Leu Ala Ala Leu
 500 505 510
 Ile Ser Ala Ile Pro Lys Val Ser Gly Gly Thr Asp Tyr His Gln Ile
 515 520 525
 Trp Asp Tyr Ile Gln Ile Asn Pro Gln Arg Gln Glu Arg Met Asn Leu
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 Val Leu Thr Asp Phe Gly Phe Met Pro Asn Arg Gly Leu Asn Ile Asp
 545 550 555 560
 His Pro Ser Ser Ile Phe Tyr Val Pro Ile Leu Pro Asp Tyr Gly Ser
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<223> RXA01046
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				Met	Ile	Pro	Phe	Pro	5												163					
ggg	caa	ccg	cag	cag	caa	agc	gca	ccc	aat	gac	gag	acc	cgt	ttc	atc						163					
Gly	Gln	Pro	Gln	Gln	Gln	Ser	Ala	Pro	Asn	Asp	Glu	Thr	Arg	Phe	Ile	20					163					
				10					15					20							163					
gac	ctt	aac	gaa	cgt	cat	aaa	gat	gat	gaa	cca	gcc	ctg	ttt	cgc	gat						211					
Asp	Leu	Asn	Glu	Arg	His	Lys	Asp	Asp	Glu	Pro	Ala	Leu	Phe	Arg	Asp						211					
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gat	gtt	att	gat	caa	act	ctc	gct	att	ttg	atc	agt	aaa	aat	aag	ccc						259					
Asp	Val	Ile	Asp	Gln	Thr	Leu	Ala	Ile	Leu	Ile	Ser	Lys	Asn	Lys	Pro						259					
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Asn	Ala	Leu	Leu	Val	Gly	Pro	Ala	Gly	Thr	Gly	Lys	Ser	Arg	Ile	Ala						307					
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gaa	gat	att	gcg	cgc	cgc	ctt	gcc	aat	gat	gac	gta	tct	att	ccc	gat						355					
Glu	Asp	Ile	Ala	Arg	Arg	Leu	Ala	Asn	Asp	Asp	Val	Ser	Ile	Pro	Asp	85					355					
	70				75					80											355					
cag	ctt	gtc	ggc	cac	cgt	att	ctt	gat	gtc	tcc	att	gca	gag	ctt	gtt						403					
Gln	Leu	Val	Gly	His	Arg	Ile	Leu	Asp	Val	Ser	Ile	Ala	Glu	Leu	Val						403					
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gct	ggt	gct	ggc	gtt	gtt	ggt	cag	ctc	aag	aaa	cgc	att	ctg	gat	ctc						451					
Ala	Gly	Ala	Gly	Val	Val	Gly	Gln	Leu	Lys	Lys	Arg	Ile	Leu	Asp	Leu						451					
			105				110					115									451					
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 Asp Pro Ala Leu Lys Arg Arg Phe Ser Arg Val Asn Val Asp Glu Phe
 185 190 195

gat cga gat caa acg ctc act att ctt cat gct gca cgt gat ggt tac 739
 Asp Arg Asp Gln Thr Leu Thr Ile Leu His Ala Ala Arg Asp Gly Tyr
 200 205 210

ctc aaa cat ttc aac aac gct gtc acg gta tct gac gac gta ctg ggc 787
 Leu Lys His Phe Asn Asn Ala Val Thr Val Ser Asp Asp Val Leu Gly
 215 220 225

tat gtc tac acc tac tcg cag caa ttc aac cca ggc aat aca gca caa 835
 Tyr Val Tyr Thr Tyr Ser Gln Gln Phe Asn Pro Gly Asn Thr Ala Gln
 230 235 240 245

cct gat gca gca ctg acg ctg ttt gat aag gcg ttg gct tcc cta act 883
 Pro Asp Ala Ala Leu Thr Leu Phe Asp Lys Ala Leu Ala Ser Leu Thr
 250 255 260

atg gag aaa cag cgt ctg atc aac aac cat gtc att gcg ccg tcg ctc 931
 Met Glu Lys Gln Arg Leu Ile Asn Asn His Val Ile Ala Pro Ser Leu
 265 270 275

aag ttc cct gtg tca gaa agg cac atc cat aac acc gct cgc aaa ctt 979
 Lys Phe Pro Val Ser Glu Arg His Ile His Asn Thr Ala Arg Lys Leu
 280 285 290

gcc ttt ggc tct caa gtg cca gcc tcc atc aat act gat gat gct cgt 1027
 Ala Phe Gly Ser Gln Val Pro Ala Ser Ile Asn Thr Asp Asp Ala Arg
 295 300 305

gac aaa ctc gaa acg ttg ttt ggt caa gat cat att att gag cca gta 1075
 Asp Lys Leu Glu Thr Leu Phe Gly Gln Asp His Ile Ile Glu Pro Val
 310 315 320 325

ctc acc gct atc aag cgt gaa cag ctt ggt att ttc cct cgc acc aaa 1123
 Leu Thr Ala Ile Lys Arg Glu Gln Leu Gly Ile Phe Pro Arg Thr Lys
 330 335 340

coa ttg agc tgg gtg ttt gct ggt tca tct ggt gtg ggt aaa aca gaa 1171
 Pro Leu Ser Trp Val Phe Ala Gly Ser Ser Gly Val Gly Lys Thr Glu
 345 350 355

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 360 365 370

atc aat ggt ccc gaa tac att agt cct gag tcc att act ggc ctt atc 1267
 Ile Asn Gly Pro Glu Tyr Ile Ser Pro Glu Ser Ile Thr Gly Leu Ile
 375 380 385

gga tca tcc gat ggc tat atc gcc tct aat tct aag cgt gct aaa cca 1315
 Gly Ser Ser Asp Gly Tyr Ile Gly Ser Asn Ser Lys Arg Ala Lys Pro
 390 395 400 405

ctc gac ccg ctg att tct aat ccg cgt cag gtg att gtg ctc gat gaa 1363
 Leu Asp Pro Leu Ile Ser Asn Pro Arg Gln Val Ile Val Leu Asp Glu
 410 415 420

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 Lys Ser Arg Ile Ala Glu Asp Ile Ala Arg Arg Leu Ala Asn Asp Asp
 65 70 75 80
 Val Ser Ile Pro Asp Gln Leu Val Gly His Arg Ile Leu Asp Val Ser
 85 90 95
 Ile Ala Glu Leu Val Ala Gly Ala Gly Val Val Gly Gln Leu Lys Lys
 100 105 110
 Arg Ile Leu Asp Leu Ile Lys Tyr Ala Thr Asp Pro Ser Asn Lys Val
 115 120 125
 Ile Ile Phe Ile Asp Glu Ile His Gln Ile Ala Gly Asp Gln Ser Ser
 130 135 140
 His Ser Gly Ser Gln Ala Lys Val Ala Gln Ile Leu Lys Pro Tyr Leu
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 Ala Arg Gly Asp Leu Arg Val Ile Gly Ala Thr Thr Thr Gln Glu Ala
 165 170 175
 Arg Asp Phe Asp His Asp Pro Ala Leu Lys Arg Arg Phe Ser Arg Val
 180 185 190
 Asn Val Asp Glu Phe Asp Arg Asp Gln Thr Leu Thr Ile Leu His Ala
 195 200 205
 Ala Arg Asp Gly Tyr Leu Lys His Phe Asn Asn Ala Val Thr Val Ser
 210 215 220
 Asp Asp Val Leu Gly Tyr Val Tyr Thr Tyr Ser Gln Gln Phe Asn Pro
 225 230 235 240
 Gly Asn Thr Ala Gln Pro Asp Ala Ala Leu Thr Leu Phe Asp Lys Ala
 245 250 255
 Leu Ala Ser Leu Thr Met Glu Lys Gln Arg Leu Ile Asn Asn His Val
 260 265 270
 Ile Ala Pro Ser Leu Lys Phe Pro Val Ser Glu Arg His Ile His Asn
 275 280 285
 Thr Ala Arg Lys Leu Ala Phe Gly Ser Gln Val Pro Ala Ser Ile Asn
 290 295 300
 Thr Asp Asp Ala Arg Asp Lys Leu Glu Thr Leu Phe Gly Gln Asp His
 305 310 315 320
 Ile Ile Glu Pro Val Leu Thr Ala Ile Lys Arg Glu Gln Leu Gly Ile
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 Phe Pro Arg Thr Lys Pro Leu Ser Trp Val Phe Ala Gly Ser Ser Gly
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 Val Gly Lys Thr Glu Met Ala Arg Ile Leu Ser Arg Ala Ile Asn Gly
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 Gly Asp Pro Ile Ile Ile Asn Gly Pro Glu Tyr Ile Ser Pro Glu Ser

370

375

380

Ile Thr Gly Leu Ile Gly Ser Ser Asp Gly Tyr Ile Gly Ser Asn Ser
 385 390 395 400

Lys Arg Ala Lys Pro Leu Asp Pro Leu Ile Ser Asn Pro Arg Gln Val
 405 410 415

Ile Val Leu Asp Glu Phe Glu Lys Ser His Pro His Phe Gln Gln Leu
 420 425 430

Phe Met Ala Ala Leu Asp Thr Gly Thr Met Ala Met Ala Asn Gly Thr
 435 440 445

Thr Leu Asn Phe Ser Gln Ala Ile Ile Ile Ala Thr Thr Asn Ala Ala
 450 455 460

Arg Asp Lys Ile Gly Arg Asp Ser Phe Gly Phe Asp Ser Asp Asn Ser
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Gly Val Leu Gly Ser Ala Gln Ala Ala Thr Asp Pro Arg Ala Gln Glu
 485 490 495

Arg Leu Lys Ser Leu Met Ser Lys Asp Phe Leu Leu Asn Cys Ser Thr
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Val Ser Arg Ile Ser Leu Pro Ser Thr Ala Leu Met Gln Ala Pro Thr
 515 520 525

Val Arg Phe Trp Thr Ile Ser Thr Ser Val Ala Val Thr Pro Cys Cys
 530 535 540

Leu Ala Thr Pro His Tyr Ala Ala Gln Ile Pro Ala Asp Ile Asp Ser
 545 550 555 560

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Met

<210> 2051

<211> 597

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

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<222> (101)..(574)

<223> RXA01047

<400> 2051

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Met Ile Asp Thr Thr

1

5

gct aac agc acc tca ggc acc cta cct aca ctc act gct gac caa gct 163
Ala Asn Ser Thr Ser Gly Thr Leu Pro Thr Leu Thr Ala Asp Gln Ala
10 15 20

gcg ttt atc acc ggt ttt tgc gag gct gct atc ttc aca gcc acc gtc 211
Ala Phe Ile Thr Gly Phe Cys Glu Ala Ala Ile Phe Thr Ala Thr Val
25 30 35

aca ata gat aac gaa cct ata ttt ctt gat gaa gcg ttc ttc tta ggt 259
Thr Ile Asp Asn Glu Pro Ile Phe Leu Asp Glu Ala Phe Phe Leu Gly
40 45 50

caa gaa acc tat acc gac att ctc atg aat caa ctc cgc acc aat gaa 307
Gln Glu Thr Tyr Thr Asp Ile Leu Met Asn Gln Leu Arg Thr Asn Glu
55 60 65

gcc att gtt aaa gac tgt ctc gac ttc ttc ctt gac aac tac acc aca 355
Ala Ile Val Lys Asp Cys Leu Asp Phe Phe Leu Asp Asn Tyr Thr Thr
70 75 80 85

atg aac aag ctc att gtt gat ggt cta tgc cca gat tgg gag cac cac 403
Met Asn Lys Leu Ile Val Asp Gly Leu Cys Pro Asp Trp Glu His His
90 95 100

ggc cat gat ttc cta ctc acc cgt gac cat cat ggt gcc gga ttc tgg 451
Gly His Asp Phe Leu Leu Thr Arg Asp His His Gly Ala Gly Phe Trp
105 110 115

gat cgt ggc tac gac gaa tac ggt gcc caa ctc acc gac aat gcc gaa 499
Asp Arg Gly Tyr Asp Glu Tyr Gly Ala Gln Leu Thr Asp Asn Ala Glu
120 125 130

aaa tat tca gaa aac tgt ctc aat ttc tgg att gag cct gat agt gac 547
Lys Tyr Ser Glu Asn Cys Leu Asn Phe Trp Ile Glu Pro Asp Ser Asp
135 140 145

cct ctc att atc aac ttc gag tac cac taacaccct tgaccttatt 594
Pro Leu Ile Ile Asn Phe Glu Tyr His
150 155

ttt 597

<210> 2052

<211> 158

<212> PRT

<213> Corynebacterium glutamicum

<400> 2052

Met Ile Asp Thr Thr Ala Asn Ser Thr Ser Gly Thr Leu Pro Thr Leu
1 5 10 15

Thr Ala Asp Gln Ala Ala Phe Ile Thr Gly Phe Cys Glu Ala Ala Ile
20 25 30

Phe Thr Ala Thr Val Thr Ile Asp Asn Glu Pro Ile Phe Leu Asp Glu
35 40 45

Ala Phe Phe Leu Gly Gln Glu Thr Tyr Thr Asp Ile Leu Met Asn Gln
50 55 60

```

Leu Arg Thr Asn Glu Ala Ile Val Lys Asp Cys Leu Asp Phe Phe Leu
 65              70              75              80

Asp Asn Tyr Thr Thr Met Asn Lys Leu Ile Val Asp Gly Leu Cys Pro
              85              90              95

Asp Trp Glu His His Gly His Asp Phe Leu Leu Thr Arg Asp His His
 100              105              110

Gly Ala Gly Phe Trp Asp Arg Gly Tyr Asp Glu Tyr Gly Ala Gln Leu
 115              120              125

Thr Asp Asn Ala Glu Lys Tyr Ser Glu Asn Cys Leu Asn Phe Trp Ile
 130              135              140

Glu Pro Asp Ser Asp Pro Leu Ile Ile Asn Phe Glu Tyr His
 145              150              155

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<210> 2053

<211> 444

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(421)

<223> RXA01058

<400> 2053

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ctcccgaat aggggtaatt ttgcaattaa ctgcgcttaa agtaagaaac attgctaatac 60

tttatctggg taattaacaa tcgatttttaa ggatattctc atg cgt aaa ctt cgt 115
              Met Arg Lys Leu Arg
              1              5

act gct tcc gtt gca ctg ctg acc gca ggt gca ctt gca ctg acc gct 163
Thr Ala Ser Val Ala Leu Leu Thr Ala Gly Ala Leu Ala Leu Thr Ala
              10              15              20

act cct gca atg gct cag tcc acc acc ggt tct tct gca tct tct cag 211
Thr Pro Ala Met Ala Gln Ser Thr Thr Gly Ser Ser Ala Ser Ser Gln
              25              30              35

gtt ggc gac gca ctc ggt gct agc gac tac gag cgc gac atc tgg ggt 259
Val Gly Asp Ala Leu Gly Ala Ser Asp Tyr Glu Arg Asp Ile Trp Gly
              40              45              50

tcc tct aag gac ttc gac gat gta acc cca ttc ggt tcc gct tgg tac 307
Ser Ser Lys Asp Phe Asp Asp Val Thr Pro Phe Gly Ser Ala Trp Tyr
              55              60              65

ggc tac acc ctg gcc gca acc gca gtt gct atc tcc ggt ctt gtg tac 355
Gly Tyr Thr Leu Ala Ala Thr Ala Val Ala Ile Ser Gly Leu Val Tyr
              70              75              80

gca aac ctt cct gca atc gag cag gct gct gca cag gcc ggc atc aag 403
Ala Asn Leu Pro Ala Ile Glu Gln Ala Ala Ala Gln Ala Gly Ile Lys
              90              95              100

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ctg gag atc cca cgc tac taattgccac tgcaatctta aat 444
 Leu Glu Ile Pro Arg Tyr
 105

<210> 2054

<211> 107

<212> PRT

<213> Corynebacterium glutamicum

<400> 2054

Met Arg Lys Leu Arg Thr Ala Ser Val Ala Leu Leu Thr Ala Gly Ala
 1 5 10 15

Leu Ala Leu Thr Ala Thr Pro Ala Met Ala Gln Ser Thr Thr Gly Ser
 20 25 30

Ser Ala Ser Ser Gln Val Gly Asp Ala Leu Gly Ala Ser Asp Tyr Glu
 35 40 45

Arg Asp Ile Trp Gly Ser Ser Lys Asp Phe Asp Asp Val Thr Pro Phe
 50 55 60

Gly Ser Ala Trp Tyr Gly Tyr Thr Leu Ala Ala Thr Ala Val Ala Ile
 65 70 75 80

Ser Gly Leu Val Tyr Ala Asn Leu Pro Ala Ile Glu Gln Ala Ala Ala
 85 90 95

Gln Ala Gly Ile Lys Leu Glu Ile Pro Arg Tyr
 100 105

<210> 2055

<211> 453

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(430)

<223> RXA01063

<400> 2055

actttcttgt agaggtctgg gtagtggata agttaatcaa ctatgaaata gactaaacta 60

atcattaaca ttaatggatt ttccggagaat agggatagac atg gca gac gag aaa 115
 Met Ala Asp Glu Lys
 1 5

aag gtt cat gta cgt gcc aca ctg cgc ttt gat tca gac acc cac cag 163
 Lys Val His Val Arg Ala Thr Leu Arg Phe Asp Ser Asp Thr His Gln
 10 15 20

cgg gca att tat tgg gca gat cga aaa ggt atc tcg ctg agc gcg tat 211
 Arg Ala Ile Tyr Trp Ala Asp Arg Lys Gly Ile Ser Leu Ser Ala Tyr
 25 30 35

gca gaa gag gcg atc aga gag aag att gat cgt gat aac ggt gtg cac 259
 Ala Glu Glu Ala Ile Arg Glu Lys Ile Asp Arg Asp Asn Gly Val His
 40 45 50

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gtt att ccg aat tca ctg ttg gat aac cgc atg aac caa atc att gat 307
Val Ile Pro Asn Ser Leu Leu Asp Asn Arg Met Asn Gln Ile Ile Asp
    55                      60                      65

cag ctc agc tcg ttt ggt cgt gag ttg gcg aac aac acg aca gtt gta 355
Gln Leu Ser Ser Phe Gly Arg Glu Leu Ala Asn Asn Thr Thr Val Val
    70                      75                      80                      85

act agt ggt ttc aac acc att atc ggt atg act cgt ggc gac tcg tat 403
Thr Ser Gly Phe Asn Thr Ile Ile Gly Met Thr Arg Gly Asp Ser Tyr
                90                      95                      100

ctc tct gat gat ctc gat gac ctg ggt taaacccgat gaacgagcag 450
Leu Ser Asp Asp Leu Asp Asp Leu Gly
                105                      110

gaa 453

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<210> 2056
<211> 110
<212> PRT
<213> Corynebacterium glutamicum

<400> 2056
Met Ala Asp Glu Lys Lys Val His Val Arg Ala Thr Leu Arg Phe Asp
 1                      5                      10                      15

Ser Asp Thr His Gln Arg Ala Ile Tyr Trp Ala Asp Arg Lys Gly Ile
                20                      25                      30

Ser Leu Ser Ala Tyr Ala Glu Glu Ala Ile Arg Glu Lys Ile Asp Arg
    35                      40                      45

Asp Asn Gly Val His Val Ile Pro Asn Ser Leu Leu Asp Asn Arg Met
    50                      55                      60

Asn Gln Ile Ile Asp Gln Leu Ser Ser Phe Gly Arg Glu Leu Ala Asn
    65                      70                      75                      80

Asn Thr Thr Val Val Thr Ser Gly Phe Asn Thr Ile Ile Gly Met Thr
    85                      90                      95

Arg Gly Asp Ser Tyr Leu Ser Asp Asp Leu Asp Asp Leu Gly
    100                      105                      110

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<210> 2057
<211> 849
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(826)
<223> RXA01066

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<400> 2057
aaacgtattc cttgacctgc gcatacaagg tctgaagaac tggcaatccg atccaaaggc 60

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tttgaaccgc ctgggcttct agctttaagg ggggtgagttc atg cgt agg gac agt 115
 Met Arg Arg Asp Ser
 1 5

ttt cgg gac cgc gcg cta gta gtc aaa act tat gat ttt ggc gaa gcc 163
 Phe Arg Asp Arg Ala Leu Val Val Lys Thr Tyr Asp Phe Gly Glu Ala
 10 15 20

gac cgc att att gtg ctg etc acc cga gac cac ggc atc gtg cgc gga 211
 Asp Arg Ile Ile Val Leu Leu Thr Arg Asp His Gly Ile Val Arg Gly
 25 30 35

gtt gcc aaa gga gta cgc cga tcc aaa tcc cgg ttt ggg tca agg ctg 259
 Val Ala Lys Gly Val Arg Arg Ser Lys Ser Arg Phe Gly Ser Arg Leu
 40 45 50

cag ctt ttt gtg gaa ctc gac gtg cag etc tac cca ggt aga aaa ctg 307
 Gln Leu Phe Val Glu Leu Asp Val Gln Leu Tyr Pro Gly Arg Lys Leu
 55 60 65

tcc acc atc tct ggc gcg gac acc gtc ggc tac tac gca tca ggc atc 355
 Ser Thr Ile Ser Gly Ala Asp Thr Val Gly Tyr Tyr Ala Ser Gly Ile
 70 75 80 85

atc gag gac ttc act cgg tat tcc tgt gcg tcc gcc atc ctg gaa atc 403
 Ile Glu Asp Phe Thr Arg Tyr Ser Cys Ala Ser Ala Ile Leu Glu Ile
 90 95 100

gcc acc cac atc gca gga ctg gaa aac gat ccg cac ctg ttt gaa gaa 451
 Ala Thr His Ile Ala Gly Leu Glu Asn Asp Pro His Leu Phe Glu Glu
 105 110 115

acc acc cgg gcg ttg aaa aac att cag gac tcc cca gaa ccc atc ctc 499
 Thr Thr Arg Ala Leu Lys Asn Ile Gln Asp Ser Pro Glu Pro Ile Leu
 120 125 130

aac cta gac gag ttc atg ctc cgc gcc atg aac cac gcc ggc tgg gca 547
 Asn Leu Asp Glu Phe Met Leu Arg Ala Met Asn His Ala Gly Trp Ala
 135 140 145

cca agc ctt ttc gac tgc gca gcc tgc ggc cga cca gga cct cac aac 595
 Pro Ser Leu Phe Asp Cys Ala Ala Cys Gly Arg Pro Gly Pro His Asn
 150 155 160 165

gca ttc cac cca ggc gtc ggc ggg gca gtg tgc ctg tac tgc cga ccg 643
 Ala Phe His Pro Gly Val Gly Gly Ala Val Cys Leu Tyr Cys Arg Pro
 170 175 180

ccg gga agc gcc gaa gtc cca cca gaa gca cta cac atg atg tgg ttg 691
 Pro Gly Ser Ala Glu Val Pro Pro Glu Ala Leu His Met Met Trp Leu
 185 190 195

gtc gcc aac ggc caa gca gcc cgc att ccc cgg gaa cac cca gag cag 739
 Val Ala Asn Gly Gln Ala Ala Arg Ile Pro Arg Glu His Pro Glu Gln
 200 205 210

caa acc acc att cac caa ctg aca acc gcg cat ctg cag tgg cat att 787
 Gln Thr Thr Ile His Gln Leu Thr Thr Ala His Leu Gln Trp His Ile
 215 220 225

gaa aga aag ctg ccc acg ctg gcg gtg ctg gat cag gcc tagtgcttag 836

Glu Arg Lys Leu Pro Thr Leu Ala Val Leu Asp Gln Ala
 230 235 240

gccttaggcgt ccg

849

<210> 2058

<211> 242

<212> PRT

<213> Corynebacterium glutamicum

<400> 2058

Met Arg Arg Asp Ser Phe Arg Asp Arg Ala Leu Val Val Lys Thr Tyr
 1 5 10 15

Asp Phe Gly Glu Ala Asp Arg Ile Ile Val Leu Leu Thr Arg Asp His
 20 25 30

Gly Ile Val Arg Gly Val Ala Lys Gly Val Arg Arg Ser Lys Ser Arg
 35 40 45

Phe Gly Ser Arg Leu Gln Leu Phe Val Glu Leu Asp Val Gln Leu Tyr
 50 55 60

Pro Gly Arg Lys Leu Ser Thr Ile Ser Gly Ala Asp Thr Val Gly Tyr
 65 70 75 80

Tyr Ala Ser Gly Ile Ile Glu Asp Phe Thr Arg Tyr Ser Cys Ala Ser
 85 90 95

Ala Ile Leu Glu Ile Ala Thr His Ile Ala Gly Leu Glu Asn Asp Pro
 100 105 110

His Leu Phe Glu Glu Thr Thr Arg Ala Leu Lys Asn Ile Gln Asp Ser
 115 120 125

Pro Glu Pro Ile Leu Asn Leu Asp Glu Phe Met Leu Arg Ala Met Asn
 130 135 140

His Ala Gly Trp Ala Pro Ser Leu Phe Asp Cys Ala Ala Cys Gly Arg
 145 150 155 160

Pro Gly Pro His Asn Ala Phe His Pro Gly Val Gly Gly Ala Val Cys
 165 170 175

Leu Tyr Cys Arg Pro Pro Gly Ser Ala Glu Val Pro Pro Glu Ala Leu
 180 185 190

His Met Met Trp Leu Val Ala Asn Gly Gln Ala Ala Arg Ile Pro Arg
 195 200 205

Glu His Pro Glu Gln Gln Thr Thr Ile His Gln Leu Thr Thr Ala His
 210 215 220

Leu Gln Trp His Ile Glu Arg Lys Leu Pro Thr Leu Ala Val Leu Asp
 225 230 235 240

Gln Ala

<210> 2059
 <211> 1194
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1171)
 <223> RXA01068

<400> 2059
 tgggtctacca agacaagctg ttccctgatt tcacgcagca agatctgtac gacgcgggcc 60
 tggaataacgc caagcgggat cgcagattcg gaagcgcata atg ccc acc aac cag 115
 Met Pro Thr Asn Gln
 1 5
 ccg acg cca gcc caa atc aaa cgc tgg cgc gga tac ctg gcc aat gag 163
 Pro Thr Pro Ala Gln Ile Lys Arg Trp Arg Gly Tyr Leu Ala Asn Glu
 10 15 20
 caa gca gag gcc gca gcc tac cgc gac ctg gcc aaa cga cgc gaa ggc 211
 Gln Ala Glu Ala Ala Tyr Arg Asp Leu Ala Lys Arg Arg Glu Gly
 25 30 35
 gaa gag cga gac atc ctc cta gcg ctc gcc gac gct gaa cac cga cac 259
 Glu Glu Arg Asp Ile Leu Leu Ala Leu Ala Asp Ala Glu His Arg His
 40 45 50
 gcc gct tac tgg gtg gaa aag ctc gcc cct gat gcc gaa aac cca cca 307
 Ala Ala Tyr Trp Val Glu Lys Leu Gly Pro Asp Ala Glu Asn Pro Pro
 55 60 65
 aaa gcc gac gtc aaa acc cgc ctg ctc ggt ttt cta gca cgc cga ttc 355
 Lys Ala Asp Val Lys Thr Arg Leu Leu Gly Phe Leu Ala Arg Arg Phe
 70 75 80 85
 ggc tcc gtg ttc acc ctg gca ctc atg cag tcc gcc gaa acg cgc agc 403
 Gly Ser Val Phe Thr Leu Ala Leu Met Gln Ser Ala Glu Thr Arg Ser
 90 95 100
 ccc tac gac gac gat gcc gac gcc tcc cgc caa atc agc gcc gac gaa 451
 Pro Tyr Asp Asp Ala Asp Ala Ser Arg Gln Ile Ser Ala Asp Glu
 105 110 115
 cgc atc cac gcc gaa gtc gtt cga gcc cta gcc agc cgc gcc aga gaa 499
 Arg Ile His Ala Glu Val Val Arg Gly Leu Ala Ser Arg Gly Arg Glu
 120 125 130
 cgc atg agc gcc aac ttc cgt gcc gcc gta ttc gga atc aac gac gcc 547
 Arg Met Ser Gly Asn Phe Arg Ala Ala Val Phe Gly Ile Asn Asp Gly
 135 140 145
 ctg gtc tcc aac gtc gcc ctc gtc atg ggt gtc atg gcc acc gcc gtg 595
 Leu Val Ser Asn Val Ala Leu Val Met Gly Val Met Ala Thr Gly Val
 150 155 160 165
 ccc gcc caa att gtt ctc atc acc gcc att tcc ggt ctg ctc tcc gcc 643
 Pro Ala Gln Ile Val Leu Ile Thr Gly Ile Ser Gly Leu Leu Ser Gly
 170 175 180

gcg cta tcc atg gcc gcc ggc gaa tac atc tca gtg cgc tcc caa aca 691
 Ala Leu Ser Met Ala Ala Gly Glu Tyr Ile Ser Val Arg Ser Gln Thr
 185 190 195

gag ctt ctc gac gcc tcc ctc cca gac ccc aaa gcc cgc gaa gcc ctc 739
 Glu Leu Leu Asp Ala Ser Leu Pro Asp Pro Lys Ala Arg Glu Ala Leu
 200 205 210

cac gcc ctc gac gtc gaa tcc aac gaa ctg gaa ctc gtc tac cga gcc 787
 His Ala Leu Asp Val Glu Ser Asn Glu Leu Glu Val Tyr Arg Ala
 215 220 225

cgc gga atg agc gaa gac gaa gcg cgg gca aaa gcg tca caa gtt ttc 835
 Arg Gly Met Ser Glu Asp Glu Ala Arg Ala Lys Ala Ser Gln Val Phe
 230 235 240 245

caa aga atc agc gac caa aaa cgc atc agc gac aac gtc ctc gcc agc 883
 Gln Arg Ile Ser Asp Gln Lys Arg Ile Ser Asp Asn Val Leu Gly Ser
 250 255 260

acc gaa atc caa agc gcc ggc tcc gct cgt tcg gcc gcc aca ttc agc 931
 Thr Glu Ile Gln Ser Ala Gly Ser Ala Arg Ser Ala Ala Thr Phe Ser
 265 270 275

ttc ctg tcc ttt gcc atc ggc gca ttc ctc ccg atc gtc cca tac gtc 979
 Phe Leu Ser Phe Ala Ile Gly Ala Phe Leu Pro Ile Val Pro Tyr Val
 280 285 290

ttc gcc atg gaa ggc ctc gcc ggg gca gtg gtg tcc cta gtc ctc gtc 1027
 Phe Gly Met Glu Gly Leu Ala Gly Ala Val Val Ser Leu Val Leu Val
 295 300 305

gga cta tca ctg atg gca acg ggc gcg acc acc gcc ctg cta tcg gga 1075
 Gly Leu Ser Leu Met Ala Thr Gly Ala Thr Thr Gly Leu Leu Ser Gly
 310 315 320 325

aag cca ccg gga atc cgc gcg gtg cgt cag ctg tcg atc gcc tac gcc 1123
 Lys Pro Pro Gly Ile Arg Ala Val Arg Gln Leu Ser Ile Gly Tyr Gly
 330 335 340

gcg gcg ctg gtc acc tac gtg ctc ggc ctc ctg ttc gcc atg atc ctt 1171
 Ala Ala Leu Val Thr Tyr Val Leu Gly Leu Leu Phe Gly Met Ile Leu
 345 350 355

taaaagctct tgcttctcga cgt 1194

<210> 2060

<211> 357

<212> PRT

<213> Corynebacterium glutamicum

<400> 2060

Met Pro Thr Asn Gln Pro Thr Pro Ala Gln Ile Lys Arg Trp Arg Gly
 1 5 10 15

Tyr Leu Ala Asn Glu Gln Ala Glu Ala Ala Ala Tyr Arg Asp Leu Ala
 20 25 30

Lys Arg Arg Glu Gly Glu Glu Arg Asp Ile Leu Leu Ala Leu Ala Asp
 35 40 45

Ala Glu His Arg His Ala Ala Tyr Trp Val Glu Lys Leu Gly Pro Asp
 50 55 60
 Ala Glu Asn Pro Pro Lys Ala Asp Val Lys Thr Arg Leu Leu Gly Phe
 65 70 75 80
 Leu Ala Arg Arg Phe Gly Ser Val Phe Thr Leu Ala Leu Met Gln Ser
 85 90 95
 Ala Glu Thr Arg Ser Pro Tyr Asp Asp Ala Asp Ala Ser Arg Gln
 100 105 110
 Ile Ser Ala Asp Glu Arg Ile His Ala Glu Val Val Arg Gly Leu Ala
 115 120 125
 Ser Arg Gly Arg Glu Arg Met Ser Gly Asn Phe Arg Ala Ala Val Phe
 130 135 140
 Gly Ile Asn Asp Gly Leu Val Ser Asn Val Ala Leu Val Met Gly Val
 145 150 155 160
 Met Ala Thr Gly Val Pro Ala Gln Ile Val Leu Ile Thr Gly Ile Ser
 165 170 175
 Gly Leu Leu Ser Gly Ala Leu Ser Met Ala Ala Gly Glu Tyr Ile Ser
 180 185 190
 Val Arg Ser Gln Thr Glu Leu Leu Asp Ala Ser Leu Pro Asp Pro Lys
 195 200 205
 Ala Arg Glu Ala Leu His Ala Leu Asp Val Glu Ser Asn Glu Leu Glu
 210 215 220
 Leu Val Tyr Arg Ala Arg Gly Met Ser Glu Asp Glu Ala Arg Ala Lys
 225 230 235 240
 Ala Ser Gln Val Phe Gln Arg Ile Ser Asp Gln Lys Arg Ile Ser Asp
 245 250 255
 Asn Val Leu Gly Ser Thr Glu Ile Gln Ser Ala Gly Ser Ala Arg Ser
 260 265 270
 Ala Ala Thr Phe Ser Phe Leu Ser Phe Ala Ile Gly Ala Phe Leu Pro
 275 280 285
 Ile Val Pro Tyr Val Phe Gly Met Glu Gly Leu Ala Gly Ala Val Val
 290 295 300
 Ser Leu Val Leu Val Gly Leu Ser Leu Met Ala Thr Gly Ala Thr Thr
 305 310 315 320
 Gly Leu Leu Ser Gly Lys Pro Pro Gly Ile Arg Ala Val Arg Gln Leu
 325 330 335
 Ser Ile Gly Tyr Gly Ala Ala Leu Val Thr Tyr Val Leu Gly Leu Leu
 340 345 350
 Phe Gly Met Ile Leu
 355

<210> 2061
 <211> 828
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(805)
 <223> RXA01074

<400> 2061
 cgaatgaaat cactgggagg gagttcaccc tcggcgagga gcctgagcgc tactagcttt 60
 gccacatttc actaaacgcc ccgcacaacc ccaagcagcc ttg gcg gaa gcc gca 115
 Leu Ala Glu Ala Ala
 1 5
 ggt cta cgc tgg ctc gcc gaa gca tct tca gct gtg gca cag gtt gtt 163
 Gly Leu Arg Trp Leu Ala Glu Ala Ser Ser Ala Val Ala Gln Val Val
 10 15 20
 agc gcc gac gca gag cag atc acg act gtt ggc gtc gaa acg caa ttg 211
 Ser Ala Asp Ala Glu Gln Ile Thr Thr Val Gly Val Glu Thr Gln Leu
 25 30 35
 ccc aca ccc gat gcg gcc ttc aag gcc ggc gaa gag ctc gcc cgc atc 259
 Pro Thr Pro Asp Ala Ala Phe Lys Ala Gly Glu Glu Leu Ala Arg Ile
 40 45 50
 cac ctt gcc ggc gcc cca gcg ttc ggc tgt cca cca gcg ggc tgg gcg 307
 His Leu Ala Gly Ala Pro Ala Phe Gly Cys Pro Ala Gly Trp Ala
 55 60 65
 ggg tta aac tac atc gcc acc cag gga caa gca tgc tta tcg acg ccc 355
 Gly Leu Asn Tyr Ile Gly Thr Gln Gly Gln Ala Cys Leu Ser Thr Pro
 70 75 80 85
 acc tgg ggt gtt ttt tac tcc cag caa cgc gta ctc ccg ttt gcg cgc 403
 Thr Trp Gly Val Phe Tyr Ser Gln Gln Arg Val Leu Pro Phe Ala Arg
 90 95 100
 cgg gca cgc agg cga aat cac ctc acc gag cac gca ctc tgg gtc gtg 451
 Arg Ala Arg Arg Arg Asn His Leu Thr Glu His Ala Leu Trp Val Val
 105 110 115
 gaa gcc gct tgt gat ttg att agc gaa ctt ccc gat gac gtt ccc ccc 499
 Glu Ala Ala Cys Asp Leu Ile Ser Glu Leu Pro Asp Asp Val Pro Pro
 120 125 130
 gcc aga atc cac ggc gac ttg tgg ttt ggc aac cta ctt ttt ggc aca 547
 Ala Arg Ile His Gly Asp Leu Trp Phe Gly Asn Leu Leu Phe Gly Thr
 135 140 145
 gac ggg cct gtg ttt att gac ccc gca gct cac ggc ggt cat ccc gaa 595
 Asp Gly Pro Val Phe Ile Asp Pro Ala Ala His Gly Gly His Pro Glu
 150 155 160 165
 act gat ctc gcg atg ctt gat gta ttt ggc gca ccc tat ctc gat gaa 643
 Thr Asp Leu Ala Met Leu Asp Val Phe Gly Ala Pro Tyr Leu Asp Glu
 170 175 180

atc cgg gaa ggt tat ctg tct atc aac ccg ctg cca gac ggg tgg cgt 691
 Ile Arg Glu Gly Tyr Leu Ser Ile Asn Pro Leu Pro Asp Gly Trp Arg
 185 190 195
 gaa cgc acc ccc atg cac caa ctc cac cct ttg gcc gta cat gcg gcg 739
 Glu Arg Thr Pro Met His Gln Leu His Pro Leu Ala Val His Ala Ala
 200 205 210
 tct cat ggg cca agc tac ggc gtg gaa cta ctc cac gcc gcc aaa gcg 787
 Ser His Gly Pro Ser Tyr Gly Val Glu Leu Leu His Ala Ala Lys Ala
 215 220 225
 aca ctc aaa ctg ttg gat taacgccacc aattttcctg cgg 828
 Thr Leu Lys Leu Leu Asp
 230 235

<210> 2062

<211> 235

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2062

Leu Ala Glu Ala Ala Gly Leu Arg Trp Leu Ala Glu Ala Ser Ser Ala
 1 5 10 15

Val Ala Gln Val Val Ser Ala Asp Ala Glu Gln Ile Thr Thr Val Gly
 20 25 30

Val Glu Thr Gln Leu Pro Thr Pro Asp Ala Ala Phe Lys Ala Gly Glu
 35 40 45

Glu Leu Ala Arg Ile His Leu Ala Gly Ala Pro Ala Phe Gly Cys Pro
 50 55 60

Pro Ala Gly Trp Ala Gly Leu Asn Tyr Ile Gly Thr Gln Gly Gln Ala
 65 70 75 80

Cys Leu Ser Thr Pro Thr Trp Gly Val Phe Tyr Ser Gln Gln Arg Val
 85 90 95

Leu Pro Phe Ala Arg Arg Ala Arg Arg Arg Asn His Leu Thr Glu His
 100 105 110

Ala Leu Trp Val Val Glu Ala Ala Cys Asp Leu Ile Ser Glu Leu Pro
 115 120 125

Asp Asp Val Pro Pro Ala Arg Ile His Gly Asp Leu Trp Phe Gly Asn
 130 135 140

Leu Leu Phe Gly Thr Asp Gly Pro Val Phe Ile Asp Pro Ala Ala His
 145 150 155 160

Gly Gly His Pro Glu Thr Asp Leu Ala Met Leu Asp Val Phe Gly Ala
 165 170 175

Pro Tyr Leu Asp Glu Ile Arg Glu Gly Tyr Leu Ser Ile Asn Pro Leu
 180 185 190

Pro Asp Gly Trp Arg Glu Arg Thr Pro Met His Gln Leu His Pro Leu

195

200

205

Ala Val His Ala Ala Ser His Gly Pro Ser Tyr Gly Val Glu Leu Leu
210 215 220

His Ala Ala Lys Ala Thr Leu Lys Leu Leu Asp
225 230 235

<210> 2063

<211> 1143

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1120)

<223> RXA01076

<400> 2063

tcttccatt aagcaccttg tcttccggaa gcttccacc caaattccaa acccccaatt 60

ccatgccccg gatggacatt ttccattaca ctctggggct atg act cca gct cac 115
Met Thr Pro Ala His
1 5

ata ttt tct gaa ggt cca atc aat agt gtt gtt ctc agc cag gat gag 163
Ile Phe Ser Glu Gly Pro Ile Asn Ser Val Val Leu Ser Gln Asp Glu
10 15 20

gat gga aat ttc acc acc tcc tac cag gac acg ttc tct gat cca tca 211
Asp Gly Asn Phe Thr Thr Ser Tyr Gln Asp Thr Phe Ser Asp Pro Ser
25 30 35

ttt ttg ggg gaa ggt gac gtt cta att gag gtt ggt tgg tcc agc ttg 259
Phe Leu Gly Glu Gly Asp Val Leu Ile Glu Val Gly Trp Ser Ser Leu
40 45 50

aat tac aag gac gca atg gct ctg aag ggt gat aag gga gtg gtg cgt 307
Asn Tyr Lys Asp Ala Met Ala Leu Lys Gly Asp Lys Gly Val Val Arg
55 60 65

act gtg cca ctg att cca ggt atc gat gtg gtg ggc act gtg atc gag 355
Thr Val Pro Leu Ile Pro Gly Ile Asp Val Val Gly Thr Val Ile Glu
70 75 80 85

agc gct gat cct cgc ttt ggt cgt ggt gat gaa gtg gtg ctg aat ggc 403
Ser Ala Asp Pro Arg Phe Gly Arg Gly Asp Glu Val Val Leu Asn Gly
90 95 100

gct ggt ttg ggg gag aac cgg cat gga ggt ttc acg cag cgg ctg aaa 451
Ala Gly Leu Gly Glu Asn Arg His Gly Gly Phe Thr Gln Arg Leu Lys
105 110 115

gtg ccg tct gaa ccg ttg ctg cat att cca ttt aac ttc tcc gcg cag 499
Val Pro Ser Glu Pro Leu Leu His Ile Pro Phe Asn Phe Ser Ala Gln
120 125 130

cag gtg ggt gcg ttg ggt act gca ggt ttc acg gct gcg cta tcg gtg 547
Gln Val Gly Ala Leu Gly Thr Ala Gly Phe Thr Ala Ala Leu Ser Val
135 140 145

aat gct ctg gtc gat caa ggt atc aaa ccg gag gat ggg gag att ctg 595
 Asn Ala Leu Val Asp Gln Gly Ile Lys Pro Glu Asp Gly Glu Ile Leu
 150 155 160 165

gta act ggt tcg act ggt ggt gtg ggt tcg att gca ctt cac ctg ctg 643
 Val Thr Gly Ser Thr Gly Gly Val Gly Ser Ile Ala Leu His Leu Leu
 170 175 180

aat aag ttg gga tat acg acg gtc gcg gtg acg ggg cgt cga gaa gcg 691
 Asn Lys Leu Gly Tyr Thr Thr Val Ala Val Thr Gly Arg Arg Glu Ala
 185 190 195

cat gcc gaa tac ctg acc agc ctg ggc gca agc gac atc att gat cgc 739
 His Ala Glu Tyr Leu Thr Ser Leu Gly Ala Ser Asp Ile Ile Asp Arg
 200 205 210

gcg gag ctt tct gaa aag ggc cgg ccg ctg cag aag ggg cgt tgg gcg 787
 Ala Glu Leu Ser Glu Lys Gly Arg Pro Leu Gln Lys Gly Arg Trp Ala
 215 220 225

ggt gta gtg gat tca gtg gga tcc cac aca ctt gtc aat gcg att gct 835
 Gly Val Val Asp Ser Val Gly Ser His Thr Leu Val Asn Ala Ile Ala
 230 235 240 245

cag aca aaa tgg ggc gga att gtc acg gcg tgt ggc atg gct cag ggg 883
 Gln Thr Lys Trp Gly Gly Ile Val Thr Ala Cys Gly Met Ala Gln Gly
 250 255 260

ccg gat ctg ccg gga acg gtg ttg ccg ttt att ctt cgt ggc gtg cat 931
 Pro Asp Leu Pro Gly Thr Val Leu Pro Phe Ile Leu Arg Gly Val His
 265 270 275

ttg gtt ggc att aac tct gtc gat gca ccc cgt gag ctg cgt cga cgt 979
 Leu Val Gly Ile Asn Ser Val Asp Ala Pro Arg Glu Leu Arg Arg Arg
 280 285 290

gcg tgg gcg ttg ctg tcc gag cat ctt gat acc gcg gtg cta gat gat 1027
 Ala Trp Ala Leu Leu Ser Glu His Leu Asp Thr Ala Val Leu Asp Asp
 295 300 305

atg acc act gtg att gat gtc aag gat gtt gct caa gct ggc gaa gat 1075
 Met Thr Thr Val Ile Asp Val Lys Asp Val Ala Gln Ala Gly Glu Asp
 310 315 320 325

ttg atg gct ggc aag ctt cac gga cgt acc gcg gtg cgt gtt cat 1120
 Leu Met Ala Gly Lys Leu His Gly Arg Thr Ala Val Arg Val His
 330 335 340

tagcagggtca agcgcgtaat tga 1143

<210> 2064
 <211> 340
 <212> PRT
 <213> *Corynebacterium glutamicum*
 <400> 2064
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Leu Ser Gln Asp Glu Asp Gly Asn Phe Thr Thr Ser Tyr Gln Asp Thr
 20 25 30
 Phe Ser Asp Pro Ser Phe Leu Gly Glu Gly Asp Val Leu Ile Glu Val
 35 40 45
 Gly Trp Ser Ser Leu Asn Tyr Lys Asp Ala Met Ala Leu Lys Gly Asp
 50 55 60
 Lys Gly Val Val Arg Thr Val Pro Leu Ile Pro Gly Ile Asp Val Val
 65 70 75 80
 Gly Thr Val Ile Glu Ser Ala Asp Pro Arg Phe Gly Arg Gly Asp Glu
 85 90 95
 Val Val Leu Asn Gly Ala Gly Leu Gly Glu Asn Arg His Gly Gly Phe
 100 105 110
 Thr Gln Arg Leu Lys Val Pro Ser Glu Pro Leu Leu His Ile Pro Phe
 115 120 125
 Asn Phe Ser Ala Gln Gln Val Gly Ala Leu Gly Thr Ala Gly Phe Thr
 130 135 140
 Ala Ala Leu Ser Val Asn Ala Leu Val Asp Gln Gly Ile Lys Pro Glu
 145 150 155 160
 Asp Gly Glu Ile Leu Val Thr Gly Ser Thr Gly Gly Val Gly Ser Ile
 165 170 175
 Ala Leu His Leu Leu Asn Lys Leu Gly Tyr Thr Thr Val Ala Val Thr
 180 185 190
 Gly Arg Arg Glu Ala His Ala Glu Tyr Leu Thr Ser Leu Gly Ala Ser
 195 200 205
 Asp Ile Ile Asp Arg Ala Glu Leu Ser Glu Lys Gly Arg Pro Leu Gln
 210 215 220
 Lys Gly Arg Trp Ala Gly Val Val Asp Ser Val Gly Ser His Thr Leu
 225 230 235 240
 Val Asn Ala Ile Ala Gln Thr Lys Trp Gly Gly Ile Val Thr Ala Cys
 245 250 255
 Gly Met Ala Gln Gly Pro Asp Leu Pro Gly Thr Val Leu Pro Phe Ile
 260 265 270
 Leu Arg Gly Val His Leu Val Gly Ile Asn Ser Val Asp Ala Pro Arg
 275 280 285
 Glu Leu Arg Arg Arg Ala Trp Ala Leu Leu Ser Glu His Leu Asp Thr
 290 295 300
 Ala Val Leu Asp Asp Met Thr Thr Val Ile Asp Val Lys Asp Val Ala
 305 310 315 320
 Gln Ala Gly Glu Asp Leu Met Ala Gly Lys Leu His Gly Arg Thr Ala
 325 330 335
 Val Arg Val His

340

<210> 2065

<211> 957

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(934)

<223> RXA01078

<400> 2065

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tccaccaccc	gcagctaaaa	ctttttgaaa	ggagctcatc	atg	agc	aac	gca	gta	115
				Met	Ser	Asn	Ala	Val	
				1				5	

ccc	cac	aac	gtt	tcc	ttc	aac	ttt	gtt	ccc	cgc	gct	tac	cgt	cca	gaa	163
Pro	His	Asn	Val	Ser	Phe	Asn	Phe	Val	Pro	Arg	Ala	Tyr	Arg	Pro	Glu	
			10					15						20		

aag	ccc	cgc	aca	ttc	ggc	atg	aca	gaa	att	cgt	gca	ccg	tac	tac	tcc	211
Lys	Pro	Arg	Thr	Phe	Gly	Met	Thr	Glu	Ile	Arg	Ala	Pro	Tyr	Tyr	Ser	
			25					30					35			

act	ttc	ggc	acc	cga	cac	ctc	cag	gat	gtc	ttc	gat	ggt	gca	ggc	cag	259
Thr	Phe	Gly	Thr	Arg	His	Leu	Gln	Asp	Val	Phe	Asp	Val	Ala	Gly	Gln	
			40				45					50				

tgg	gtg	gac	ggc	atc	aaa	tgg	gca	ggc	ggt	tcc	ttc	tcc	ctg	gtg	ccg	307
Trp	Val	Asp	Gly	Ile	Lys	Trp	Ala	Gly	Gly	Ser	Phe	Ser	Leu	Val	Pro	
			55			60						65				

acc	gaa	cag	gtg	cgt	gct	ttt	agc	gac	atc	gcc	cat	gaa	aac	aat	gcc	355
Thr	Glu	Gln	Val	Arg	Ala	Phe	Ser	Asp	Ile	Ala	His	Glu	Asn	Asn	Ala	
			70			75				80					85	

tat	gtg	tct	tcc	ggt	ggc	tgg	att	gaa	act	gtg	ctt	cgc	tac	ggc	gac	403
Tyr	Val	Ser	Ser	Gly	Gly	Trp	Ile	Glu	Thr	Val	Leu	Arg	Tyr	Gly	Asp	
				90					95					100		

gac	gca	gtt	gat	cat	tac	tta	aag	gaa	gcc	aag	gaa	gtc	ggc	ttc	gat	451
Asp	Ala	Val	Asp	His	Tyr	Leu	Lys	Glu	Ala	Lys	Glu	Val	Gly	Phe	Asp	
			105					110					115			

gtt	att	gag	att	tcc	acc	gga	ttc	atc	atg	ctc	aac	act	tca	ggt	ctt	499
Val	Ile	Glu	Ile	Ser	Thr	Gly	Phe	Ile	Met	Leu	Asn	Thr	Ser	Gly	Leu	
			120				125						130			

cag	cgc	ctg	gta	gaa	aaa	gtg	gtc	aag	gca	ggc	ctc	aaa	gca	aaa	cct	547
Gln	Arg	Leu	Val	Glu	Lys	Val	Val	Lys	Ala	Gly	Leu	Lys	Ala	Lys	Pro	
			135			140					145					

gaa	cta	gga	cta	cag	att	ggt	tcc	gga	ggc	gac	tct	ggt	gag	gct	gaa	595
Glu	Leu	Gly	Leu	Gln	Ile	Gly	Ser	Gly	Gly	Asp	Ser	Gly	Glu	Ala	Glu	
			150			155				160					165	

ctt	gca	gcc	gaa	gga	aag	aaa	gac	att	ggc	gat	ctg	gtt	gac	cgc	ggt	643
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Leu Ala Ala Glu Gly Lys Lys Asp Ile Gly Asp Leu Val Asp Arg Gly
 170 175 180

aaa aaa gct ctc gac gcc ggc gca tcc atc atc atg atc gaa tcc gaa 691
 Lys Lys Ala Leu Asp Ala Gly Ala Ser Ile Ile Met Ile Glu Ser Glu
 185 190 195

ggc atc acc gaa aac gtc acc gaa tgg gat aca ggc gct gcc gcg tcc 739
 Gly Ile Thr Glu Asn Val Thr Glu Trp Asp Thr Gly Ala Ala Ala Ser
 200 205 210

atc atc aat gga ctg gga tta gaa aac gtc atg ttc gaa gcc gcc gac 787
 Ile Ile Asn Gly Leu Gly Leu Glu Asn Val Met Phe Glu Ala Ala Asp
 215 220 225

ggc ccc gtc ttt gag tgg tat gtc aaa aac tac ggc aac gaa tgc aac 835
 Gly Pro Val Phe Glu Trp Tyr Val Lys Asn Tyr Gly Asn Glu Cys Asn
 230 235 240 245

ctg ttc gtc gac cac agt caa att ctg caa ctt gaa ggg ctg cgc caa 883
 Leu Phe Val Asp His Ser Gln Ile Leu Gln Leu Glu Gly Leu Arg Gln
 250 255 260

aac atc tgg ggc aac aag agc acc tgg gga cga gta atc aac cct gcg 931
 Asn Ile Trp Gly Asn Lys Ser Thr Trp Gly Arg Val Ile Asn Pro Ala
 265 270 275

cct taaataccag gtcagggagg gca 957
 Pro

<210> 2066
 <211> 278
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 2066
 Met Ser Asn Ala Val Pro His Asn Val Ser Phe Asn Phe Val Pro Arg
 1 5 10 15

Ala Tyr Arg Pro Glu Lys Pro Arg Thr Phe Gly Met Thr Glu Ile Arg
 20 25 30

Ala Pro Tyr Tyr Ser Thr Phe Gly Thr Arg His Leu Gln Asp Val Phe
 35 40 45

Asp Val Ala Gly Gln Trp Val Asp Gly Ile Lys Trp Ala Gly Gly Ser
 50 55 60

Phe Ser Leu Val Pro Thr Glu Gln Val Arg Ala Phe Ser Asp Ile Ala
 65 70 75 80

His Glu Asn Asn Ala Tyr Val Ser Ser Gly Gly Trp Ile Glu Thr Val
 85 90 95

Leu Arg Tyr Gly Asp Asp Ala Val Asp His Tyr Leu Lys Glu Ala Lys
 100 105 110

Glu Val Gly Phe Asp Val Ile Glu Ile Ser Thr Gly Phe Ile Met Leu
 115 120 125

Asn Thr Ser Gly Leu Gln Arg Leu Val Glu Lys Val Val Lys Ala Gly
130 135 140

Leu Lys Ala Lys Pro Glu Leu Gly Leu Gln Ile Gly Ser Gly Gly Asp
145 150 155 160

Ser Gly Glu Ala Glu Leu Ala Ala Glu Gly Lys Lys Asp Ile Gly Asp
165 170 175

Leu Val Asp Arg Gly Lys Lys Ala Leu Asp Ala Gly Ala Ser Ile Ile
180 185 190

Met Ile Glu Ser Glu Gly Ile Thr Glu Asn Val Thr Glu Trp Asp Thr
195 200 205

Gly Ala Ala Ala Ser Ile Ile Asn Gly Leu Gly Leu Glu Asn Val Met
210 215 220

Phe Glu Ala Ala Asp Gly Pro Val Phe Glu Trp Tyr Val Lys Asn Tyr
225 230 235 240

Gly Asn Glu Cys Asn Leu Phe Val Asp His Ser Gln Ile Leu Gln Leu
245 250 255

Glu Gly Leu Arg Gln Asn Ile Trp Gly Asn Lys Ser Thr Trp Gly Arg
260 265 270

Val Ile Asn Pro Ala Pro
275

<210> 2067

<211> 399

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(376)

<223> RXA01083

<400> 2067

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gagaccttcg agcagttcct cgaaggagag tgatccacct atg ttt ccg cga att 115
Met Phe Pro Arg Ile
1 5

ccg ctg gca atg tgt gct gtc gca gca atc cct gct gtt gtg ctc agg 163
Pro Leu Ala Met Cys Ala Val Ala Ala Ile Pro Ala Val Val Leu Arg
10 15 20

ttt tct gag ctg tcg gcg tca cct gtg gcg acc atg ctg att ttt ggt 211
Phe Ser Glu Leu Ser Ala Ser Pro Val Ala Thr Met Leu Ile Phe Gly
25 30 35

acc gca gtg gtt gct gcc tct ttt gtg ttg gcg tgg gca gct gaa gct 259
Thr Ala Val Val Ala Ala Ser Phe Val Leu Ala Trp Ala Ala Glu Ala
40 45 50

gtg cgc aaa gat att tct ggt gcg ttg gca gtg gcc ttg ctt gcg tta 307
 Val Arg Lys Asp Ile Ser Gly Ala Leu Ala Val Ala Leu Leu Ala Leu
 55 60 65

gtt gca gtg ctt cct gaa tat gct tct gaa acg gtt gtc gag cac act 355
 Val Ala Val Leu Pro Glu Tyr Ala Ser Glu Thr Val Val Glu His Thr
 70 75 80 85

tat caa aca tcg gcg gcg aat taagaaggtg aacagttgac gca 399
 Tyr Gln Thr Ser Ala Ala Asn
 90

<210> 2068

<211> 92

<212> PRT

<213> Corynebacterium glutamicum

<400> 2068

Met Phe Pro Arg Ile Pro Leu Ala Met Cys Ala Val Ala Ala Ile Pro
 1 5 10 15

Ala Val Val Leu Arg Phe Ser Glu Leu Ser Ala Ser Pro Val Ala Thr
 20 25 30

Met Leu Ile Phe Gly Thr Ala Val Val Ala Ala Ser Phe Val Leu Ala
 35 40 45

Trp Ala Ala Glu Ala Val Arg Lys Asp Ile Ser Gly Ala Leu Ala Val
 50 55 60

Ala Leu Leu Ala Leu Val Ala Val Leu Pro Glu Tyr Ala Ser Glu Thr
 65 70 75 80

Val Val Glu His Thr Tyr Gln Thr Ser Ala Ala Asn
 85 90

<210> 2069

<211> 1305

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1282)

<223> RXA01088

<400> 2069
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gtgaaccgaa ttttttaact gatttgaaga agcgagaata atg gga ctg tgg atc 115
 Met Gly Leu Trp Ile
 1 5

gat gca acc gct gcc gtt gca ggg gat atg ttg ctg gga gca ctc att 163
 Asp Ala Thr Ala Gly Val Ala Gly Asp Met Leu Leu Gly Ala Leu Ile
 10 15 20

gat gca ggt gca gaa cta gaa aaa atc caa cag gtt gtg gaa gca gtc 211
 Asp Ala Gly Ala Glu Leu Glu Lys Ile Gln Gln Val Val Glu Ala Val

	25	30	35	
atc ccc ggt gac gtg ctc ttg cgc acc gaa gag gta gtg cgc caa ggc				259
Ile Pro Gly Asp Val Leu Leu Arg Thr Glu Glu Val Val Arg Gln Gly				
	40	45	50	
caa cga ggc atc aag ctg cat gtg gac gca caa cat gaa cac cat cat				307
Gln Arg Gly Ile Lys Leu His Val Asp Ala Gln His Glu His His His				
	55	60	65	
cac cgc cac tta agc acc att aaa gaa ctg ctt gtc aat gct gac atc				355
His Arg His Leu Ser Thr Ile Lys Glu Leu Leu Val Asn Ala Asp Ile				
	70	75	80	85
cct gaa caa acc aag cag gat gcc tta ggc gtt ttt gaa ctc atc gct				403
Pro Glu Gln Thr Lys Gln Asp Ala Leu Gly Val Phe Glu Leu Ile Ala				
	90	95	100	
atc gct gaa gga aaa gtc cac ggc atc gag ccg gag aaa atc cac ttc				451
Ile Ala Glu Gly Lys Val His Gly Ile Glu Pro Glu Lys Ile His Phe				
	105	110	115	
cat gag gta gga gct tgg gat tcc atc gca gac att gtg ggt gtg tgc				499
His Glu Val Gly Ala Trp Asp Ser Ile Ala Asp Ile Val Gly Val Cys				
	120	125	130	
gaa gcg atc agg cag ctt aac cca ggt ttg att gct gca tct ccg att				547
Glu Ala Ile Arg Gln Leu Asn Pro Gly Leu Ile Ala Ala Ser Pro Ile				
	135	140	145	
gct tta gga ttc gga cgc atc aag gca gct cac gga gat att cca gtg				595
Ala Leu Gly Phe Gly Arg Ile Lys Ala Ala His Gly Asp Ile Pro Val				
	150	155	160	165
cca gtt cca gcc gtg gca gag ctg gtg aaa ggc tgg ccc acc caa acc				643
Pro Val Pro Ala Val Ala Glu Leu Val Lys Gly Trp Pro Thr Gln Thr				
	170	175	180	
gga gct ctt atg gag agc acc gaa cct gtt ggt gaa tta gcc acc cca				691
Gly Ala Leu Met Glu Ser Thr Glu Pro Val Gly Glu Leu Ala Thr Pro				
	185	190	195	
act ggt gtt gcg ttg atc cgt cac ttt gcc acc caa gat ggc cct ttc				739
Thr Gly Val Ala Leu Ile Arg His Phe Ala Thr Gln Asp Gly Pro Phe				
	200	205	210	
cca ggt ggc atc atc aat gaa gtt ggc att ggt gca gga aca aaa gat				787
Pro Gly Gly Ile Ile Asn Glu Val Gly Ile Gly Ala Gly Thr Lys Asp				
	215	220	225	
aca gaa ggc cgt cca aat ata gtg cgc gca att ttg ttc aac acc tct				835
Thr Glu Gly Arg Pro Asn Ile Val Arg Ala Ile Leu Phe Asn Thr Ser				
	230	235	240	245
agg agt aac cca gat acc cgc aca ctg gtg caa tta gaa gcc aat gtt				883
Arg Ser Asn Pro Asp Thr Arg Thr Leu Val Gln Leu Glu Ala Asn Val				
	250	255	260	
gat gat caa gac cca cgg ctg tgg cca gga gta ata gag atc etc ttt				931
Asp Asp Gln Asp Pro Arg Leu Trp Pro Gly Val Ile Glu Ile Leu Phe				
	265	270	275	

gcc gct ggc gca gta gat gca tgg ctg act cca att ttg atg aag aag 979
 Ala Ala Gly Ala Val Asp Ala Trp Leu Thr Pro Ile Leu Met Lys Lys
 280 285 290

ggc cgt cct gca cat agg gtg tca gca ttg gtg gat agc tcc gag gtg 1027
 Gly Arg Pro Ala His Arg Val Ser Ala Leu Val Asp Ser Ser Glu Val
 295 300 305

gaa gca gtg aaa acc gca tta ttt gca gcc acc acg act ttt ggg atc 1075
 Glu Ala Val Lys Thr Ala Leu Phe Ala Ala Thr Thr Phe Gly Ile
 310 315 320 325

aga tca tgg gaa gtc gaa cga gaa ggc ttg gac cgt cgt ttc gaa caa 1123
 Arg Ser Trp Glu Val Glu Arg Glu Gly Leu Asp Arg Arg Phe Glu Gln
 330 335 340

gtc gag gtg gac gga cac acc atc aac atc aaa atc ggt tcc cgt gat 1171
 Val Glu Val Asp Gly His Thr Ile Asn Ile Lys Ile Gly Ser Arg Asp
 345 350 355

gat caa gta atc agt gca cag tcc gag ttt gaa gat att cgg tct gca 1219
 Asp Gln Val Ile Ser Ala Gln Ser Glu Phe Glu Asp Ile Arg Ser Ala
 360 365 370

gcg gtg gcc ttg gga att tca gag cgg gaa gtt gtg gca aga att ccg 1267
 Ala Val Ala Leu Gly Ile Ser Glu Arg Glu Val Val Ala Arg Ile Pro
 375 380 385

caa ggc acc acc gag taacaaccaa aaggtcgact gct 1305
 Gln Gly Thr Thr Glu
 390

<210> 2070
 <211> 394
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 2070
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 Leu Gly Ala Leu Ile Asp Ala Gly Ala Glu Leu Glu Lys Ile Gln Gln
 20 25 30
 Val Val Glu Ala Val Ile Pro Gly Asp Val Leu Leu Arg Thr Glu Glu
 35 40 45
 Val Val Arg Gln Gly Gln Arg Gly Ile Lys Leu His Val Asp Ala Gln
 50 55 60
 His Glu His His His Arg His Leu Ser Thr Ile Lys Glu Leu Leu
 65 70 75 80
 Val Asn Ala Asp Ile Pro Glu Gln Thr Lys Gln Asp Ala Leu Gly Val
 85 90 95
 Phe Glu Leu Ile Ala Ile Ala Glu Gly Lys Val His Gly Ile Glu Pro
 100 105 110

Glu Lys Ile His Phe His Glu Val Gly Ala Trp Asp Ser Ile Ala Asp
 115 120 125
 Ile Val Gly Val Cys Glu Ala Ile Arg Gln Leu Asn Pro Gly Leu Ile
 130 135 140
 Ala Ala Ser Pro Ile Ala Leu Gly Phe Gly Arg Ile Lys Ala Ala His
 145 150 155 160
 Gly Asp Ile Pro Val Pro Val Pro Ala Val Ala Glu Leu Val Lys Gly
 165 170 175
 Trp Pro Thr Gln Thr Gly Ala Leu Met Glu Ser Thr Glu Pro Val Gly
 180 185 190
 Glu Leu Ala Thr Pro Thr Gly Val Ala Leu Ile Arg His Phe Ala Thr
 195 200 205
 Gln Asp Gly Pro Phe Pro Gly Gly Ile Ile Asn Glu Val Gly Ile Gly
 210 215 220
 Ala Gly Thr Lys Asp Thr Glu Gly Arg Pro Asn Ile Val Arg Ala Ile
 225 230 235 240
 Leu Phe Asn Thr Ser Arg Ser Asn Pro Asp Thr Arg Thr Leu Val Gln
 245 250 255
 Leu Glu Ala Asn Val Asp Asp Gln Asp Pro Arg Leu Trp Pro Gly Val
 260 265 270
 Ile Glu Ile Leu Phe Ala Ala Gly Ala Val Asp Ala Trp Leu Thr Pro
 275 280 285
 Ile Leu Met Lys Lys Gly Arg Pro Ala His Arg Val Ser Ala Leu Val
 290 295 300
 Asp Ser Ser Glu Val Glu Ala Val Lys Thr Ala Leu Phe Ala Ala Thr
 305 310 315 320
 Thr Thr Phe Gly Ile Arg Ser Trp Glu Val Glu Arg Glu Gly Leu Asp
 325 330 335
 Arg Arg Phe Glu Gln Val Glu Val Asp Gly His Thr Ile Asn Ile Lys
 340 345 350
 Ile Gly Ser Arg Asp Asp Gln Val Ile Ser Ala Gln Ser Glu Phe Glu
 355 360 365
 Asp Ile Arg Ser Ala Ala Val Ala Leu Gly Ile Ser Glu Arg Glu Val
 370 375 380
 Val Ala Arg Ile Pro Gln Gly Thr Thr Glu
 385 390

<210> 2071

<211> 594

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101).. (571)

<223> RXA01091

<400> 2071

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gggtctatgct ggactatcgc cttttgacac gagtatcgca atg gtc ccg aac aca 115
                                     Met Val Pro Asn Thr
                                     1 5

gtc ctt atc cat gac gaa acc gcc gat ctg gcg acg cag atc cag cgg 163
Val Leu Ile His Asp Glu Thr Ala Asp Leu Ala Thr Gln Ile Gln Arg
                                     10 15 20

ctg gaa cat atc atg gcg tgc ctg cgc gat ccg gtc agc gga tgc ccg 211
Leu Glu His Ile Met Ala Cys Leu Arg Asp Pro Val Ser Gly Cys Pro
                                     25 30 35

tgg gat att gaa cag acc ttt gcc agc atc gcg ccc cac acg att gag 259
Trp Asp Ile Glu Gln Thr Phe Ala Ser Ile Ala Pro His Thr Ile Glu
                                     40 45 50

gaa gcc tac gag gtt gcc gac gcc atc gcg cag gaa gac tgg ccc gag 307
Glu Gly Tyr Glu Val Ala Asp Ala Ile Ala Gln Glu Asp Trp Pro Glu
                                     55 60 65

cta cgc gcc gag ttg gcc gat ttg ctg ttt cag acc gtg ttt cac gcc 355
Leu Arg Gly Glu Leu Gly Asp Leu Leu Phe Gln Thr Val Phe His Ala
                                     70 75 80 85

caa atg gcg cgc gag gca gcc cat ttc gct ttg gtt gac gtg gtg aag 403
Gln Met Ala Arg Glu Ala Gly His Phe Ala Leu Val Asp Val Val Lys
                                     90 95 100

gca att tcg gac aag atg gtt ttg cgc cat ccg cac gtg ttc gcc gcg 451
Ala Ile Ser Asp Lys Met Val Leu Arg His Pro His Val Phe Gly Ala
                                     105 110 115

cag tcg aac gcg aaa tcc gcc gac cag cag gtg aag att ggg aag tca 499
Gln Ser Asn Ala Lys Ser Ala Asp Gln Gln Val Lys Ile Gly Lys Ser
                                     120 125 130

tca agg cgc ccg agc gcg cgg gca aag cgc aaa agg gcg ttt tgg atg 547
Ser Arg Arg Pro Ser Ala Arg Ala Lys Arg Lys Arg Ala Phe Trp Met
                                     135 140 145

gcg tcg cgc tgg gac tgc ctg ccc tgatgcgcgc gacgaagctg caa 594
Ala Ser Arg Trp Asp Cys Leu Pro
150 155

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<210> 2072

<211> 157

<212> PRT

<213> Corynebacterium glutamicum

<400> 2072

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Met Val Pro Asn Thr Val Leu Ile His Asp Glu Thr Ala Asp Leu Ala
1 5 10 15

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Thr Gln Ile Gln Arg Leu Glu His Ile Met Ala Cys Leu Arg Asp Pro
20 25 30

Val Ser Gly Cys Pro Trp Asp Ile Glu Gln Thr Phe Ala Ser Ile Ala
35 40 45

Pro His Thr Ile Glu Glu Gly Tyr Glu Val Ala Asp Ala Ile Ala Gln
50 55 60

Glu Asp Trp Pro Glu Leu Arg Gly Glu Leu Gly Asp Leu Leu Phe Gln
65 70 75 80

Thr Val Phe His Ala Gln Met Ala Arg Glu Ala Gly His Phe Ala Leu
85 90 95

Val Asp Val Val Lys Ala Ile Ser Asp Lys Met Val Leu Arg His Pro
100 105 110

His Val Phe Gly Ala Gln Ser Asn Ala Lys Ser Ala Asp Gln Gln Val
115 120 125

Lys Ile Gly Lys Ser Ser Arg Arg Pro Ser Ala Arg Ala Lys Arg Lys
130 135 140

Arg Ala Phe Trp Met Ala Ser Arg Trp Asp Cys Leu Pro
145 150 155

<210> 2073

<211> 280

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(280)

<223> RXA01092

<400> 2073

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gcgtcacctg catcaaaacc ccgaaatcag ctttgattgt gtg gaa act gcg gcc 115
Val Glu Thr Ala Ala
1 5

ttc gtg gcc gag cag ctg cgc agc ttc ggg gtg gat gaa att cac acc 163
Phe Val Ala Glu Gln Leu Arg Ser Phe Gly Val Asp Glu Ile His Thr
10 15 20

ggc atc gcg aaa acc ggt atc atc gcc ctg att cac ggg cgc gag gct 211
Gly Ile Ala Lys Thr Gly Ile Ile Ala Leu Ile His Gly Arg Glu Ala
25 30 35

ggc ccc gtc gtc ggc ctg cgc gcc gat atg gac gcg ctg ccg ctg acc 259
Gly Pro Val Val Gly Leu Arg Ala Asp Met Asp Ala Leu Pro Leu Thr
40 45 50

gag att acc ggc gtc tac tat 280
Glu Ile Thr Gly Val Tyr Tyr
55 60

<210> 2074

<211> 60

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2074

Val	Glu	Thr	Ala	Ala	Phe	Val	Ala	Glu	Gln	Leu	Arg	Ser	Phe	Gly	Val
1				5					10					15	

Asp	Glu	Ile	His	Thr	Gly	Ile	Ala	Lys	Thr	Gly	Ile	Ile	Ala	Leu	Ile
		20						25					30		

His	Gly	Arg	Glu	Ala	Gly	Pro	Val	Val	Gly	Leu	Arg	Ala	Asp	Met	Asp
		35					40					45			

Ala	Leu	Pro	Leu	Thr	Glu	Ile	Thr	Gly	Val	Tyr	Tyr
	50					55				60	

<210> 2075

<211> 280

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(280)

<223> RXA01092

<400> 2075

tgaacccatg cccgttatca atagtatcgc cagtttttcc gacgagatga cccgctggcg 60

gcgtcacctg	catcaaaacc	ccgaaatcag	ctttgattgt	gtg	gaa	act	gcg	gcc	115
				Val	Glu	Thr	Ala	Ala	
				1				5	

ttc	gtg	gcc	gag	cag	ctg	cgc	agc	ttc	ggg	gtg	gat	gaa	att	cac	acc	163
Phe	Val	Ala	Glu	Gln	Leu	Arg	Ser	Phe	Gly	Val	Asp	Glu	Ile	His	Thr	
			10						15				20			

ggc	atc	gcg	aaa	acc	ggt	atc	atc	gcc	ctg	att	cac	ggg	cgc	gag	gct	211
Gly	Ile	Ala	Lys	Thr	Gly	Ile	Ile	Ala	Leu	Ile	His	Gly	Arg	Glu	Ala	
			25					30					35			

ggc	ccc	gtc	gtc	ggc	ctg	cgc	gcc	gat	atg	gac	gcg	ctg	ccg	ctg	acc	259
Gly	Pro	Val	Val	Gly	Leu	Arg	Ala	Asp	Met	Asp	Ala	Leu	Pro	Leu	Thr	
		40					45					50				

gag	att	acc	ggc	gtc	tac	tat										280
Glu	Ile	Thr	Gly	Val	Tyr	Tyr										
		55				60										

<210> 2076

<211> 60

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2076

Val Glu Thr Ala Ala Phe Val Ala Glu Gln Leu Arg Ser Phe Gly Val

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1           5           10           15
Asp Glu Ile His Thr Gly Ile Ala Lys Thr Gly Ile Ile Ala Leu Ile
      20           25           30
His Gly Arg Glu Ala Gly Pro Val Val Gly Leu Arg Ala Asp Met Asp
      35           40           45
Ala Leu Pro Leu Thr Glu Ile Thr Gly Val Tyr Tyr
      50           55           60

<210> 2077
<211> 822
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(799)
<223> RXA01096

<400> 2077
accgtgaaac aaaccggcgg tcggtgccac actggtgcc acacatgttt cgacaatgac 60
gttttgctgt aaaagcaaca acgattaagg aagaaatctt atg aag cca cgc gtg 115
      Met Lys Pro Arg Val
      1           5
ctg tca gca tta ggc att gga gct ggc gcc ctg gtt gtc tgg atc agc 163
Leu Ser Ala Leu Gly Ile Gly Ala Gly Ala Leu Val Val Trp Ile Ser
      10           15           20
tca cgc atg aac tgg gta acc atc gag gct ttc gac gat aaa tca ggt 211
Ser Arg Met Asn Trp Val Thr Ile Glu Ala Phe Asp Asp Lys Ser Gly
      25           30           35
agt gtc acc caa tct att gtg ggt gca acc tgg tct aca gaa atc atg 259
Ser Val Thr Gln Ser Ile Val Gly Ala Thr Trp Ser Thr Glu Ile Met
      40           45           50
gcg ctt gca ctt gct ttg ctc gct gcc ttc gcc gcc gcg ttg gtg ctc 307
Ala Leu Ala Leu Ala Leu Leu Ala Ala Phe Ala Ala Ala Leu Val Leu
      55           60           65
aag cgc atg ggt cgg cgc atc att ggt ggt att tcg gcg ctg atc gcg 355
Lys Arg Met Gly Arg Arg Ile Ile Gly Gly Ile Ser Ala Leu Ile Ala
      70           75           80           85
gtg ggt gcc agc ctg tct cca ctc gcg ctt ctc acc caa gac cca gac 403
Val Gly Ala Ser Leu Ser Pro Leu Ala Leu Leu Thr Gln Asp Pro Asp
      90           95           100
gca gaa cgg gcc cga acc ctg ctg acc tcc ggt gtg gcc tca cag aag 451
Ala Glu Arg Ala Arg Thr Leu Leu Thr Ser Gly Val Ala Ser Gln Lys
      105           110           115
gct aat tcc gga acc ctg ctg tct gat tgg gcg gag atc atc aat acc 499
Ala Asn Ser Gly Thr Leu Leu Ser Asp Trp Ala Glu Ile Ile Asn Thr
      120           125           130

```

acc acc cat cca ctg gcg gca gtg gta gcc atg att ggc tgc gcg cta 547
 Thr Thr His Pro Leu Ala Ala Val Val Ala Met Ile Gly Cys Ala Leu
 135 140 145

gcc cta gtc ggc ggc gtt gtc ctt gcc atg cgc cct gcc gag gac acc 595
 Ala Leu Val Gly Gly Val Val Leu Ala Met Arg Pro Ala Glu Asp Thr
 150 155 160 165

gcg aaa agc aat cag tat gag cgt aaa cag gct cgc gct gag aaa atc 643
 Ala Lys Ser Asn Gln Tyr Glu Arg Lys Gln Ala Arg Ala Glu Lys Ile
 170 175 180

cac acc gat ttg gcc caa gat cca gac tcc ggt cgt gtg atg tgg acg 691
 His Thr Asp Leu Ala Gln Asp Pro Asp Ser Gly Arg Val Met Trp Thr
 185 190 195

cac tcg atg aag aca ttg act tca ccg aga aga ctc aga aat cca aag 739
 His Ser Met Lys Thr Leu Thr Ser Pro Arg Arg Leu Arg Asn Pro Lys
 200 205 210

aaa ccc cag gtc aaa gct agg gtg tgg cac cct gat ttc ttt cgc cat 787
 Lys Pro Gln Val Lys Ala Arg Val Trp His Pro Asp Phe Phe Arg His
 215 220 225

gtg tgt tcg gga taaccttaaa cacagcattg gtt 822
 Val Cys Ser Gly
 230

<210> 2078
 <211> 233
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 2078
 Met Lys Pro Arg Val Leu Ser Ala Leu Gly Ile Gly Ala Gly Ala Leu
 1 5 10 15

Val Val Trp Ile Ser Ser Arg Met Asn Trp Val Thr Ile Glu Ala Phe
 20 25 30

Asp Asp Lys Ser Gly Ser Val Thr Gln Ser Ile Val Gly Ala Thr Trp
 35 40 45

Ser Thr Glu Ile Met Ala Leu Ala Leu Ala Leu Leu Ala Ala Phe Ala
 50 55 60

Ala Ala Leu Val Leu Lys Arg Met Gly Arg Arg Ile Ile Gly Gly Ile
 65 70 75 80

Ser Ala Leu Ile Ala Val Gly Ala Ser Leu Ser Pro Leu Ala Leu Leu
 85 90 95

Thr Gln Asp Pro Asp Ala Glu Arg Ala Arg Thr Leu Leu Thr Ser Gly
 100 105 110

Val Ala Ser Gln Lys Ala Asn Ser Gly Thr Leu Leu Ser Asp Trp Ala
 115 120 125

Glu Ile Ile Asn Thr Thr Thr His Pro Leu Ala Ala Val Val Ala Met
 130 135 140

```

Ile Gly Cys Ala Leu Ala Leu Val Gly Gly Val Val Leu Ala Met Arg
145                      150                      155                      160

Pro Ala Glu Asp Thr Ala Lys Ser Asn Gln Tyr Glu Arg Lys Gln Ala
                      165                      170                      175

Arg Ala Glu Lys Ile His Thr Asp Leu Ala Gln Asp Pro Asp Ser Gly
                      180                      185                      190

Arg Val Met Trp Thr His Ser Met Lys Thr Leu Thr Ser Pro Arg Arg
195                      200                      205

Leu Arg Asn Pro Lys Lys Pro Gln Val Lys Ala Arg Val Trp His Pro
210                      215                      220

Asp Phe Phe Arg His Val Cys Ser Gly
225                      230

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<210> 2079

<211> 1368

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1345)

<223> RXA01102

<400> 2079

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attctatggat tgtggggaga gatgacttaa ttggaatca cgggctttaa cacgcgctga 60

cattgagcaa cttccagca tgtggaaaag cccagggttc gtg gct gtc ctc gtg 115
                      Val Ala Val Leu Val
                      1                      5

gcg gtt gca gca gcg ttc ggc agt tgg tca ctc ctt ctt ccc gtc gta 163
Ala Val Ala Ala Ala Phe Gly Ser Trp Ser Leu Leu Leu Pro Val Val
                      10                      15                      20

ccg cta gcg gtc ctc aac aac ggc gga tca agc gct gtc gcc ggt gcc 211
Pro Leu Ala Val Leu Asn Asn Gly Gly Ser Ser Ala Val Ala Gly Ala
                      25                      30                      35

acc act ggc atc ttc atg gca gct aca gtg atc act cag att ttc act 259
Thr Thr Gly Ile Phe Met Ala Ala Thr Val Ile Thr Gln Ile Phe Thr
                      40                      45                      50

ccc gct gcg ctg cgg aaa att ggc tac acc cca gtg atg gct ttc gcc 307
Pro Ala Ala Leu Arg Lys Ile Gly Tyr Thr Pro Val Met Ala Phe Ala
                      55                      60                      65

gca ttc atg ctg ggt gtg cca gcc atc ggg tac atc ttc agc gtc gag 355
Ala Phe Met Leu Gly Val Pro Ala Ile Gly Tyr Ile Phe Ser Val Glu
                      70                      75                      80

cca att cca gtg ctg gta gtg tcc gca ctt cga gga att ggg ttc ggt 403
Pro Ile Pro Val Leu Val Val Ser Ala Leu Arg Gly Ile Gly Phe Gly
                      90                      95                      100

```

gcg ctc acc gtc gca gaa tct gcg ttg gtg gct gaa ctc gtt ccc gta	451
Ala Leu Thr Val Ala Glu Ser Ala Leu Val Ala Glu Leu Val Pro Val	
105 110 115	
cgc ttc ttg ggc aaa gct tct gga atg ttg ggc gta ttt att ggc ctt	499
Arg Phe Leu Gly Lys Ala Ser Gly Met Leu Gly Val Phe Ile Gly Leu	
120 125 130	
tcc caa atg ctt ttc ctg cct gcc ggg ttg gcg tta ggt gac caa ttt	547
Ser Gln Met Leu Phe Leu Pro Ala Gly Leu Ala Leu Gly Asp Gln Phe	
135 140 145	
ggc tac aac gtg gtc tat gtt tta ggt gcc gtt atc gca cta gtt gca	595
Gly Tyr Asn Val Val Tyr Val Leu Gly Ala Val Ile Ala Leu Val Ala	
150 155 160 165	
gcg gtg atg tgt ctg cgt att ccg cag gtt aag gca gcg gca aag cag	643
Ala Val Met Cys Leu Arg Ile Pro Gln Val Lys Ala Ala Ala Lys Gln	
170 175 180	
caa cca cag gtg agc gaa cag gag cgt tct gtt tcc acc tgg aag ttg	691
Gln Pro Gln Val Ser Glu Gln Glu Arg Ser Val Ser Thr Trp Lys Leu	
185 190 195	
gtg ctg gtt ccc tcc ttg gct gtt acc agt ttg tca atg act ttt ggc	739
Val Leu Val Pro Ser Leu Ala Val Thr Ser Leu Ser Met Thr Phe Gly	
200 205 210	
gca gtg tct tca ttc ctt cca gct gca gtc att gag tta gat cca gga	787
Ala Val Ser Ser Phe Leu Pro Ala Ala Val Ile Glu Leu Asp Pro Gly	
215 220 225	
tta ggt gct gca tta gcg ggt att att tta tcc att acc ggt ggt tct	835
Leu Gly Ala Ala Leu Ala Gly Ile Ile Leu Ser Ile Thr Gly Gly Ser	
230 235 240 245	
tca atg gtg ttc cgc tac ctg tcc gcc gtt atc gct gac cgc cgc ggt	883
Ser Met Val Phe Arg Tyr Leu Ser Gly Val Ile Ala Asp Arg Arg Gly	
250 255 260	
gtg cct ggt acc acg atg att cct gct cag atc att ggg ttc tta ggt	931
Val Pro Gly Thr Thr Met Ile Pro Ala Gln Ile Ile Gly Phe Leu Gly	
265 270 275	
gtc gtt tta atc acc gtc aca atc ttc caa ggc tgg tcc gtg tgg ctt	979
Val Val Leu Ile Thr Val Thr Ile Phe Gln Gly Trp Ser Val Trp Leu	
280 285 290	
ttg att ata ggt gca gtg atg ttt ggt ggt gct ttt ggc atg gtg caa	1027
Leu Ile Ile Gly Ala Val Met Phe Gly Gly Ala Phe Gly Met Val Gln	
295 300 305	
aac gaa gcg ttg ctt tca atg ttt ttc cgg ctt cct cgc act aga gtc	1075
Asn Glu Ala Leu Leu Ser Met Phe Phe Arg Leu Pro Arg Thr Arg Val	
310 315 320 325	
tcc gaa gcc tcc gcc atc tgg aat atc gcc ttt gat tgg gga aca gga	1123
Ser Glu Ala Ser Ala Ile Trp Asn Ile Ala Phe Asp Ser Gly Thr Gly	
330 335 340	
atc gga agc ttc ctc ctt gcc ata gtt gcc gca tgg ctt gct tac agt	1171

```

Ile Gly Ser Phe Leu Leu Gly Ile Val Ala Ala Ser Leu Ala Tyr Ser
      345                      350                      355

ggt gct ttt ggt tcc gga gcc gtg gtg att ttg ttt gga atc gtt ttg 1219
Gly Ala Phe Gly Ser Gly Ala Val Val Ile Leu Phe Gly Ile Val Leu
      360                      365                      370

acc acc gcc gat cga atc att ggg cgg cac cgc att act gaa tac aac 1267
Thr Thr Ala Asp Arg Ile Ile Gly Arg His Arg Ile Thr Glu Tyr Asn
      375                      380                      385

aac acc cgc gcg cgt ttg cgc cag gtg cca gtc gct cgg cgt gca gtg 1315
Asn Thr Arg Ala Arg Leu Arg Gln Val Pro Val Ala Arg Arg Ala Val
      390                      395                      400                      405

caa ggg ctg cgc aac agg cgc aaa gat cgc taaaacgctt ttgcagccca 1365
Gln Gly Leu Arg Asn Arg Arg Lys Asp Arg 415

ccc 1368

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<210> 2080

<211> 415

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2080

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Val Ala Val Leu Val Ala Val Ala Ala Phe Gly Ser Trp Ser Leu
      1                      5                      10                      15

```

```

Leu Leu Pro Val Val Pro Leu Ala Val Leu Asn Asn Gly Gly Ser Ser
      20                      25                      30

```

```

Ala Val Ala Gly Ala Thr Thr Gly Ile Phe Met Ala Ala Thr Val Ile
      35                      40                      45

```

```

Thr Gln Ile Phe Thr Pro Ala Ala Leu Arg Lys Ile Gly Tyr Thr Pro
      50                      55                      60

```

```

Val Met Ala Phe Ala Ala Phe Met Leu Gly Val Pro Ala Ile Gly Tyr
      65                      70                      75                      80

```

```

Ile Phe Ser Val Glu Pro Ile Pro Val Leu Val Val Ser Ala Leu Arg
      85                      90                      95

```

```

Gly Ile Gly Phe Gly Ala Leu Thr Val Ala Glu Ser Ala Leu Val Ala
      100                      105                      110

```

```

Glu Leu Val Pro Val Arg Phe Leu Gly Lys Ala Ser Gly Met Leu Gly
      115                      120                      125

```

```

Val Phe Ile Gly Leu Ser Gln Met Leu Phe Leu Pro Ala Gly Leu Ala
      130                      135                      140

```

```

Leu Gly Asp Gln Phe Gly Tyr Asn Val Val Tyr Val Leu Gly Ala Val
      145                      150                      155                      160

```

```

Ile Ala Leu Val Ala Ala Val Met Cys Leu Arg Ile Pro Gln Val Lys
      165                      170                      175

```

Ala Ala Ala Lys Gln Gln Pro Gln Val Ser Glu Gln Glu Arg Ser Val
 180 185 190
 Ser Thr Trp Lys Leu Val Leu Val Pro Ser Leu Ala Val Thr Ser Leu
 195 200 205
 Ser Met Thr Phe Gly Ala Val Ser Ser Phe Leu Pro Ala Ala Val Ile
 210 215 220
 Glu Leu Asp Pro Gly Leu Gly Ala Ala Leu Ala Gly Ile Ile Leu Ser
 225 230 235 240
 Ile Thr Gly Gly Ser Ser Met Val Phe Arg Tyr Leu Ser Gly Val Ile
 245 250 255
 Ala Asp Arg Arg Gly Val Pro Gly Thr Thr Met Ile Pro Ala Gln Ile
 260 265 270
 Ile Gly Phe Leu Gly Val Val Leu Ile Thr Val Thr Ile Phe Gln Gly
 275 280 285
 Trp Ser Val Trp Leu Leu Ile Ile Gly Ala Val Met Phe Gly Gly Ala
 290 295 300
 Phe Gly Met Val Gln Asn Glu Ala Leu Leu Ser Met Phe Phe Arg Leu
 305 310 315 320
 Pro Arg Thr Arg Val Ser Glu Ala Ser Ala Ile Trp Asn Ile Ala Phe
 325 330 335
 Asp Ser Gly Thr Gly Ile Gly Ser Phe Leu Leu Gly Ile Val Ala Ala
 340 345 350
 Ser Leu Ala Tyr Ser Gly Ala Phe Gly Ser Gly Ala Val Val Ile Leu
 355 360 365
 Phe Gly Ile Val Leu Thr Thr Ala Asp Arg Ile Ile Gly Arg His Arg
 370 375 380
 Ile Thr Glu Tyr Asn Asn Thr Arg Ala Arg Leu Arg Gln Val Pro Val
 385 390 395 400
 Ala Arg Arg Ala Val Gln Gly Leu Arg Asn Arg Arg Lys Asp Arg
 405 410 415

<210> 2081

<211> 348

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(325)

<223> RXA01103

<400> 2081

ccgaagcaga gtacaaggct gttgcccggtg cgctgcgcgg tgccgtagag atggatctct 60

 gtcaaacagg aatcccatcc actaaggagg cgctctagac atg aac tct tct ccc 115
 Met Asn Ser Ser Pro

gtg aat gat cga aac gtc cct gca ccc aac acc tcc att cct ttc cca 163
Val Asn Asp Arg Asn Val Pro Ala Pro Asn Thr Ser Ile Pro Phe Pro
10 15 20

gtt gac ctg aat cga gtg acg gag gct gtt gat tcc ttg ggc tac cac 211
Val Asp Leu Asn Arg Val Thr Glu Ala Val Asp Ser Leu Gly Tyr His
25 30 35

tat ttg agc tca gaa gat cgc atc atc gtg ccg tgg caa gat cac cgc 259
Tyr Leu Ser Ser Glu Asp Arg Ile Ile Val Pro Trp Gln Asp His Arg
40 45 50

att tcg atg tac ttc agc cac gaa tca ggg caa atg ctc acc atc ctt 307
Ile Ser Met Tyr Phe Ser His Glu Ser Gly Gln Met Leu Thr Ile Leu
55 60 65

ggc cgc acg cgc ctt aat ttg gac atg ttt gcc atc aac gat cgc cgc 355
Gly Arg Thr Arg Leu Asn Leu Asp Met Phe Ala Ile Asn Asp Ala Ala
70 75 80 85

cga gct gtc acc gaa tgg aat gcc gaa cgc atc ggg cca aca gcc ctc 403
Arg Ala Val Thr Glu Trp Asn Ala Glu Arg Ile Gly Pro Thr Ala Leu
90 95 100

gtc cat ctg ggc aac gac ggc gaa gtg gaa ttg aaa ttc cgc acg acc 451
Val His Leu Gly Asn Asp Gly Glu Val Glu Leu Lys Phe Arg Thr Thr
105 110 115

atc tgc atc gat gaa ggg tta agc acc caa cag cta cgc caa ttc atc 499
Ile Cys Ile Asp Glu Gly Leu Ser Thr Gln Gln Leu Arg Gln Phe Ile
120 125 130

aac ctg tcc ttg gac acc acc gcc atg gct gtg acc tat att ctg gag 547
Asn Leu Ser Leu Asp Thr Thr Ala Met Ala Val Thr Tyr Ile Leu Glu
135 140 145

cgt ttt tca gaa ctt aac ttc agc gac acc gga agc cct gac gac acg 595
Arg Phe Ser Glu Leu Asn Phe Ser Asp Thr Gly Ser Pro Asp Asp Thr
150 155 160 165

aac aat gcc gat gaa ctc agc gac gaa caa gac caa gca gat ctc gta 643
Asn Asn Ala Asp Glu Leu Ser Asp Glu Gln Asp Gln Ala Asp Leu Val
170 175 180

gag aaa atc cgg ggg ctg tac gtt ccc act cca gtt gaa gag ctc atc 691
Glu Lys Ile Arg Gly Leu Tyr Val Pro Thr Pro Val Glu Glu Leu Ile
185 190 195

gaa tcc cta gaa gac gca gag tgg gaa gaa tca gac atg gca gac gag 739
Glu Ser Leu Glu Asp Ala Glu Trp Glu Glu Ser Asp Met Ala Asp Glu
200 205 210

gat gca gaa gac gac tac cta gac gat gac tca gaa atc gaa tgg gaa 787
Asp Ala Glu Asp Asp Tyr Leu Asp Asp Asp Ser Glu Ile Glu Trp Glu
215 220 225

aca gac gat gac tac ttc gaa cct gaa gaa gtc gac atg gac gaa ctc 835
Thr Asp Asp Asp Tyr Phe Glu Pro Glu Glu Val Asp Met Asp Glu Leu
230 235 240 245

```

ctc aac ggt ttc ctc gaa gat tct gac atc ccc cag gaa gtc acc ttg      883
Leu Asn Gly Phe Leu Glu Asp Ser Asp Ile Pro Gln Glu Val Thr Leu
                250                255                260

gaa cgc att cgg gca caa ctg cat gcc atc ggc gtg gta aaa acc agc      931
Glu Arg Ile Arg Ala Gln Leu His Ala Ile Gly Val Val Lys Thr Ser
                265                270                275

ggc gaa gac gat ttc atc atc gcg tgg atc aac gaa gtg ttt tta ggc      979
Gly Glu Asp Asp Phe Ile Ile Ala Trp Ile Asn Glu Val Phe Leu Gly
                280                285                290

ttc ttc gtt gat aat ggc ccc act ttc ctg gtg aaa ggt cac tgg gat      1027
Phe Phe Val Asp Asn Gly Pro Thr Phe Leu Val Lys Gly His Trp Asp
                295                300                305

ccc agc atg gac ccc aca cgc gac ttc atg aaa ctg ttc atg atg tgc      1075
Pro Ser Met Asp Pro Thr Arg Asp Phe Met Lys Leu Phe Met Met Cys
                310                315                320                325

aat cag tgg aac gaa aac tct ctg act acc aaa gct ttt tgc cat act      1123
Asn Gln Trp Asn Glu Asn Ser Leu Thr Thr Lys Ala Phe Cys His Thr
                330                335                340

gat gac aag ggt ctc cag gtc cgg gta gag ttc gcg gtc tct gtc gct      1171
Asp Asp Lys Gly Leu Gln Val Arg Val Glu Phe Ala Val Ser Val Ala
                345                350                355

gaa ggc ctc aac gac gat caa cta cag cac aac atc gca ctg tca att      1219
Glu Gly Leu Asn Asp Asp Gln Leu Gln His Asn Ile Ala Leu Ser Ile
                360                365                370

cat cat att ttg caa gcg att gat tcc atc agc aca gaa gcc act gga      1267
His His Ile Leu Gln Ala Ile Asp Ser Ile Ser Thr Glu Ala Thr Gly
                375                380                385

tca tca acg gtg gaa tgg ccg gag aaa aac cgc tgatcattaa ggtcttccaa 1320
Ser Ser Thr Val Glu Trp Pro Glu Lys Asn Arg
                390                395                400

gaa                                                                    1323

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<210> 2084

<211> 400

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2084

```

Met Asp Phe Thr Ser Val Asn Asp Arg Asn Val Pro Ala Pro Asn Thr
  1          5          10          15

```

```

Ser Ile Pro Phe Pro Val Asp Leu Asn Arg Val Thr Glu Ala Val Asp
  20          25          30

```

```

Ser Leu Gly Tyr His Tyr Leu Ser Ser Glu Asp Arg Ile Ile Val Pro
  35          40          45

```

```

Trp Gln Asp His Arg Ile Ser Met Tyr Phe Ser His Glu Ser Gly Gln
  50          55          60

```

Met Leu Thr Ile Leu Gly Arg Thr Arg Leu Asn Leu Asp Met Phe Ala
 65 70 75 80
 Ile Asn Asp Ala Ala Arg Ala Val Thr Glu Trp Asn Ala Glu Arg Ile
 85 90 95
 Gly Pro Thr Ala Leu Val His Leu Gly Asn Asp Gly Glu Val Glu Leu
 100 105 110
 Lys Phe Arg Thr Thr Ile Cys Ile Asp Glu Gly Leu Ser Thr Gln Gln
 115 120 125
 Leu Arg Gln Phe Ile Asn Leu Ser Leu Asp Thr Thr Ala Met Ala Val
 130 135 140
 Thr Tyr Ile Leu Glu Arg Phe Ser Glu Leu Asn Phe Ser Asp Thr Gly
 145 150 155 160
 Ser Pro Asp Asp Thr Asn Asn Ala Asp Glu Leu Ser Asp Glu Gln Asp
 165 170 175
 Gln Ala Asp Leu Val Glu Lys Ile Arg Gly Leu Tyr Val Pro Thr Pro
 180 185 190
 Val Glu Glu Leu Ile Glu Ser Leu Glu Asp Ala Glu Trp Glu Glu Ser
 195 200 205
 Asp Met Ala Asp Glu Asp Ala Glu Asp Asp Tyr Leu Asp Asp Asp Ser
 210 215 220
 Glu Ile Glu Trp Glu Thr Asp Asp Asp Tyr Phe Glu Pro Glu Glu Val
 225 230 235 240
 Asp Met Asp Glu Leu Leu Asn Gly Phe Leu Glu Asp Ser Asp Ile Pro
 245 250 255
 Gln Glu Val Thr Leu Glu Arg Ile Arg Ala Gln Leu His Ala Ile Gly
 260 265 270
 Val Val Lys Thr Ser Gly Glu Asp Phe Ile Ile Ala Trp Ile Asn
 275 280 285
 Glu Val Phe Leu Gly Phe Phe Val Asp Asn Gly Pro Thr Phe Leu Val
 290 295 300
 Lys Gly His Trp Asp Pro Ser Met Asp Pro Thr Arg Asp Phe Met Lys
 305 310 315 320
 Leu Phe Met Met Cys Asn Gln Trp Asn Glu Asn Ser Leu Thr Thr Lys
 325 330 335
 Ala Phe Cys His Thr Asp Asp Lys Gly Leu Gln Val Arg Val Glu Phe
 340 345 350
 Ala Val Ser Val Ala Glu Gly Leu Asn Asp Asp Gln Leu Gln His Asn
 355 360 365
 Ile Ala Leu Ser Ile His His Ile Leu Gln Ala Ile Asp Ser Ile Ser
 370 375 380
 Thr Glu Ala Thr Gly Ser Ser Thr Val Glu Trp Pro Glu Lys Asn Arg

385

390

395

400

<210> 2085

<211> 774

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(751)

<223> RXA01108

<400> 2085

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gttgcaaaagt taacagtcaa cggctgtatt ctttagagcc atg aca tac ccc ggc 115
 Met Thr Tyr Pro Gly
 1 5

atc acc tct gac cac aat cct tat gat gga tac aca ggc gat gac ggg 163
 Ile Thr Ser Asp His Asn Pro Tyr Asp Gly Tyr Thr Gly Asp Asp Gly
 10 15 20

gcc gga aac aag cgc aac ctc cca aac cga aag aaa ata aac aaa tcg 211
 Ala Gly Asn Lys Arg Asn Leu Pro Asn Arg Lys Lys Ile Asn Lys Ser
 25 30 35

gtg gga gtt tac gct ggt gtg ttt gcc cta aca ttg gct tta tac gcc 259
 Val Gly Val Tyr Ala Gly Val Phe Ala Leu Thr Leu Ala Leu Tyr Ala
 40 45 50

att ggg gga gcc gca tgg gga ctg ctc cga ccc act tat acc gct tat 307
 Ile Gly Gly Ala Ala Trp Gly Leu Leu Arg Pro Thr Tyr Thr Ala Tyr
 55 60 65

gtt gaa gac gct gaa aca gcc tcc ata gcg gtg gaa acc aac act tct 355
 Val Glu Asp Ala Glu Thr Ala Ser Ile Ala Val Glu Thr Asn Thr Ser
 70 75 80 85

ttt gcc ggc tat gcc tgg ttt gcg atc gcc acc ggt gtg ctt gca gca 403
 Phe Ala Gly Tyr Ala Trp Phe Ala Ile Ala Thr Gly Val Leu Ala Ala
 90 95 100

gca atc gca tta ttc gtt ttc ctg cgc acc cct caa cat cga ggc cca 451
 Ala Ile Ala Leu Phe Val Phe Leu Arg Thr Pro Gln His Arg Gly Pro
 105 110 115

gtt atg ctc cta tgg ctg gga att gta tct atc gca ggt tcc gtg gca 499
 Val Met Leu Leu Trp Leu Gly Ile Val Ser Ile Ala Gly Ser Val Ala
 120 125 130

ttc ctg gtg ttt gga aac gtg gcc tcg acg atg ctt cat ggt tca cca 547
 Phe Leu Val Phe Gly Asn Val Ala Ser Thr Met Leu His Gly Ser Pro
 135 140 145

tct gat tac gcc tca gcg atc ggt gcg tct ttc cag gta gca ccc act 595
 Ser Asp Tyr Ala Ser Ala Ile Gly Ala Ser Phe Gln Val Ala Pro Thr

```

150              155              160              165
att acc cct ggt gtt gcg ttt ggg gtc gct cca ttt ttg agt gtg tgc 643
Ile Thr Pro Gly Val Ala Phe Gly Val Ala Pro Phe Leu Ser Val Cys
              170              175              180

atg tat tgg tgc gcg gca ttt gtg aca cct gaa gaa gag ata gac cag 691
Met Tyr Trp Cys Ala Ala Phe Val Thr Pro Glu Glu Glu Ile Asp Gln
              185              190              195

gac gac gca ggc cag ggg act tcg aaa gca tcg ggg tct gag atg act 739
Asp Asp Ala Gly Gln Gly Thr Ser Lys Ala Ser Gly Ser Glu Met Thr
              200              205              210

ggg gct agt ggc taggggctag atgtgcgcaa aca 774
Gly Ala Ser Gly
              215

<210> 2086
<211> 217
<212> PRT
<213> Corynebacterium glutamicum

<400> 2086
Met Thr Tyr Pro Gly Ile Thr Ser Asp His Asn Pro Tyr Asp Gly Tyr
 1          5          10          15

Thr Gly Asp Asp Gly Ala Gly Asn Lys Arg Asn Leu Pro Asn Arg Lys
          20          25          30

Lys Ile Asn Lys Ser Val Gly Val Tyr Ala Gly Val Phe Ala Leu Thr
          35          40          45

Leu Ala Leu Tyr Ala Ile Gly Gly Ala Ala Trp Gly Leu Leu Arg Pro
 50          55          60

Thr Tyr Thr Ala Tyr Val Glu Asp Ala Glu Thr Ala Ser Ile Ala Val
 65          70          75          80

Glu Thr Asn Thr Ser Phe Ala Gly Tyr Ala Trp Phe Ala Ile Ala Thr
          85          90          95

Gly Val Leu Ala Ala Ala Ile Ala Leu Phe Val Phe Leu Arg Thr Pro
          100          105          110

Gln His Arg Gly Pro Val Met Leu Leu Trp Leu Gly Ile Val Ser Ile
          115          120          125

Ala Gly Ser Val Ala Phe Leu Val Phe Gly Asn Val Ala Ser Thr Met
          130          135          140

Leu His Gly Ser Pro Ser Asp Tyr Ala Ser Ala Ile Gly Ala Ser Phe
          145          150          155          160

Gln Val Ala Pro Thr Ile Thr Pro Gly Val Ala Phe Gly Val Ala Pro
          165          170          175

Phe Leu Ser Val Cys Met Tyr Trp Cys Ala Ala Phe Val Thr Pro Glu
          180          185          190

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Glu Glu Ile Asp Gln Asp Asp Ala Gly Gln Gly Thr Ser Lys Ala Ser
 195 200 205

Gly Ser Glu Met Thr Gly Ala Ser Gly
 210 215

<210> 2087

<211> 765

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(742)

<223> RXA01109

<400> 2087

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gttttcgcga gcatgtcgat gatttatcag gacgagaact ttg tct att agc ctt 115
 Leu Ser Ile Ser Leu
 1 5

tcc tca aag aag gtt gct ttc gca gca ctc atg gtc acc cca ctt ctc 163
 Ser Ser Lys Lys Val Ala Phe Ala Ala Leu Met Val Thr Pro Leu Leu
 10 15 20

ttg acc gca tgt ggc agt gat tca tct gat act gaa gca gcc tca tcc 211
 Leu Thr Ala Cys Gly Ser Asp Ser Ser Asp Thr Glu Ala Ala Ser Ser
 25 30 35

agc gca gcg acg acg aca aat tct tcc tca tcc agc gca gcg acc tcg 259
 Ser Ala Ala Thr Thr Thr Asn Ser Ser Ser Ser Ala Ala Thr Ser
 40 45 50

gcg gaa gca gca gaa acc acc tcg tcc gaa tct gaa tct tcc gaa gca 307
 Ala Glu Ala Ala Glu Thr Thr Ser Ser Glu Ser Glu Ser Ser Glu Ala
 55 60 65

aca acc att aac gaa gag cag caa gca cag ctt gat gta ctg tct caa 355
 Thr Thr Ile Asn Glu Glu Gln Gln Ala Gln Leu Asp Val Leu Ser Gln
 70 75 80 85

gag ctg tct gag aac cca att acc ttc gct gaa gct gcg cca gtt gaa 403
 Glu Leu Ser Glu Asn Pro Ile Thr Phe Ala Glu Ala Ala Pro Val Glu
 90 95 100

aac ggc gag acc gct tcc cca gaa gac aca gct gcc atc gag gct ctg 451
 Asn Gly Glu Thr Ala Ser Pro Glu Asp Thr Ala Ala Ile Glu Ala Leu
 105 110 115

gtt cgc gga tac act gac acc aac acc ttg cgt agc tcc ctt gcg tac 499
 Val Arg Gly Tyr Thr Asp Thr Asn Thr Leu Arg Ser Ser Leu Ala Tyr
 120 125 130

acc atc aac aac acc tgc acc cgc gtt ctt gaa gcc agc ggc gct gac 547
 Thr Ile Asn Asn Thr Cys Thr Arg Val Leu Glu Ala Ser Gly Ala Asp
 135 140 145

gct acc cag ctt gat ctc aac acc atc cct gat atc cca ctg ggt ggc 595

Ala Thr Gln Leu Asp Leu Asn Thr Ile Pro Asp Ile Pro Leu Gly Gly
 150 155 160 165

gaa ggc acc gga act gtt gat tcc atc acc gat gtt gtg gtc aac ggc 643
 Glu Gly Thr Gly Thr Val Asp Ser Ile Thr Asp Val Val Val Asn Gly
 170 175 180

cag gaa gca tcc gca tgg gtc gta gca acc gcc ggt gga acc acc gac 691
 Gln Glu Ala Ser Ala Trp Val Val Ala Thr Ala Gly Gly Thr Thr Asp
 185 190 195

tct gca acc cag cgc ttc ttc aac gaa ggt ggc cag tgg aag ttc tgc 739
 Ser Ala Thr Gln Arg Phe Phe Asn Glu Gly Gly Gln Trp Lys Phe Cys
 200 205 210

gac taatccacag agcttaaaac tcc 765
 Asp

<210> 2088

<211> 214

<212> PRT

<213> Corynebacterium glutamicum

<400> 2088

Leu Ser Ile Ser Leu Ser Ser Lys Lys Val Ala Phe Ala Ala Leu Met
 1 5 10 15

Val Thr Pro Leu Leu Leu Thr Ala Cys Gly Ser Asp Ser Ser Asp Thr
 20 25 30

Glu Ala Ala Ser Ser Ser Ala Ala Thr Thr Thr Asn Ser Ser Ser Ser
 35 40 45

Ser Ala Ala Thr Ser Ala Glu Ala Ala Glu Thr Thr Ser Ser Glu Ser
 50 55 60

Glu Ser Ser Glu Ala Thr Thr Ile Asn Glu Glu Gln Gln Ala Gln Leu
 65 70 75 80

Asp Val Leu Ser Gln Glu Leu Ser Glu Asn Pro Ile Thr Phe Ala Glu
 85 90 95

Ala Ala Pro Val Glu Asn Gly Glu Thr Ala Ser Pro Glu Asp Thr Ala
 100 105 110

Ala Ile Glu Ala Leu Val Arg Gly Tyr Thr Asp Thr Asn Thr Leu Arg
 115 120 125

Ser Ser Leu Ala Tyr Thr Ile Asn Asn Thr Cys Thr Arg Val Leu Glu
 130 135 140

Ala Ser Gly Ala Asp Ala Thr Gln Leu Asp Leu Asn Thr Ile Pro Asp
 145 150 155 160

Ile Pro Leu Gly Gly Glu Gly Thr Gly Thr Val Asp Ser Ile Thr Asp
 165 170 175

Val Val Val Asn Gly Gln Glu Ala Ser Ala Trp Val Val Ala Thr Ala
 180 185 190

Gly Gly Thr Thr Asp Ser Ala Thr Gln Arg Phe Phe Asn Glu Gly Gly
195 200 205

Gln Trp Lys Phe Cys Asp
210

<210> 2089

<211> 1053

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1030)

<223> RXA01119

<400> 2089

ccgtaaagac gttggcgaag tcatcatcaa cggtgccgtt gcccgtaggcg aagccgaacc 60

agagatgttg gaagctgtcg cagaagaaaa gaccgcgtag ttg gca gga gtt atc 115
Leu Ala Gly Val Ile
1 5

acc ggc ttt gcc atc atc ctg tcg gtt atc ggc gtt gga ttt ctt ctg 163
Thr Gly Phe Ala Ile Ile Leu Ser Val Ile Gly Val Gly Phe Leu Leu
10 15 20

gca aag ctg ggg gtc atc aat gat gac aaa cag cgc ttg gtg tta aac 211
Ala Lys Leu Gly Val Ile Asn Asp Asp Lys Gln Arg Leu Val Leu Asn
25 30 35

cgc att gct ttt tat gcg gca act cca gcg ctg ctt ttc aat gtc gtt 259
Arg Ile Ala Phe Tyr Ala Ala Thr Pro Ala Leu Leu Phe Asn Val Val
40 45 50

gcc cga tca gat ccc agc gcg ttg atc tca ccg gtc att gtg gtg aca 307
Ala Arg Ser Asp Pro Ser Ala Leu Ile Ser Pro Val Ile Val Val Thr
55 60 65

ttt gtg gcc acg atc gtc aca gca gct gtg tac tgc gtg att tcg gcg 355
Phe Val Ala Thr Ile Val Thr Ala Ala Val Tyr Cys Val Ile Ser Ala
70 75 80 85

att ttc ttt aag aag gat atc gcc act acg gcg aca gga gct gcg gct 403
Ile Phe Phe Lys Lys Asp Ile Ala Thr Thr Ala Thr Gly Ala Ala
90 95 100

tct gcc tac gtg aac tcc aac aac att ggc ctg ccg gtg tct att tat 451
Ser Ala Tyr Val Asn Ser Asn Asn Ile Gly Leu Pro Val Ser Ile Tyr
105 110 115

gtg ctg gga aca ggc gca tat gtg gca ccg att ctg gtc atg cag atg 499
Val Leu Gly Thr Gly Ala Tyr Val Ala Pro Ile Leu Val Met Gln Met
120 125 130

gtg att ttc gcg ccc atg atc ctg gcc gcg ctg acc tct ggt gat gtg 547
Val Ile Phe Ala Pro Met Ile Leu Ala Ala Leu Thr Ser Gly Asp Val
135 140 145

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aaa ggc tgc cgc ggg caa aaa ata tgg gct gcg gtg aaa ggt tca ctg 595
Lys Gly Ser Arg Gly Gln Lys Ile Trp Ala Val Lys Gly Ser Leu
150 155 160 165

ctc agc cca att gtg ttg gcc tct atc gcg ggc ctg atc gtg tgt ctg 643
Leu Ser Pro Ile Val Leu Ala Ser Ile Ala Gly Leu Ile Val Cys Leu
170 175 180

tta gaa att cag ctg cca gcc gca gtc atg gaa ccc acc atc att ttg 691
Leu Glu Ile Gln Leu Pro Ala Ala Val Met Glu Pro Thr Ile Leu
185 190 195

ggc ggc gca tcc att ccg ttg att ctg atg agc ttc ggc gca tca ttg 739
Gly Gly Ala Ser Ile Pro Leu Ile Leu Met Ser Phe Gly Ala Ser Leu
200 205 210

ccc tca acc aac gtg ctg gct tcc aag gcg gat cgc ccc agc gtt ctt 787
Pro Ser Thr Asn Val Leu Ala Ser Lys Ala Asp Arg Pro Ser Val Leu
215 220 225

act gct act gcg ata aaa att gtg ggt atg ccc gcc atc act tgg ctg 835
Thr Ala Thr Ala Ile Lys Ile Val Gly Met Pro Ala Ile Thr Trp Leu
230 235 240 245

atc gcc aag gcg ttt ggt ctg gag ggc gat tac ctc tac gcc gct gtt 883
Ile Ala Lys Ala Phe Gly Leu Glu Gly Asp Tyr Leu Tyr Ala Ala Val
250 255 260

att ttg gcg gcg ctg ccc gcc gcg cag aat gtg tac aac tac gcg gcg 931
Ile Leu Ala Ala Leu Pro Ala Ala Gln Asn Val Tyr Asn Tyr Ala Ala
265 270 275

acg tac cgc aag ggc gag atc gtc gcc cgc gat acg gtc ttc ctc acc 979
Thr Tyr Arg Lys Gly Glu Ile Val Ala Arg Asp Thr Val Phe Leu Thr
280 285 290

acg ttc cta gcg ctg ctg ggc atg cta gga atc gcg gcc cta ttt ggt 1027
Thr Phe Leu Ala Leu Leu Gly Met Leu Gly Ile Ala Ala Leu Phe Gly
295 300 305

cgc tagggcttca ggctgctttt cga 1053
Arg
310

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<210> 2090

<211> 310

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2090

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Leu Ala Gly Val Ile Thr Gly Phe Ala Ile Ile Leu Ser Val Ile Gly
1 5 10 15

Val Gly Phe Leu Leu Ala Lys Leu Gly Val Ile Asn Asp Asp Lys Gln
20 25 30

Arg Leu Val Leu Asn Arg Ile Ala Phe Tyr Ala Ala Thr Pro Ala Leu
35 40 45

Leu Phe Asn Val Val Ala Arg Ser Asp Pro Ser Ala Leu Ile Ser Pro

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50 55 60
 Val Ile Val Val Thr Phe Val Ala Thr Ile Val Thr Ala Ala Val Tyr
 65 70 75 80
 Cys Val Ile Ser Ala Ile Phe Phe Lys Lys Asp Ile Ala Thr Thr Ala
 85 90 95
 Thr Gly Ala Ala Ala Ser Ala Tyr Val Asn Ser Asn Asn Ile Gly Leu
 100 105 110
 Pro Val Ser Ile Tyr Val Leu Gly Thr Gly Ala Tyr Val Ala Pro Ile
 115 120 125
 Leu Val Met Gln Met Val Ile Phe Ala Pro Met Ile Leu Ala Ala Leu
 130 135 140
 Thr Ser Gly Asp Val Lys Gly Ser Arg Gly Gln Lys Ile Trp Ala Ala
 145 150 155 160
 Val Lys Gly Ser Leu Leu Ser Pro Ile Val Leu Ala Ser Ile Ala Gly
 165 170 175
 Leu Ile Val Cys Leu Leu Glu Ile Gln Leu Pro Ala Ala Val Met Glu
 180 185 190
 Pro Thr Ile Ile Leu Gly Gly Ala Ser Ile Pro Leu Ile Leu Met Ser
 195 200 205
 Phe Gly Ala Ser Leu Pro Ser Thr Asn Val Leu Ala Ser Lys Ala Asp
 210 215 220
 Arg Pro Ser Val Leu Thr Ala Thr Ala Ile Lys Ile Val Gly Met Pro
 225 230 235 240
 Ala Ile Thr Trp Leu Ile Ala Lys Ala Phe Gly Leu Glu Gly Asp Tyr
 245 250 255
 Leu Tyr Ala Ala Val Ile Leu Ala Ala Leu Pro Ala Ala Gln Asn Val
 260 265 270
 Tyr Asn Tyr Ala Ala Thr Tyr Arg Lys Gly Glu Ile Val Ala Arg Asp
 275 280 285
 Thr Val Phe Leu Thr Thr Phe Leu Ala Leu Leu Gly Met Leu Gly Ile
 290 295 300
 Ala Ala Leu Phe Gly Arg
 305 310

<210> 2091

<211> 645

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(622)

<223> RXA01122

[illegible]

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1 5 10 15
 Ala Ala Leu Ser Ser Trp Ala Val Ser Arg Ala Leu Pro Leu Arg Ala
 20 25 30
 Asp Asn Ser Ile Glu Ile Asp Ala Pro Val Glu Lys Val Trp Asp Phe
 35 40 45
 Ile Glu Glu Thr Asn Arg Val Pro Glu Trp Asn Glu His Ile Leu Tyr
 50 55 60
 Val Gln Ala Pro Gly Glu Ile Glu Gln Gly Met Lys Leu Lys Met Lys
 65 70 75 80
 Thr Arg His Pro Glu Thr Asn Arg Leu Thr Leu Lys Phe Arg Pro Thr
 85 90 95
 Ile Asp Val Leu Arg Pro His Arg Glu Leu Thr Trp Ser Thr Lys Ile
 100 105 110
 Val Ala Arg Trp Leu Leu Thr Val Thr Asp Thr Ile Glu Leu Lys Pro
 115 120 125
 Leu Glu Asp Gly Arg Thr Glu Val Asp Gln Ser Met Ser Phe Ser Gly
 130 135 140
 Val Leu Ser Pro Gly Val Pro Phe Leu Ala Ser Ile Ser Arg Ile Lys
 145 150 155 160
 Glu Asn Ser Asn Arg Gln Leu Lys Ala Leu Ile Glu Ala Glu
 165 170

 <210> 2093
 <211> 570
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (101)..(547)
 <223> RXA01123

 <400> 2093
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 gtggcggttg gtggaaacac gtggctgggc gaatgtgagc atg cga acc ctg gcc 115
 Met Arg Thr Leu Ala
 1 5
 gcg gag cta aat atc aag gcg ccg tcg ctg tac aag cat gta aaa acg 163
 Ala Glu Leu Asn Ile Lys Ala Pro Ser Leu Tyr Lys His Val Lys Thr
 10 15 20
 cgc gag gat atc gcc gca cac atc gcc acg aag gca ttt att cag ctg 211
 Arg Glu Asp Ile Ala Ala His Ile Ala Thr Lys Ala Phe Ile Gln Leu
 25 30 35
 ggg caa agc ctg cat gaa cat tgt gaa agt gtg gag gat ttg ctt gcg 259
 Gly Gln Ser Leu His Glu His Cys Glu Ser Val Glu Asp Leu Leu Ala
 40 45 50

gaa tac cgc tcc atg gct cgg gaa aat cca aat att tac cgg ctt ctc 307
 Glu Tyr Arg Ser Met Ala Arg Glu Asn Pro Asn Ile Tyr Arg Leu Leu
 55 60 65

acc agt tca gag ttc ccc cgc gag cta ctt cca gaa ggc cta gaa act 355
 Thr Ser Ser Glu Phe Pro Arg Glu Leu Leu Pro Glu Gly Leu Glu Thr
 70 75 80 85

tgg gca gga acg cca ttc tac ctg gtc acc ggc cac gat ccg atc aag 403
 Trp Ala Gly Thr Pro Phe Tyr Leu Val Thr Gly His Asp Pro Ile Lys
 90 95 100

ggt caa gca ctg tgg gca ttc gcg cac ggc atg gcc atc ctg gaa atc 451
 Gly Gln Ala Leu Trp Ala Phe Ala His Gly Met Ala Ile Leu Glu Ile
 105 110 115

gac gcc cga ttc gcc ggc ccc aac aat gga tcc ccc gcg gat ggc gtg 499
 Asp Ala Arg Phe Ala Gly Pro Asn Asn Gly Ser Pro Ala Asp Gly Val
 120 125 130

tgg gag atc ggc gcg cgg gca ttt gac aca caa gta ttc gac caa ggc 547
 Trp Glu Ile Gly Ala Arg Ala Phe Asp Thr Gln Val Phe Asp Gln Gly
 135 140 145

tgagcaaaaa ggcgctaagc tgt 570

<210> 2094
 <211> 149
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 2094
 Met Arg Thr Leu Ala Ala Glu Leu Asn Ile Lys Ala Pro Ser Leu Tyr
 1 5 10 15
 Lys His Val Lys Thr Arg Glu Asp Ile Ala Ala His Ile Ala Thr Lys
 20 25 30
 Ala Phe Ile Gln Leu Gly Gln Ser Leu His Glu His Cys Glu Ser Val
 35 40 45
 Glu Asp Leu Leu Ala Glu Tyr Arg Ser Met Ala Arg Glu Asn Pro Asn
 50 55 60
 Ile Tyr Arg Leu Leu Thr Ser Ser Glu Phe Pro Arg Glu Leu Leu Pro
 65 70 75 80
 Glu Gly Leu Glu Thr Trp Ala Gly Thr Pro Phe Tyr Leu Val Thr Gly
 85 90 95
 His Asp Pro Ile Lys Gly Gln Ala Leu Trp Ala Phe Ala His Gly Met
 100 105 110
 Ala Ile Leu Glu Ile Asp Ala Arg Phe Ala Gly Pro Asn Asn Gly Ser
 115 120 125
 Pro Ala Asp Gly Val Trp Glu Ile Gly Ala Arg Ala Phe Asp Thr Gln
 130 135 140

Val Phe Asp Gln Gly
145

<210> 2095
<211> 302
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (1)..(279)
<223> RXA01127

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<400> 2095
gga att ggc ctc gca gca tcc ggc aac atc gat gcc acg ggc acc aac 48
Gly Ile Gly Leu Ala Ala Ser Gly Asn Ile Asp Ala Thr Gly Thr Asn
1 5 10 15

cct tcc atg ttc gag cca gtc cac ggc tct gca cca gat atc gca ggc 96
Pro Ser Met Phe Glu Pro Val His Gly Ser Ala Pro Asp Ile Ala Gly
20 25 30

cag gga atc gca gac cca acg gca gca atc cta tcc gct gcg atg ctg 144
Gln Gly Ile Ala Asp Pro Thr Ala Ala Ile Leu Ser Ala Ala Met Leu
35 40 45

ctg cgt cac tta ggt gat gaa gac aac gca gta cgt att gaa aca gcc 192
Leu Arg His Leu Gly Asp Glu Asp Asn Ala Val Arg Ile Glu Thr Ala
50 55 60

atc gca gct gat gtg gct ggc cga gat aac tct cag ccg att tct acc 240
Ile Ala Ala Asp Val Ala Gly Arg Asp Asn Ser Gln Pro Ile Ser Thr
65 70 75 80

act gag gtg gga gac cgc atc gtc aag gcg ctg caa agc taaatttcaa 289
Thr Glu Val Gly Asp Arg Ile Val Lys Ala Leu Gln Ser
85 90

cgccgacccc ctt 302

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<210> 2096
<211> 93
<212> PRT
<213> *Corynebacterium glutamicum*

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<400> 2096
Gly Ile Gly Leu Ala Ala Ser Gly Asn Ile Asp Ala Thr Gly Thr Asn
1 5 10 15

Pro Ser Met Phe Glu Pro Val His Gly Ser Ala Pro Asp Ile Ala Gly
20 25 30

Gln Gly Ile Ala Asp Pro Thr Ala Ala Ile Leu Ser Ala Ala Met Leu
35 40 45

Leu Arg His Leu Gly Asp Glu Asp Asn Ala Val Arg Ile Glu Thr Ala
50 55 60

Ile Ala Ala Asp Val Ala Gly Arg Asp Asn Ser Gln Pro Ile Ser Thr

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65

Thr Glu Val Gly Asp Arg Ile Val Lys Ala Leu Gln Ser
85 90

<210> 2097

 $\langle 220 \rangle$

<400> 2097

cgaatgcagg atttcgagac aatgaggcag tttttctttt atg gtt aat ctc atg 115
Met Val Asn Leu Met
1 5

tcg gtc gaa ctc gaa gaa atc cgc gat ttc tta gca gga ttt gaa cct 163
Ser Val Glu Leu Glu Glu Ile Arg Asp Phe Leu Ala Gly Phe Glu Pro
10 15 20

ttc gcg cag cta cca gcc gag gaa cta gat cag tta cct gga aaa atg 211
Phe Ala Gln Leu Pro Ala Glu Glu Leu Asp Gln Leu Pro Gly Lys Met
25 30 35

agc ttg cgc tat ttt cgg cgt ggg gaa gag atc atc cca att ggt gtg 259
Ser Leu Arg Tyr Phe Arg Arg Gly Glu Glu Ile Ile Pro Ile Gly Val

40 45 50

ccc aat cat tac atg ggg gta atc aga tgc ggt gcc att gat gtt ctt 307
Pro Asn His Tyr Met Gly Val Ile Arg Ser Gly Ala Ile Asp Val Leu
55 60 65

gat cag gag ggc gta ctg ctg gat cgc cgt gac gcg ggg cgc tcg ttt 355
Asp Gln Glu Gly Val Leu Leu Asp Arg Arg Asp Ala Gly Arg Ser Phe
70 75 80 85

ggc tat tcc acg atg ggg cca gaa cga aat tct cgg tac cgt atg gtt 403
Gly Tyr Ser Thr Met Gly Pro Glu Arg Asn Ser Arg Tyr Arg Met Val
90 95 100

gcc gtg gaa gat tcc ttg gtg ttg cgt ctg ggg cgt gat gat ttt gat 451
Ala Val Glu Asp Ser Leu Val Leu Arg Leu Gly Arg Asp Asp Phe Asp
105 110 115

gag tta gcc aag cgc aac cct gat ctg aac cgt tac tac tcc agc tgg 499
Glu Leu Ala Lys Arg Asn Pro Asp Leu Asn Arg Tyr Tyr Ser Ser Trp
120 125 130

tcg aag cgt atc cgc gcc gct gct gat caa ttg cgc caa gaa tct agt 547
Ser Lys Arg Ile Arg Ala Ala Ala Asp Gln Leu Arg Gln Glu Ser Ser
135 140 145

tgc aag gtg ctg cgc acg aag ttg ggg gag ttc aag atc gcc aac ccg 595
Ser Lys Val Leu Arg Thr Lys Leu Gly Glu Phe Lys Ile Ala Asn Pro

150	155										160										165																				
att tcc tgc agc ccg gac acc acg atc atg gat gct gcc atc aag atg	ile ser cys ser pro asp thr thr ile met asp ala ala ile lys met										cat gag ttc ggg gtg tct tcg ttg ctg gtg cag atc gat ggg gaa ctg										his glu phe gly val ser ser leu leu val gln ile asp gly glu leu										643										
	170										175										190										195										
aaa ggc atc atc acc gat cac tat atg cgc agc agg gtg gtg gcg aag	lys gly ile thr asp his tyr met arg ser arg val val ala lys										cat ttg gat att cag ctg ccg gtc tct gag gtc atg acg gtg gat ccg										his leu asp ile gln leu pro val ser glu val met thr val asp pro										739										
	200										205										220										225										
cgt tgc gcg acc tcg cag ggg ttg gct ttt gag gcc atg ttg ttg atg	arg cys ala thr ser gln gly leu ala phe glu ala met leu leu met										tcg gag ctg cgc att cac cac ttg ccg att gtg gat gat ggc caa atc										ser glu leu arg ile his his leu pro ile val asp asp gly gln ile										835										
	230										235										250										255										
tcc ggc atc gtc act gca gct gac atc atg cgc ttg ctg cgc cac gat	ser gly ile val thr ala ala asp ile met arg leu leu arg his asp										ccg att tac ctc act cgc gat ctg tcg cga aaa aat acc gtg gag gaa										pro ile tyr leu thr ala asp leu ser arg lys asn thr val glu glu										931										
	265										270										275										290										
ttg gcc aac acc ttc cag tcg gca gcg gag gtg gct tcg aga ttt att	leu ala asn thr phe gln ser ala ala glu val ala ser arg phe ile										gat cgg gga gct tct gcg gaa gaa gtc agt agc ttg ctc acc gtg gct										asp arg gly ala ser ala glu glu val ser ser leu leu thr val ala										1027										
	295										300										310										315										
gcg gat tct ttg gca aga agg ctc ctt gtg ctg gcg gag cgg aaa ttt	ala asp ser leu ala arg arg leu leu val leu ala glu arg lys phe										ggt gca ccg cca gtt ccg tat tgc phe val gtg gtg ggc tcg cag ggc										gly ala pro pro val pro tyr cys										agg aaa gaa atg gga ctg gcc tct gat caa gac aat gcc ctt gtt ctg										1075
	330										335										350										355										
agg aaa gaa atg gga ctg gcc tct gat caa gac aat gcc ctt gtt ctg	arg lys glu met gly leu ala ser asp gln asp asn ala leu val leu										ggt gca ccg cca gtt ccg tat tgc phe val gtg gtg ggc tcg cag ggc										gly ala pro pro val pro tyr cys										agg aaa gaa atg gga ctg gcc tct gat caa gac aat gcc ctt gtt ctg										1123
	360										365										380										385										
gac aat tcc tac aat gac cgc gag cat gga cag tat ttt gca gcg ctg	asp asn ser tyr asn asp arg glu his gly gln										ggt gca ccg cca gtt ccg tat tgc phe val gtg gtg ggc tcg cag ggc										gly ala pro pro val pro tyr cys										agg aaa gaa atg gga ctg gcc tct gat caa gac aat gcc ctt gtt ctg										1171
	375										380										390										400										
agt gaa ttc gtg tgc cag ggc ctc gac cgc gca gga cag gtg ctg tgt	ser glu phe val cys gln gly leu asp arg ala gly gln val leu cys										ggt gca ccg cca gtt ccg tat tgc phe val gtg gtg ggc tcg cag ggc										gly ala pro pro val pro tyr cys										agg aaa gaa atg gga ctg gcc tct gat caa gac aat gcc ctt gtt ctg										1219
	395										400										410										420										
gac aat tcc tac aat gac cgc gag cat gga cag tat ttt gca gcg ctg	asp asn ser tyr asn asp arg glu his gly gln										ggt gca ccg cca gtt ccg tat tgc phe val gtg gtg ggc tcg cag ggc										gly ala pro pro val pro tyr cys										agg aaa gaa atg gga ctg gcc tct gat caa gac aat gcc ctt gtt ctg										1267
	435										440										450										460										
agt gaa ttc gtg tgc cag ggc ctc gac cgc gca gga cag gtg ctg tgt	ser glu phe val cys gln gly leu asp arg ala gly gln val leu cys										ggt gca ccg cca gtt ccg tat tgc phe val gtg gtg ggc tcg cag ggc										gly ala pro pro val pro tyr cys										agg aaa gaa atg gga ctg gcc tct gat caa gac aat gcc ctt gtt ctg										1315
	470										475										480										490										

ccg ggt gac atg atg gca tcc aat ccg gag tgg cgg aaa act gct gac 1363
 Pro Gly Asp Met Met Ala Ser Asn Pro Glu Trp Arg Lys Thr Ala Asp
 410 415 420

cag tgg atc tcc acc ttc cat tcc tgg att act gcg ccg gag ccg gat 1411
 Gln Trp Ile Ser Thr Phe His Ser Trp Ile Thr Ala Pro Glu Pro Asp
 425 430 435

gcg ttg ctg cat gcc cag aca ttc ttt gat ttc agg gga att tac ggc 1459
 Ala Leu Leu His Ala Gln Thr Phe Phe Asp Phe Arg Gly Ile Tyr Gly
 440 445 450

gac acc gag atg gct aag gat gtc cac caa aat gcg gtg aat atg gcc 1507
 Asp Thr Glu Met Ala Lys Asp Val His Gln Asn Ala Val Asn Met Ala
 455 460 465

agg ggt gcg cgt cgc atg cat gca cac ttg gct agt ctt gcg gcc cgg 1555
 Arg Gly Ala Arg Arg Met His Ala His Leu Ala Ser Leu Ala Ala Arg
 470 475 480 485

cgc gat cct ccg ctg ggg ttt ttc cgt ggt ctt gtg gtg gag cgt tct 1603
 Arg Asp Pro Pro Leu Gly Phe Phe Arg Gly Leu Val Val Glu Arg Ser
 490 495 500

ggt gaa tac ggc gcg acg atg gat att aag aag ggt ggc acc gcg ggc 1651
 Gly Glu Tyr Gly Ala Thr Met Asp Ile Lys Lys Gly Gly Thr Ala Gly
 505 510 515

atc gtg cag atg gcg agg ctg tat gcg ctg gcc acg ggt agt gat gcg 1699
 Ile Val Gln Met Ala Arg Leu Tyr Ala Leu Ala Thr Gly Ser Asp Ala
 520 525 530

att ggg act ccg gag cgg ttg att gct gcg tcg ggc cat ggt cag gtg 1747
 Ile Gly Thr Arg Glu Arg Leu Ile Ala Ala Ser Gly His Gly Gln Val
 535 540 545

tcg cgt aag ggt gcg cag gat ttg ttg gat gcc ttt gat ttc tta gcg 1795
 Ser Arg Lys Gly Ala Gln Asp Leu Leu Asp Ala Phe Asp Phe Leu Ala
 550 555 560 565

gcg atg gcg ttc cag cac cag gcg cgg ttg atc aag gtg ggg gag aag 1843
 Ala Met Ala Phe Gln His Gln Ala Arg Leu Ile Lys Val Gly Glu Lys
 570 575 580

ccg aac tat cac att gat ccc aag acg ttg ggc aag atg gat ccg gag 1891
 Pro Asn Tyr His Ile Asp Pro Lys Thr Leu Gly Lys Met Asp Arg Glu
 585 590 595

cat ttg cgc gat gca ttt tcc att att aaa gat atg cag tcg gcg tta 1939
 His Leu Arg Asp Ala Phe Ser Ile Ile Lys Asp Met Gln Ser Ala Leu
 600 605 610

gct act aaa tat ccg gtg agg aac atc tagtggtggg gcgtcgaaaa 1986
 Ala Thr Lys Tyr Pro Val Arg Asn Ile
 615 620

gcg 1989

<211> 622

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2098

Met Val Asn Leu Met Ser Val Glu Leu Glu Glu Ile Arg Asp Phe Leu
 1 5 10 15

Ala Gly Phe Glu Pro Phe Ala Gln Leu Pro Ala Glu Glu Leu Asp Gln
 20 25 30

Leu Pro Gly Lys Met Ser Leu Arg Tyr Phe Arg Arg Gly Glu Glu Ile
 35 40 45

Ile Pro Ile Gly Val Pro Asn His Tyr Met Gly Val Ile Arg Ser Gly
 50 55 60

Ala Ile Asp Val Leu Asp Gln Glu Gly Val Leu Leu Asp Arg Arg Asp
 65 70 75 80

Ala Gly Arg Ser Phe Gly Tyr Ser Thr Met Gly Pro Glu Arg Asn Ser
 85 90 95

Arg Tyr Arg Met Val Ala Val Glu Asp Ser Leu Val Leu Arg Leu Gly
 100 105 110

Arg Asp Asp Phe Asp Glu Leu Ala Lys Arg Asn Pro Asp Leu Asn Arg
 115 120 125

Tyr Tyr Ser Ser Trp Ser Lys Arg Ile Arg Ala Ala Ala Asp Gln Leu
 130 135 140

Arg Gln Glu Ser Ser Ser Lys Val Leu Arg Thr Lys Leu Gly Glu Phe
 145 150 155 160

Lys Ile Ala Asn Pro Ile Ser Cys Ser Pro Asp Thr Thr Ile Met Asp
 165 170 175

Ala Ala Ile Lys Met His Glu Phe Gly Val Ser Ser Leu Leu Val Gln
 180 185 190

Ile Asp Gly Glu Leu Lys Gly Ile Ile Thr Asp His Tyr Met Arg Ser
 195 200 205

Arg Val Val Ala Lys His Leu Asp Ile Gln Leu Pro Val Ser Glu Val
 210 215 220

Met Thr Val Asp Pro Arg Cys Ala Thr Ser Gln Gly Leu Ala Phe Glu
 225 230 235 240

Ala Met Leu Leu Met Ser Glu Leu Arg Ile His His Leu Pro Ile Val
 245 250 255

Asp Asp Gly Gln Ile Ser Gly Ile Val Thr Ala Ala Asp Ile Met Arg
 260 265 270

Leu Leu Arg His Asp Pro Ile Tyr Leu Thr Ala Asp Leu Ser Arg Lys
 275 280 285

Asn Thr Val Glu Glu Leu Ala Asn Thr Phe Gln Ser Ala Ala Glu Val
 290 295 300

Ala Ser Arg Phe Ile Asp Arg Gly Ala Ser Ala Glu Glu Val Ser Ser
 305 310 315 320
 Leu Leu Thr Val Ala Ala Asp Ser Leu Ala Arg Arg Leu Leu Val Leu
 325 330 335
 Ala Glu Arg Lys Phe Gly Ala Pro Pro Val Pro Tyr Cys Phe Val Val
 340 345 350
 Val Gly Ser Gln Gly Arg Lys Glu Met Gly Leu Ala Ser Asp Gln Asp
 355 360 365
 Asn Ala Leu Val Leu Asp Asn Ser Tyr Asn Asp Arg Glu His Gly Gln
 370 375 380
 Tyr Phe Ala Ala Leu Ser Glu Phe Val Cys Gln Gly Leu Asp Arg Ala
 385 390 395 400
 Gly Gln Val Leu Cys Pro Gly Asp Met Met Ala Ser Asn Pro Glu Trp
 405 410 415
 Arg Lys Thr Ala Asp Gln Trp Ile Ser Thr Phe His Ser Trp Ile Thr
 420 425 430
 Ala Pro Glu Pro Asp Ala Leu Leu His Ala Gln Thr Phe Phe Asp Phe
 435 440 445
 Arg Gly Ile Tyr Gly Asp Thr Glu Met Ala Lys Asp Val His Gln Asn
 450 455 460
 Ala Val Asn Met Ala Arg Gly Ala Arg Arg Met His Ala His Leu Ala
 465 470 475 480
 Ser Leu Ala Ala Arg Arg Asp Pro Pro Leu Gly Phe Phe Arg Gly Leu
 485 490 495
 Val Val Glu Arg Ser Gly Glu Tyr Gly Ala Thr Met Asp Ile Lys Lys
 500 505 510
 Gly Gly Thr Ala Gly Ile Val Gln Met Ala Arg Leu Tyr Ala Leu Ala
 515 520 525
 Thr Gly Ser Asp Ala Ile Gly Thr Arg Glu Arg Leu Ile Ala Ala Ser
 530 535 540
 Gly His Gly Gln Val Ser Arg Lys Gly Ala Gln Asp Leu Leu Asp Ala
 545 550 555 560
 Phe Asp Phe Leu Ala Ala Met Ala Phe Gln His Gln Ala Arg Leu Ile
 565 570 575
 Lys Val Gly Glu Lys Pro Asn Tyr His Ile Asp Pro Lys Thr Leu Gly
 580 585 590
 Lys Met Asp Arg Glu His Leu Arg Asp Ala Phe Ser Ile Ile Lys Asp
 595 600 605
 Met Gln Ser Ala Leu Ala Thr Lys Tyr Pro Val Arg Asn Ile
 610 615 620

gct tct ggg cgc atc agc ttt gag ctg ggt gac acc cca gtg gat gtg 691
 Ala Ser Gly Arg Ile Ser Phe Glu Leu Gly Asp Thr Pro Val Asp Val
 185 190 195

att ttg gat gat ccc gag ttg ttg aag atc caa gcc gtg gtg gtt gct 739
 Ile Leu Asp Asp Pro Glu Leu Leu Lys Ile Gln Ala Val Val Val Ala
 200 205 210

gac cgc gat gtg gaa gcc act gaa gtt tta cat ttg tgt aat cga gcg 787
 Asp Arg Asp Val Glu Ala Thr Glu Val Leu His Leu Cys Asn Arg Ala
 215 220 225

aac ctg gat tct gat cac tcc acc att ttt atg cgt tcg gat ggg gat 835
 Asn Leu Asp Ser Asp His Ser Thr Ile Phe Met Arg Ser Asp Gly Asp
 230 235 240 245

gat gtg gat ttc gtc gcc acg gtt gcg gtg ccg att cgt gct ggt ctg 883
 Asp Val Asp Phe Val Ala Thr Val Ala Val Pro Ile Arg Ala Gly Leu
 250 255 260

aac gat ttc cag ttg agt caa gcc ctg cat gat ggg gta gtg ggg gtt 931
 Asn Asp Phe Gln Leu Ser Gln Ala Leu His Asp Gly Val Val Gly Val
 265 270 275

gtt ggg cag gta cga gct gtg atc aat cag cta cac tagtgaagtc 977
 Val Gly Gln Val Arg Ala Val Ile Asn Gln Leu His
 280 285

catatagtga gaa 990

<210> 2100
 <211> 289
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 2100
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 1 5 10 15

Pro His Gln Ser Gly Asp Ala Ile Val Val Glu Ser Ala His Phe Thr
 20 25 30

Leu Thr Phe Thr Trp Asp Glu Trp Leu Arg Ala Gln Ala Thr Trp Val
 35 40 45

Gly Glu Leu Ser Ala Ser Asp Tyr Val Arg Ser Ile Val Ala Ile Asn
 50 55 60

Ser Ala His Asp Ala Arg Ala Thr Pro Lys Met Met Leu Asp Ala Pro
 65 70 75 80

Thr Gly Leu Thr Thr Val Leu Lys Ala Asp Lys Gly Gln Leu Gln Ala
 85 90 95

Phe Ala Val Glu Ala Leu Pro Ile Gly Asp Gly Leu Ser Glu Ala Gln
 100 105 110

Leu Ala Gly Phe Val Ala Ala Phe Asp Gly Ala Ile Asp Leu Thr
 115 120 125

Arg Glu Phe His Ala Leu Tyr Pro Glu Arg Ser Pro Gln Glu Arg Gly
130 135 140

Ala Met Leu Asn Ile Lys Leu Val Asp Ala Ser Pro Ser Gln Thr Val
145 150 155 160

Thr Pro Val Arg Val Ala Asn Trp Phe Met Asp Gln Gly Val Glu Glu
165 170 175

Val Pro Tyr Asp Ala Ala Ser Gly Arg Ile Ser Phe Glu Leu Gly Asp
180 185 190

Thr Pro Val Asp Val Ile Leu Asp Asp Pro Glu Leu Leu Lys Ile Gln
195 200 205

Ala Val Val Val Ala Asp Arg Asp Val Glu Ala Thr Glu Val Leu His
210 215 220

Leu Cys Asn Arg Ala Asn Leu Asp Ser Asp His Ser Thr Ile Phe Met
225 230 235 240

Arg Ser Asp Gly Asp Asp Val Asp Phe Val Ala Thr Val Ala Val Pro
245 250 255

Ile Arg Ala Gly Leu Asn Asp Phe Gln Leu Ser Gln Ala Leu His Asp
260 265 270

Gly Val Val Gly Val Val Gly Gln Val Arg Ala Val Ile Asn Gln Leu
275 280 285

His

<210> 2101

<211> 483

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(460)

<223> RXA01137

<400> 2101

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ctcagattct aagccacgat ttcttaacct tgtggcatcg gtg cgc cca acc ttc 115
Val Arg Pro Thr Phe
1 5

gtg atc cta cgg atc tcc gaa tac ttc ggt gtc gct gaa gct gcg att 163
Val Ile Leu Arg Ile Ser Glu Tyr Phe Gly Val Ala Glu Ala Ala Ile
10 15 20

aat gca gcc act gga cgt ctg acc agc ctc agc gaa gtg ttt atc gac 211
Asn Ala Ala Thr Gly Arg Leu Thr Ser Leu Ser Glu Val Phe Ile Asp
25 30 35

aac gct gcc gag atc caa gac aac ctt tct tcg ctg gtc gcg ctt cag 259

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Asn Ala Ala Glu Ile Gln Asp Asn Leu Ser Ser Leu Val Ala Leu Gln
   40                               45                               50

aaa gat ttg gca gag cga gtc aac gtt gaa gga gtc aat cct gtt act   307
Lys Asp Leu Ala Glu Arg Val Asn Val Glu Gly Val Asn Pro Val Thr
   55                               60                               65

cca gtt gat cta ctg gaa ctt cgc ctc ggt tcc gcg cag ctg gcc gtt   355
Pro Val Asp Leu Leu Glu Leu Arg Leu Gly Ser Ala Gln Leu Ala Val
   70                               75                               80                               85

gct gca act gcc att gag gtt cgt gtt gct gga gga gca ggt tat gta   403
Ala Ala Thr Ala Ile Glu Val Arg Val Ala Ala Gly Gly Ala Gly Tyr Val
   90                               95                               100

aag tct tca tca acg tct cgt cgt ttc cgt gtt gaa atg gga gct tgc   451
Lys Ser Ser Ser Thr Ser Arg Arg Phe Arg Val Glu Met Gly Ala Cys
   105                               110                               115

acg ggt ccg tgatctacag gccacgcaaa act   483
Thr Gly Pro
   120

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<210> 2102

<211> 120

<212> PRT

<213> Corynebacterium glutamicum

<400> 2102

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Val Arg Pro Thr Phe Val Ile Leu Arg Ile Ser Glu Tyr Phe Gly Val
   1           5           10           15

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Ala Glu Ala Ala Ile Asn Ala Ala Thr Gly Arg Leu Thr Ser Leu Ser
   20           25

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```

Glu Val Phe Ile Asp Asn Ala Ala Glu Ile Gln Asp Asn Leu Ser Ser
   35           40           45

```

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Leu Val Ala Leu Gln Lys Asp Leu Ala Glu Arg Val Asn Val Glu Gly
   50           55           60

```

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Val Asn Pro Val Thr Pro Val Asp Leu Leu Glu Leu Arg Leu Gly Ser
   65           70           75           80

```

```

Ala Gln Leu Ala Val Ala Ala Thr Ala Ile Glu Val Arg Val Ala Gly
   85           90           95

```

```

Gly Ala Gly Tyr Val Lys Ser Ser Ser Thr Ser Arg Arg Phe Arg Val
   100          105          110

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Glu Met Gly Ala Cys Thr Gly Pro
   115          120

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<210> 2103

<211> 257

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (34)..(234)

<223> RXA01156

<400> 2103

aagaactaag aaataccgat ttacggcagg agagtg agt gta gtg aac gca aag 54
 Val Ser Val Val Asn Ala Lys
 1 5

caa acc caa att atg ggt ggc ggc gga cgt gac gag gac aac gcc gag 102
 Gln Thr Gln Ile Met Gly Gly Gly Arg Asp Glu Asp Asn Ala Glu
 10 15 20

gat tcc gca cag gca tct gga cag gtt cag atc aac acc gaa ggt gtg 150
 Asp Ser Ala Gln Ala Ser Gly Gln Val Gln Ile Asn Thr Glu Gly Val
 25 30 35

gac agc ttg ctg gat gaa atc gac gga ctg ttg gaa aac aac gcc gag 198
 Asp Ser Leu Leu Asp Glu Ile Asp Gly Leu Leu Glu Asn Asn Ala Glu
 40 45 50 55

gaa ttc gtt cgt tcc tat gta caa aag ggt ggc gaa tagtactgt 244
 Glu Phe Val Arg Ser Tyr Val Gln Lys Gly Gly Glu
 60 65

gagtaccgtg gaa 257

<210> 2104

<211> 67

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2104

Val Ser Val Val Asn Ala Lys Gln Thr Gln Ile Met Gly Gly Gly Gly
 1 5 10 15

Arg Asp Glu Asp Asn Ala Glu Asp Ser Ala Gln Ala Ser Gly Gln Val
 20 25 30

Gln Ile Asn Thr Glu Gly Val Asp Ser Leu Leu Asp Glu Ile Asp Gly
 35 40 45

Leu Leu Glu Asn Asn Ala Glu Glu Phe Val Arg Ser Tyr Val Gln Lys
 50 55 60

Gly Gly Glu
 65

<210> 2105

<211> 1065

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1042)

<223> RXA01158

<400> 2105

taggacgttc aaggaattgg ctgaatcaac aagcgccaag gtggttaagc gccctcggcg 60

agttatctca aaaaagaaga agaagtctcc tacggggagag atg tcc att gtt gag 115
Met Ser Ile Val Glu
1 5

cac atc aaa gag ttt cga cgc cga ctt ctt atc gct ctg cgc ggc atc 163
His Ile Lys Glu Phe Arg Arg Arg Leu Leu Ile Ala Leu Ala Gly Ile
10 15 20

ctc gtg ggc acc att atc ggc ttt att tgg tac gat ttc tca ttt tgg 211
Leu Val Gly Thr Ile Ile Gly Phe Ile Trp Tyr Asp Phe Ser Phe Trp
25 30 35

cag atc ccc act ttg ggc gag ctg ctg agg gat ccg tac tgt tct ctg 259
Gln Ile Pro Thr Leu Gly Glu Leu Arg Asp Pro Tyr Cys Ser Leu
40 45 50

cct gct gaa tcc cgc tgg gcc atg agc gac tca gag gaa tgt cga ctg 307
Pro Ala Glu Ser Arg Trp Ala Met Ser Asp Ser Glu Glu Cys Arg Leu
55 60 65

ctc gca acc ggc ccg ttt gat cca ttc atg ctt cgc ctt aaa gta gcg 355
Leu Ala Thr Gly Pro Phe Asp Pro Phe Met Leu Arg Leu Lys Val Ala
70 75 80 85

gcg ttg gtg ggt atg gtt ctt ggc tca ccc gtg tgg ctg agc cag ctg 403
Ala Leu Val Gly Met Val Leu Gly Ser Pro Val Trp Leu Ser Gln Leu
90 95 100

tgg ggc ttt atc acc cca ggt ttg atg aag aat gag cgc cgt tac acc 451
Trp Gly Phe Ile Thr Pro Gly Leu Met Lys Asn Glu Arg Tyr Thr
105 110 115

gca atc ttc gtc acg att gct gtt gtg ctg ttt gtc ggc ggt gct gtt 499
Ala Ile Phe Val Thr Ile Ala Val Val Leu Phe Val Gly Gly Ala Val
120 125 130

ctt gcg tac ttc gtc gtt gca tat ggt ttg gag ttc ctc ctt acc att 547
Leu Ala Tyr Phe Val Val Ala Tyr Gly Leu Glu Phe Leu Leu Thr Ile
135 140 145

ggt gga gac acc cag gca gcg gcc ctg act ggt gat aag tac ttc gga 595
Gly Gly Asp Thr Gln Ala Ala Ala Leu Thr Gly Asp Lys Tyr Phe Gly
150 155 160 165

ttc ttg ctc gcg ttg ttg gcg att ttc ggc gtg agc ttc gaa gtt cca 643
Phe Leu Leu Ala Leu Leu Ala Ile Phe Gly Val Ser Phe Glu Val Pro
170 175 180

ctg gtg atc ggc atg ctc aac att gtg ggt atc ttg cct tac gat gcc 691
Leu Val Ile Gly Met Leu Asn Ile Val Gly Ile Leu Pro Tyr Asp Ala
185 190 195

att aaa gat aag cga cgc atg atc atc atg att ttg ttc gtg ttc gct 739
Ile Lys Asp Lys Arg Arg Met Ile Ile Met Ile Leu Phe Val Phe Ala
200 205 210

gct ttc atg aca ccc ggc cag gat cct ttc acc atg ttg gtg ttg gcg 787
Ala Phe Met Thr Pro Gly Gln Asp Pro Phe Thr Met Leu Val Leu Ala
215 220 225

ctt tca ctc acc gtt ctg gta gag ctt gcc ctg cag ttc tgt cgc ttc 835
 Leu Ser Leu Thr Val Leu Val Glu Leu Ala Leu Gln Phe Cys Arg Phe
 230 235 240 245

aac gac aaa cgc cgg gac aag aag cgc cca gaa tgg ctt gat ggc gat 883
 Asn Asp Lys Arg Arg Asp Lys Lys Arg Pro Glu Trp Leu Asp Gly Asp
 250 255 260

gac ctc tct gca tca cca ctg gat act tct gct ggt gga gaa gat gct 931
 Asp Leu Ser Ala Ser Pro Leu Asp Thr Ser Ala Gly Gly Glu Asp Ala
 265 270 275

cca agc cca gtc gaa acc cca gag gcg gtg gag cct tcg cgg atg ctg 979
 Pro Ser Pro Val Glu Thr Pro Glu Ala Val Glu Pro Ser Arg Met Leu
 280 285 290

aac cca agt ggg gag gcg tcg ata agc tat aaa ccc ggg cgc gcc gac 1027
 Asn Pro Ser Gly Glu Ala Ser Ile Ser Tyr Lys Pro Gly Arg Ala Asp
 295 300 305

ttc ggt gac gtg ctc tagggcctag ccaggtaccc tta 1065
 Phe Gly Asp Val Leu
 310

<210> 2106

<211> 314

<212> PRT

<213> Corynebacterium glutamicum

<400> 2106

Met Ser Ile Val Glu His Ile Lys Glu Phe Arg Arg Arg Leu Leu Ile
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Ala Leu Ala Gly Ile Leu Val Gly Thr Ile Ile Gly Phe Ile Trp Tyr
 20 25 30

Asp Phe Ser Phe Trp Gln Ile Pro Thr Leu Gly Glu Leu Leu Arg Asp
 35 40 45

Pro Tyr Cys Ser Leu Pro Ala Glu Ser Arg Trp Ala Met Ser Asp Ser
 50 55 60

Glu Glu Cys Arg Leu Leu Ala Thr Gly Pro Phe Asp Pro Phe Met Leu
 65 70 75 80

Arg Leu Lys Val Ala Ala Leu Val Gly Met Val Leu Gly Ser Pro Val
 85 90 95

Trp Leu Ser Gln Leu Trp Gly Phe Ile Thr Pro Gly Leu Met Lys Asn
 100 105 110

Glu Arg Arg Tyr Thr Ala Ile Phe Val Thr Ile Ala Val Val Leu Phe
 115 120 125

Val Gly Gly Ala Val Leu Ala Tyr Phe Val Val Ala Tyr Gly Leu Glu
 130 135 140

Phe Leu Leu Thr Ile Gly Gly Asp Thr Gln Ala Ala Ala Leu Thr Gly
 145 150 155 160

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Asp Lys Tyr Phe Gly Phe Leu Leu Ala Leu Leu Ala Ile Phe Gly Val
      165                      170                      175

Ser Phe Glu Val Pro Leu Val Ile Gly Met Leu Asn Ile Val Gly Ile
      180                      185                      190

Leu Pro Tyr Asp Ala Ile Lys Asp Lys Arg Arg Met Ile Ile Met Ile
      195                      200                      205

Leu Phe Val Phe Ala Ala Phe Met Thr Pro Gly Gln Asp Pro Phe Thr
      210                      215                      220

Met Leu Val Leu Ala Leu Ser Leu Thr Val Leu Val Glu Leu Ala Leu
      225                      230                      235                      240

Gln Phe Cys Arg Phe Asn Asp Lys Arg Arg Asp Lys Lys Arg Pro Glu
      245                      250                      255

Trp Leu Asp Gly Asp Asp Leu Ser Ala Ser Pro Leu Asp Thr Ser Ala
      260                      265                      270

Gly Gly Glu Asp Ala Pro Ser Pro Val Glu Thr Pro Glu Ala Val Glu
      275                      280                      285

Pro Ser Arg Met Leu Asn Pro Ser Gly Glu Ala Ser Ile Ser Tyr Lys
      290                      295                      300

Pro Gly Arg Ala Asp Phe Gly Asp Val Leu
      305                      310

<210> 2107
<211> 438
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(415)
<223> RXA01159

<400> 2107
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catgaacaag cttgtttaat gtgaatttgg agtagaccac atg tcc ctc gga cca 115
                        Met Ser Leu Gly Pro
                        1 5

tgg gaa att gga atc att gtc ctg ctg atc atc gtg ctg ttc ggc gcg 163
Trp Glu Ile Gly Ile Ile Val Leu Leu Ile Ile Val Leu Phe Gly Ala
                        10 15 20

aag aag ctg cct gat gca gct cgt tcc atc ggc cgt tcc atg cgc atc 211
Lys Lys Leu Pro Asp Ala Ala Arg Ser Ile Gly Arg Ser Met Arg Ile
                        25 30 35

ttc aag tct gaa gtc aaa gaa atg aac aag gac ggc gat acc cca gaa 259
Phe Lys Ser Glu Val Lys Glu Met Asn Lys Asp Gly Asp Thr Pro Glu
                        40 45 50

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caa cag cag cag cct cag cag cag att gcg ccc aac cag atc gag gct 307
Gln Gln Gln Gln Pro Gln Gln Gln Ile Ala Pro Asn Gln Ile Glu Ala
55 60 65

cct cag cca aac ttt gag cag cac tac cag gga cag cag gtt cag cag 355
Pro Gln Pro Asn Phe Glu Gln His Tyr Gln Gly Gln Gln Val Gln Gln
70 75 80 85

cct cag aac cct cag acc cct gac tac cgt cag aac tac gag gat cca 403
Pro Gln Asn Pro Gln Thr Pro Asp Tyr Arg Gln Asn Tyr Glu Asp Pro
90 95 100

aac cgc acc tct taaagttggg cagtttgcac cta 438
Asn Arg Thr Ser
105

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<210> 2108

<211> 105

<212> PRT

<213> Corynebacterium glutamicum

<400> 2108

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Met Ser Leu Gly Pro Trp Glu Ile Gly Ile Ile Val Leu Leu Ile Ile
1 5 10 15

Val Leu Phe Gly Ala Lys Lys Leu Pro Asp Ala Ala Arg Ser Ile Gly
20 25 30

Arg Ser Met Arg Ile Phe Lys Ser Glu Val Lys Glu Met Asn Lys Asp
35 40 45

Gly Asp Thr Pro Glu Gln Gln Gln Pro Gln Gln Ile Ala Pro
50 55 60

Asn Gln Ile Glu Ala Pro Gln Pro Asn Phe Glu Gln His Tyr Gln Gly
65 70 75 80

Gln Gln Val Gln Gln Pro Gln Asn Pro Gln Thr Pro Asp Tyr Arg Gln
85 90 95

Asn Tyr Glu Asp Pro Asn Arg Thr Ser
100 105

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<210> 2109

<211> 998

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(975)

<223> RXA01160

<400> 2109

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aaa tca tcc aac aaa atc agc gac ctt gcc cgc cag ctt aat ctg ttg 48
Lys Ser Ser Asn Lys Ile Ser Asp Leu Ala Arg Gln Leu Asn Leu Leu
1 5 10 15

ccg tat ttc acc agg tat aaa ggc cgt acc gtc atg gaa gca gcg cgc 96

```

Pro	Tyr	Phe	Thr	Arg	Tyr	Lys	Gly	Arg	Thr	Val	Met	Glu	Ala	Ala	Arg	
			20						25					30		
gat	ctt	ggc	caa	ccc	tcc	tcc	caa	atc	atg	gaa	gac	ctc	aac	aga	tta	144
Asp	Leu	Gly	Gln	Pro	Ser	Ser	Gln	Ile	Met	Glu	Asp	Leu	Asn	Arg	Leu	
		35					40					45				
tgg	atg	tgt	ggc	ctg	cca	gga	ctt	ctt	cca	ggc	gac	ttg	gtg	gag	ctt	192
Trp	Met	Cys	Gly	Leu	Pro	Gly	Leu	Leu	Pro	Gly	Asp	Leu	Val	Glu	Leu	
	50					55					60					
gat	cat	tcc	ttt	aag	gaa	gta	aaa	atc	cac	aat	gct	caa	ggc	atg	gat	240
Asp	His	Ser	Phe	Lys	Glu	Val	Lys	Ile	His	Asn	Ala	Gln	Gly	Met	Asp	
	65				70					75					80	
aaa	ccc	ttg	cgc	ctc	aca	cca	act	gaa	gcc	ggc	gtt	ttg	ctg	ctg	aca	288
Lys	Pro	Leu	Arg	Leu	Thr	Pro	Thr	Glu	Ala	Gly	Val	Leu	Leu	Leu	Thr	
			85						90					95		
ctt	gaa	tcc	ctg	gaa	tcc	ctc	ccc	ggc	att	gcg	aaa	cag	gaa	gag	gtc	336
Leu	Glu	Ser	Leu	Glu	Ser	Leu	Pro	Gly	Ile	Ala	Lys	Gln	Glu	Ala	Val	
			100					105					110			
gta	tct	gct	gag	aac	aag	cta	cgc	gcc	atc	atg	ggg	gag	tat	tcc	tcg	384
Val	Ser	Ala	Ala	Asn	Lys	Leu	Arg	Ala	Ile	Met	Gly	Glu	Tyr	Ser	Ser	
		115					120					125				
act	gtt	ttc	gac	tcc	act	gga	gaa	gac	ctc	gat	gct	gaa	gtt	cta	gag	432
Thr	Val	Phe	Asp	Ser	Thr	Gly	Glu	Asp	Leu	Asp	Ala	Glu	Val	Leu	Glu	
	130					135					140					
atc	atc	cgc	gac	gcc	atg	gat	tta	cac	cag	cag	gtc	agt	ttt	gaa	tac	480
Ile	Ile	Arg	Asp	Ala	Met	Asp	Leu	His	Gln	Gln	Val	Ser	Phe	Glu	Tyr	
	145				150					155				160		
cac	tcg	cac	aga	tca	gac	aac	acc	agc	ctg	agg	caa	gtc	agc	cct	gct	528
His	Ser	His	Arg	Ser	Asp	Asn	Thr	Ser	Leu	Arg	Gln	Val	Ser	Pro	Ala	
			165					170						175		
cat	atc	ttc	acc	cat	gaa	ggc	gaa	acc	tac	atc	aaa	gcc	tgg	gaa	gaa	576
His	Ile	Phe	Thr	His	Glu	Gly	Glu	Thr	Tyr	Ile	Lys	Ala	Trp	Glu	Glu	
		180						185					190			
gct	gtg	aac	caa	tgg	cgg	acg	ttt	agg	ctt	gat	cgc	atc	cga	agc	att	624
Ala	Val	Asn	Gln	Trp	Arg	Thr	Phe	Arg	Leu	Asp	Arg	Ile	Arg	Ser	Ile	
		195				200						205				
gtg	ctt	ctt	gac	agc	aaa	gca	gtg	cac	ccg	gag	cga	ggg	gtt	tca	gta	672
Val	Leu	Leu	Asp	Ser	Lys	Ala	Val	His	Pro	Ala	Arg	Gly	Val	Ser	Val	
	210					215					220					
tcc	acg	gac	gat	cct	ttt	gag	ttc	gca	aaa	tct	tcc	gat	att	gcc	acg	720
Ser	Thr	Asp	Asp	Pro	Phe	Glu	Phe	Ala	Lys	Ser	Ser	Asp	Ile	Ala	Thr	
	225				230					235				240		
tta	ttg	ctg	cgt	gag	gac	gca	atg	tgg	tta	ggc	aat	tac	atg	gcc	atg	768
Leu	Leu	Leu	Arg	Glu	Asp	Ala	Met	Trp	Leu	Gly	Asn	Tyr	Met	Ala	Met	
			245					250					255			
gag	gtg	gat	gaa	acg	gtg	gaa	ccg	att	cgc	gat	agc	gac	gga	ttc	agc	816
Glu	Val	Asp	Glu	Thr	Val	Glu	Pro	Ile	Arg	Asp	Ser	Asp	Gly	Phe	Ser	

260	265	270	
tgg cac aca gtc cac ttt ccg ctg ctt tct agg gat	tgg ttc gtc cga	864	
Trp His Thr Val His Phe Pro Leu Leu Ser Arg Asp	Trp Phe Val Arg		
275	280	285	
ttc gcg att ggc cat gct gag cat ttg aaa gta act	agt ccc gaa gat	912	
Phe Ala Ile Gly His Ala Glu His Leu Lys Val Thr	Ser Pro Glu Asp		
290	295	300	
ctt cgg aaa tgc ata aag caa aag gct ttt agt ggt	ttg tca gcg tat	960	
Leu Arg Lys Cys Ile Lys Gln Lys Ala Phe Ser Gly	Leu Ser Ala Tyr		
305	310	315	
gat cat cac gta gag taacacccaa gagtaagacg caa		998	
Asp His His Val Glu			
325			

<210> 2110

<211> 325

<212> PRT

<213> Corynebacterium glutamicum

<400> 2110

Lys Ser Ser Asn Lys Ile Ser Asp Leu Ala Arg Gln Leu Asn Leu Leu	
1 5 10 15	

Pro Tyr Phe Thr Arg Tyr Lys Gly Arg Thr Val Met Glu Ala Ala Arg	
20 25 30	

Asp Leu Gly Gln Pro Ser Ser Gln Ile Met Glu Asp Leu Asn Arg Leu	
35 40 45	

Trp Met Cys Gly Leu Pro Gly Leu Leu Pro Gly Asp Leu Val Glu Leu	
50 55 60	

Asp His Ser Phe Lys Glu Val Lys Ile His Asn Ala Gln Gly Met Asp	
65 70 75 80	

Lys Pro Leu Arg Leu Thr Pro Thr Glu Ala Gly Val Leu Leu Leu Thr	
85 90 95	

Leu Glu Ser Leu Glu Ser Leu Pro Gly Ile Ala Lys Gln Glu Ala Val	
100 105 110	

Val Ser Ala Ala Asn Lys Leu Arg Ala Ile Met Gly Glu Tyr Ser Ser	
115 120 125	

Thr Val Phe Asp Ser Thr Gly Glu Asp Leu Asp Ala Glu Val Leu Glu	
130 135 140	

Ile Ile Arg Asp Ala Met Asp Leu His Gln Gln Val Ser Phe Glu Tyr	
145 150 155 160	

His Ser His Arg Ser Asp Asn Thr Ser Leu Arg Gln Val Ser Pro Ala	
165 170 175	

His Ile Phe Thr His Glu Gly Glu Thr Tyr Ile Lys Ala Trp Glu Glu	
180 185 190	

Ala Val Asn Gln Trp Arg Thr Phe Arg Leu Asp Arg Ile Arg Ser Ile
195 200 205

Val Leu Leu Asp Ser Lys Ala Val His Pro Ala Arg Gly Val Ser Val
210 215 220

Ser Thr Asp Asp Pro Phe Glu Phe Ala Lys Ser Ser Asp Ile Ala Thr
225 230 235 240

Leu Leu Leu Arg Glu Asp Ala Met Trp Leu Gly Asn Tyr Met Ala Met
245 250 255

Glu Val Asp Glu Thr Val Glu Pro Ile Arg Asp Ser Asp Gly Phe Ser
260 265 270

Trp His Thr Val Val His Phe Pro Leu Leu Ser Arg Asp Trp Phe Val Arg
275 280 285

Phe Ala Ile Gly His Ala Glu His Leu Lys Val Thr Ser Pro Glu Asp
290 295 300

Leu Arg Lys Cys Ile Lys Gln Lys Ala Phe Ser Gly Leu Ser Ala Tyr
305 310 315 320

Asp His His Val Glu
325

<210> 2111

<211> 805

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(805)

<223> RXA01163

<400> 2111

accgtaccca cagacacacc agaattaaca gaaacagact gaaaaacaac atcgctcgac 60

atgcgcgttaa tcctaaccgc cgcacactaa tgtggccgat atg ggc tac acc aac 115
Met Gly Tyr Thr Asn
1 5

ctc aac gac aca cgg gtc ttg cgc gcc ggg tca tgt gat gcc tgg tgg 163
Leu Asn Asp Thr Arg Val Leu Arg Ala Gly Ser Cys Asp Ala Trp Trp
10 15 20

cgc acg atg tct ccg cta gtg cag cag gga agt gag gca gtc ttt cgg 211
Arg Thr Met Ser Pro Leu Val Gln Gln Gly Ser Glu Ala Val Phe Arg
25 30 35

cgc atc atg ggt ctc tcg cgg cgt cct gat cgg aaa cct ggc ttt gac 259
Arg Ile Met Gly Leu Ser Arg Arg Pro Asp Arg Lys Pro Gly Phe Asp
40 45 50

gat gtc cca cat ttc ggc gca gct gtt cga gtt ccc ggt cta aaa cac 307
Asp Val Pro His Phe Gly Ala Ala Val Arg Val Pro Gly Leu Lys His
55 60 65

ggc acg ttg gtc aat gct gca ccc ttg aaa gtt ttg ggc gca cgg ggc 355
 Gly Thr Leu Val Asn Ala Pro Leu Lys Val Leu Gly Ala Arg Gly
 70 75 80 85

gag ccc aac ccc gcg agt tcg tac cgt ttt gaa tac atc acc ggt gat 403
 Glu Pro Asn Pro Ala Ser Ser Tyr Arg Phe Glu Tyr Ile Thr Gly Asp
 90 95 100

tcc gca ggt cga gcc atc act gcg acc ggc gct gtc ctc ttt tcc aca 451
 Ser Ala Gly Arg Ala Ile Thr Ala Thr Gly Ala Val Leu Phe Ser Thr
 105 110 115

cgc ccc tgg aca acc ggc ccg cgt ccc gcg atc gcc atg gct cca tcc 499
 Arg Pro Trp Thr Thr Gly Pro Arg Pro Ala Ile Ala Met Ala Pro Ser
 120 125 130

acc caa ggc gtc gca cag cac tgc gat ccc tcc cac acc tgc gcc atc 547
 Thr Gln Gly Val Ala Gln His Cys Asp Pro Ser His Thr Cys Ala Ile
 135 140 145

gga ctc aac gca ttc tat gac aaa ccc ttc gac gca atc att gct tac 595
 Gly Leu Asn Ala Phe Tyr Asp Lys Pro Phe Asp Ala Ile Ile Ala Tyr
 150 155 160 165

gaa ctc ccc gtc atc ctc tgg ttt cta gct cac gga ctt gac gtt gtg 643
 Glu Leu Pro Val Ile Leu Trp Phe Leu Ala His Gly Leu Asp Val Val
 170 175 180

ttc atc gat tac ccc gcg gac ccc gca acc ggc gtc caa tac tat tgc 691
 Phe Ile Asp Tyr Pro Arg Asp Pro Ala Thr Gly Val Gln Tyr Tyr Cys
 185 190 195

gat tcc atc gct gca gct aaa tcg ctt ctc gac gcc gtc ctc gcc tcc 739
 Asp Ser Ile Ala Ala Ala Lys Ser Leu Leu Asp Ala Val Leu Ala Ser
 200 205 210

aga caa ctc ggc ctt tca ccg gaa gca ccg ctt ggc ctg tgg gga ttc 787
 Arg Gln Leu Gly Leu Ser Pro Glu Ala Pro Leu Gly Leu Trp Gly Phe
 215 220 225

tcc caa gga ggc gcc gcc 805
 Ser Gln Gly Gly Gly Ala
 230 235

<210> 2112

<211> 235

<212> PRT

<213> Corynebacterium glutamicum

<400> 2112

Met Gly Tyr Thr Asn Leu Asn Asp Thr Arg Val Leu Arg Ala Gly Ser
 1 5 10 15

Cys Asp Ala Trp Trp Arg Thr Met Ser Pro Leu Val Gln Gln Gly Ser
 20 25 30

Glu Ala Val Phe Arg Arg Ile Met Gly Leu Ser Arg Arg Pro Asp Arg
 35 40 45

Lys Pro Gly Phe Asp Asp Val Pro His Phe Gly Ala Ala Val Arg Val

50

55

60

Pro Gly Leu Lys His Gly Thr Leu Val Asn Ala Ala Pro Leu Lys Val
65 70 75 80

Leu Gly Ala Arg Gly Glu Pro Asn Pro Ala Ser Ser Tyr Arg Phe Glu
85 90 95

Tyr Ile Thr Gly Asp Ser Ala Gly Arg Ala Ile Thr Ala Thr Gly Ala
100 105 110

Val Leu Phe Ser Thr Arg Pro Trp Thr Thr Gly Pro Arg Pro Ala Ile
115 120 125

Ala Met Ala Pro Ser Thr Gln Gly Val Ala Gln His Cys Asp Pro Ser
130 135 140

His Thr Cys Ala Ile Gly Leu Asn Ala Phe Tyr Asp Lys Pro Phe Asp
145 150 155 160

Ala Ile Ile Ala Tyr Glu Leu Pro Val Ile Leu Trp Phe Leu Ala His
165 170 175

Gly Leu Asp Val Val Phe Ile Asp Tyr Pro Arg Asp Pro Ala Thr Gly
180 185 190

Val Gln Tyr Tyr Cys Asp Ser Ile Ala Ala Ala Lys Ser Leu Leu Asp
195 200 205

Ala Val Leu Ala Ser Arg Gln Leu Gly Leu Ser Pro Glu Ala Pro Leu
210 215 220

Gly Leu Trp Gly Phe Ser Gln Gly Gly Gly Ala
225 230 235

<210> 2113

<211> 696

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(673)

<223> RXA01165

<400> 2113

agaccactca cattgcacat ctgcagctgc caggaagtct ccaccaaca gttttctagg 60

tcacagggat ccattagcca ttgtgtcctt gtcgaaaggt atg gtg ggg cat gtg 115
Met Val Gly His Val
1 5

cct gca gca ata gca atc cca tat ttc att att gag atc etc gcc ttc 163
Pro Ala Ala Ile Ala Ile Pro Tyr Phe Ile Ile Glu Ile Leu Ala Phe
10 15 20

att ggt gtc gtc atg tgg ctc ggt ttc ggc tgg gct ttg ggt etc etc 211
Ile Gly Val Val Met Trp Leu Gly Phe Gly Trp Ala Leu Gly Leu Leu
25 30 35

gta ttg ttc ttc gtc ggt gga ctt ctt cta gcc ggc gtg gag ctt cgt 259
 Val Leu Phe Phe Val Gly Gly Leu Leu Ala Gly Val Glu Leu Arg
 40 45 50
 cgc att agt aag agt gcc gcc att cat cag gct tcg ggc cag gga agt 307
 Arg Ile Ser Lys Ser Ala Ala Ile His Gln Ala Ser Gly Gln Gly Ser
 55 60 65
 gcg gga gcg atc gcc gga aac att ggg ctg acc gca gct ggt gcc att 355
 Ala Gly Ala Ile Ala Gly Asn Ile Gly Leu Thr Ala Ala Gly Ala Ile
 70 75 80 85
 ttg gtg gcc atg ccg ggg ttt gtg tct tcg att atc ggt ttg ttg ttc 403
 Leu Val Ala Met Pro Gly Phe Val Ser Ser Ile Ile Gly Leu Leu Phe
 90 95 100
 att ttt gca cca acc agg gcg ctg ttc cgc aag gtt ttg gcc aag cgc 451
 Ile Phe Ala Pro Thr Arg Ala Leu Phe Arg Lys Val Leu Ala Lys Arg
 105 110 115
 atg cgc agt gcc atc gag aac cta ggt gtg cgt ggt ttt gaa gcc gtt 499
 Met Arg Ser Ala Ile Glu Asn Leu Gly Val Arg Gly Phe Glu Ala Val
 120 125 130
 aat ggt tac cgc acc cag gca tcc tac gga aac ttc gga gcg gca ttc 547
 Asn Gly Tyr Arg Thr Gln Ala Ser Tyr Gly Asn Phe Gly Ala Ala Phe
 135 140 145
 aat ggt ggt gcg caa caa cca tca aat gag ccg atc gtg att gat gaa 595
 Asn Gly Gly Ala Gln Gln Pro Ser Asn Glu Pro Ile Val Ile Asp Glu
 150 155 160 165
 gac gag atc caa gcc tgg act tct gat ctg aaa cct gaa gat ttc acc 643
 Asp Glu Ile Gln Ala Trp Thr Ser Asp Leu Lys Pro Glu Asp Phe Thr
 170 175 180
 aaa ggt aaa gat gaa tcc gac ggt gag aaa taagtgcac tgttgttcg 693
 Lys Gly Lys Asp Glu Ser Asp Gly Glu Lys
 185 190
 gct 696

<210> 2114

<211> 191

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2114

Met Val Gly His Val Pro Ala Ala Ile Ala Ile Pro Tyr Phe Ile Ile
 1 5 10 15
 Glu Ile Leu Ala Phe Ile Gly Val Val Met Trp Leu Gly Phe Gly Trp
 20 25 30
 Ala Leu Gly Leu Leu Val Leu Phe Phe Val Gly Gly Leu Leu Leu Ala
 35 40 45
 Gly Val Glu Leu Arg Arg Ile Ser Lys Ser Ala Ala Ile His Gln Ala
 50 55 60

Ser Gly Gln Gly Ser Ala Gly Ala Ile Ala Gly Asn Ile Gly Leu Thr
 65 70 75 80

Ala Ala Gly Ala Ile Leu Val Ala Met Pro Gly Phe Val Ser Ser Ile
 85 90 95

Ile Gly Leu Leu Phe Ile Phe Ala Pro Thr Arg Ala Leu Phe Arg Lys
 100 105 110

Val Leu Ala Lys Arg Met Arg Ser Ala Ile Glu Asn Leu Gly Val Arg
 115 120 125

Gly Phe Glu Ala Val Asn Gly Tyr Arg Thr Gln Ala Ser Tyr Gly Asn
 130 135 140

Phe Gly Ala Ala Phe Asn Gly Gly Ala Gln Gln Pro Ser Asn Glu Pro
 145 150 155 160

Ile Val Ile Asp Glu Asp Glu Ile Gln Ala Trp Thr Ser Asp Leu Lys
 165 170 175

Pro Glu Asp Phe Thr Lys Gly Lys Asp Glu Ser Asp Gly Glu Lys
 180 185 190

<210> 2115

<211> 506

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(483)

<223> RXA01166

<400> 2115

ctc acc gga gtg att gcc tac gcc atc gcg gga ctt gca gtg aac tct 48

Leu Thr Gly Val Ile Ala Tyr Ala Ile Ala Gly Leu Ala Val Asn Ser

1

5

10

15

tca gag atg ttt gag gaa atc atg tcg gtg tta aat gaa cgc gga gtc 96

Ser Glu Met Phe Glu Glu Ile Met Ser Val Leu Asn Glu Arg Gly Val

20

25

30

agt gat gtg ctg aaa aat atc acc agc tgc gcg gga ggt tcc ttg ttg 144

Ser Asp Val Leu Lys Asn Ile Thr Ser Cys Ala Gly Gly Ser Leu Leu

35

40

45

gcc agt ggc tac tcg tct tcc cgc ggg tgg aca cat cag ggc acg ccg 192

Ala Ser Gly Tyr Ser Ser Ser Arg Gly Trp Thr His Gln Gly Thr Pro

50

55

60

ctg gca gac att ctg gac gat ctg cca ctt gtt gtc gct gag ttt ggg 240

Leu Ala Asp Ile Leu Asp Asp Leu Pro Leu Val Val Ala Glu Phe Gly

65

70

75

80

aag caa aag ctg ggt cgt gtg gcg cca gaa atc cca gtg ctg ttg tgg 288

Lys Gln Lys Leu Gly Arg Val Ala Pro Glu Ile Pro Val Leu Leu Trp

85

90

95

ggc tct aaa aat gat gat gtc att ccc att gat ccc att agg gaa ttg 336

```

Gly Ser Lys Asn Asp Asp Val Ile Pro Ile Asp Pro Ile Arg Glu Leu
      100                      105                      110

cgt gat agc tgg gcg gac aag ggt acg cca ttg acc tgg cat gaa tcc 384
Arg Asp Ser Trp Ala Asp Lys Gly Thr Pro Leu Thr Trp His Glu Ser
      115                      120                      125

caa gcg ccg cgt gtg cca gga cgc aca ggt ctc aac cat ttc ggg ccc 432
Gln Ala Pro Arg Val Pro Gly Arg Thr Gly Leu Asn His Phe Gly Pro
      130                      135                      140

tat ttt aga aac ctg gaa aag tac tcg gga tgg ctc ata gat cat ctt 480
Tyr Phe Arg Asn Leu Glu Lys Tyr Ser Gly Trp Leu Ile Asp His Leu
      145                      150                      155

gtc tgagtgccgt tttaaaggct cgg 506
Val

```

<210> 2116

<211> 161

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2116

```

Leu Thr Gly Val Ile Ala Tyr Ala Ile Ala Gly Leu Ala Val Asn Ser
  1                      5                      10                      15

```

```

Ser Glu Met Phe Glu Glu Ile Met Ser Val Leu Asn Glu Arg Gly Val
      20                      25                      30

```

```

Ser Asp Val Leu Lys Asn Ile Thr Ser Cys Ala Gly Gly Ser Leu Leu
      35                      40                      45

```

```

Ala Ser Gly Tyr Ser Ser Ser Arg Gly Trp Thr His Gln Gly Thr Pro
      50                      55                      60

```

```

Leu Ala Asp Ile Leu Asp Asp Leu Pro Leu Val Val Ala Glu Phe Gly
      65                      70                      75                      80

```

```

Lys Gln Lys Leu Gly Arg Val Ala Pro Glu Ile Pro Val Leu Leu Trp
      85                      90                      95

```

```

Gly Ser Lys Asn Asp Asp Val Ile Pro Ile Asp Pro Ile Arg Glu Leu
      100                      105                      110

```

```

Arg Asp Ser Trp Ala Asp Lys Gly Thr Pro Leu Thr Trp His Glu Ser
      115                      120                      125

```

```

Gln Ala Pro Arg Val Pro Gly Arg Thr Gly Leu Asn His Phe Gly Pro
      130                      135                      140

```

```

Tyr Phe Arg Asn Leu Glu Lys Tyr Ser Gly Trp Leu Ile Asp His Leu
      145                      150                      155                      160

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Val

<210> 2117

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<220>
<221> CDS
<222> (101) .. (583)
<223> RXA01170
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400> 2117	tacaggaaac	tttcaggcat	aggggagtc	atgaacacagaa	cggaagacta	aggtgacata	60
	gtcacttaaa	ctaaacaaga	aggggtggagg	acccaagcac	gtg agt ctt tca aac		115
					Val Ser Leu Ser Asn	5	
					1		
aaa gct aaa gga atc gtt gca gta atc atc gtc gcc tgg atc gtc gcg	163						
Lys Ala Lys Gly Ile Val Ala Val Ile Ile Val Ala Trp Ile Val Ala							
	10				15		20
atg gct ggc atg gtc gca tac gcg tca agc aat aat gct gat aag aca	211						
Met Ala Gly Met Val Ala Tyr Ala Ser Ser Asn Asn Ala Asp Lys Thr							
	25				30		35
ttt cca act gca ggt gcg cta gaa caa acc gtc gca gca ttt gat agg	259						
Phe Pro Thr Ala Gly Ala Leu Gln Thr Val Ala Ala Phe Asp Arg							
	40				45		50
caa ggc ctt cag gtc tct gca gtc gca ctg gca gac atc tac ggc gat	307						
Gln Gly Leu Gln Val Ser Ala Val Ala Leu Ala Asp Ile Tyr Gly Asp							
	55				60		65
gaa tac gtc tcc gcg gcg att ctg tgc gaa gga act cca acc gca aca	355						
Glu Tyr Val Ser Ala Ala Ile Leu Cys Glu Gly Thr Pro Thr Ala Thr							
	70				75		80
etc gag cag tca ctg gcc gta gac ctg tct gag ctg aac ctg gac gag	403						
Lec Glu Gln Ser Leu Gly Val Asp Leu Ser Glu Leu Asn Leu Asp Glu							
	90				95		100
tct ggt gtt cct tgg gcc gtg tcc tac ttg gct ctg tcc aat cag gat	451						
Ser Gly Val Pro Ser Ser Gly Val Ser Tyr Leu Ala Leu Ser Asn Gln Asp							
	105				110		115
ggg gaa gtt gtc tac gac aag att gat cgt gcc aac gtt gat ctc tgc	499						
Gly Glu Val Val Tyr Asp Lys Ile Asp Arg Ala Asn Val Asp Leu Cys							
	120				125		130
gca acg cca ctc aat ggt gct ttc agc gct tat tca ttg atg cca gtt	547						
Ala Thr Pro Leu Asn Gly Ala Phe Ser Ala Tyr Ser Leu Met Pro Val							
	135				140		145
gcc aag gtt gcc gag aac tcc tgg gcg atc gcc gct taggggtttta	593						
Ala Lys Val Gly Glu Asn Ser Trp Ala Ile Ala Ala							
	150				155		160
agggtcaatc cgc	606						

<210> 2118
<211> 161

<212> PRT

<213> Corynebacterium glutamicum

<400> 2118

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Val Ser Leu Ser Asn Lys Ala Lys Gly Ile Val Ala Val Ile Ile Val
 1             5             10             15

Ala Trp Ile Val Ala Met Ala Gly Met Val Ala Tyr Ala Ser Ser Asn
 20             25             30

Asn Ala Asp Lys Thr Phe Pro Thr Ala Gly Ala Leu Glu Gln Thr Val
 35             40             45

Ala Ala Phe Asp Arg Gln Gly Leu Gln Val Ser Ala Val Ala Leu Ala
 50             55             60

Asp Ile Tyr Gly Asp Glu Tyr Val Ser Ala Ala Ile Leu Cys Glu Gly
 65             70             75             80

Thr Pro Thr Ala Thr Leu Glu Gln Ser Leu Gly Val Asp Leu Ser Glu
 85             90             95

Leu Asn Leu Asp Glu Ser Gly Val Pro Ser Gly Val Ser Tyr Leu Ala
100             105             110

Leu Ser Asn Gln Asp Gly Glu Val Val Tyr Asp Lys Ile Asp Arg Ala
115             120             125

Asn Val Asp Leu Cys Ala Thr Pro Leu Asn Gly Ala Phe Ser Ala Tyr
130             135             140

Ser Leu Met Pro Val Ala Lys Val Gly Glu Asn Ser Trp Ala Ile Ala
145             150             155             160

Ala

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<210> 2119

<211> 816

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(793)

<223> RXA01171

<400> 2119

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gtagaaattt tccattcgca ggaaagccga taatggggca gaaccccttc ccgccaaat 60

gacataatgt acattatcgg acaattatcc atatctggcc atg tcg cag gcc gct 115
                               Met Ser Gln Ala Ala
                               1             5

ggg aag ttt aag ccc atg act tca acg ctc gcc gaa tca aca ctt aca 163
Gly Lys Phe Lys Pro Met Thr Ser Thr Leu Ala Glu Ser Thr Leu Thr
              10             15             20

tcc ctt aaa gaa ctt gag gat cca aag atc ctt tcc gtc aat gaa cgc 211
Ser Leu Lys Glu Leu Glu Asp Pro Lys Ile Leu Ser Val Asn Glu Arg

```

	25	30	35	
	cac ggc gat gat	cac gca gtg aac ctc acc aag ctt	cgc gcc gtt gcc	259
	His Gly Asp Asp	His Ala Val Asn Leu Thr Lys Leu Arg Ala Val Ala		
	40	45	50	
	aaa gag ctg aaa aag aac	cag ccg ctg gct cgt gag ctt tgg gca acc	307	
	Lys Glu Leu Lys Lys Asn Gln Pro Leu Ala Arg Glu Leu Trp Ala Thr			
	55	60	65	
	gac gat aca gcc gca cgt ttg gtg gcg ttg ctt att tgc cga ccc aag	355		
	Asp Asp Thr Ala Ala Arg Leu Val Ala Leu Ser Met Ile Cys Arg Pro Lys			
	70	75	80	85
	gaa ttt gat cag tct gaa ctc gac tcg atg atc cat gag gct cgc acg	403		
	Glu Phe Asp Gln Ser Glu Leu Asp Ser Met Ile His Glu Ala Arg Thr			
	90	95	100	
	ccg aag gtt ctt gat tgg ttg atc aat tat gtg gtc aag aag aat cct	451		
	Pro Lys Val Leu Asp Trp Leu Ile Asn Tyr Val Val Lys Lys Asn Pro			
	105	110	115	
	cat tgg aac gat ctc cgt gtg ctc tgg ctt gaa gat ccc gcc gag aat	499		
	His Trp Asn Asp Leu Arg Val Leu Trp Leu Glu Asp Pro Ala Glu Asn			
	120	125	130	
	gtt gcg gcc gcc ggc tgg gct ctc aac act cat gcc gtt atc aca aag	547		
	Val Ala Ala Ala Gly Trp Ala Leu Asn Thr His Ala Val Ile Thr Lys			
	135	140	145	
	ccg gac gca ttg gac gat tcc gaa atc ctt gac acc att gaa gct cag	595		
	Pro Asp Ala Leu Asp Asp Ser Glu Ile Leu Asp Thr Ile Glu Ala Gln			
	150	155	160	165
	atg aaa act gcc gag cct cgc gta cag tgg tca atg aat gaa tgt ttg	643		
	Met Lys Thr Ala Glu Pro Arg Val Gln Trp Ser Met Asn Glu Cys Leu			
	170	175	180	
	gcg caa atc ggc atc cat cgt cca gag ctt cgt gat cgt gcc att gcc	691		
	Ala Gln Ile Gly Ile His Arg Pro Glu Leu Arg Asp Arg Ala Ile Ala			
	185	190	195	
	att ggt gag cgc ctg gaa gtt ctc aaa gat tat ccg acc cct cca aat	739		
	Ile Gly Glu Arg Leu Glu Val Leu Lys Asp Tyr Pro Thr Pro Pro Asn			
	200	205	210	
	tgc acc tcg cct ttt gct ccg att tgg atc gaa gag atg gtt cgc agg	787		
	Cys Thr Ser Pro Phe Ala Pro Ile Trp Ile Glu Glu Met Val Arg Arg			
	215	220	225	
	aaa aaa taaccgacct gttccctatc ttt	816		
	Lys Lys			
	230			

<210> 2120

<211> 231

<212> PRT

<213> Corynebacterium glutamicum

<400> 2120


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Met Ser Gln Ala Ala Gly Lys Phe Lys Pro Met Thr Ser Thr Leu Ala
 1          5          10          15

Glu Ser Thr Leu Thr Ser Leu Lys Glu Leu Glu Asp Pro Lys Ile Leu
          20          25          30

Ser Val Asn Glu Arg His Gly Asp Asp His Ala Val Asn Leu Thr Lys
          35          40          45

Leu Arg Ala Val Ala Lys Glu Leu Lys Lys Asn Gln Pro Leu Ala Arg
          50          55          60

Glu Leu Trp Ala Thr Asp Asp Thr Ala Ala Arg Leu Val Ala Leu Leu
          65          70          75          80

Ile Cys Arg Pro Lys Glu Phe Asp Gln Ser Glu Leu Asp Ser Met Ile
          85          90          95

His Glu Ala Arg Thr Pro Lys Val Leu Asp Trp Leu Ile Asn Tyr Val
          100          105          110

Val Lys Lys Asn Pro His Trp Asn Asp Leu Arg Val Leu Trp Leu Glu
          115          120          125

Asp Pro Ala Glu Asn Val Ala Ala Ala Gly Trp Ala Leu Asn Thr His
          130          135          140

Ala Val Ile Thr Lys Pro Asp Ala Leu Asp Asp Ser Glu Ile Leu Asp
          145          150          155          160

Thr Ile Glu Ala Gln Met Lys Thr Ala Glu Pro Arg Val Gln Trp Ser
          165          170          175

Met Asn Glu Cys Leu Ala Gln Ile Gly Ile His Arg Pro Glu Leu Arg
          180          185          190

Asp Arg Ala Ile Ala Ile Gly Glu Arg Leu Glu Val Leu Lys Asp Tyr
          195          200          205

Pro Thr Pro Pro Asn Cys Thr Ser Pro Phe Ala Pro Ile Trp Ile Glu
          210          215          220

Glu Met Val Arg Arg Lys Lys
225          230

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<210> 2121

<211> 627

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(604)

<223> RXA01176

<400> 2121

gagctgtgca ctttgtgacc ttttgtgaca ctgctcaatg ctttacggct acgatgaaca 60

acaaaccgac gttttgacg ctgtgaagga ctaattgcta gtg cgt tat ttt tac 115
 Val Arg Tyr Phe Tyr

1

5

gat act gag ttc att gaa gat ggg cgc acg atc gaa ttg gtc tct att 163
 Asp Thr Glu Phe Ile Glu Asp Gly Arg Thr Ile Glu Leu Val Ser Ile
 10 15 20

gga atc gtc gca gaa gac ggt cgc gag tat tac gca gtt agc aca cag 211
 Gly Ile Val Ala Glu Asp Gly Arg Glu Tyr Tyr Ala Val Ser Thr Gln
 25 30 35

ttt gat tcc tcc aag gcg aac gct tgg gtg cgc gcc aac gtg ttg gac 259
 Phe Asp Ser Ser Lys Ala Asn Ala Trp Val Arg Ala Asn Val Leu Asp
 40 45 50

aaa ttg cct aat cct tcc tcc aaa gtg tgg aaa tct gca gac act ata 307
 Lys Leu Pro Asn Pro Ser Ser Lys Val Trp Lys Ser Ala Asp Thr Ile
 55 60 65

aag cgc gaa gtt tat gag ttt ctc acc tcc acc gga cca acc cct gaa 355
 Lys Arg Glu Val Tyr Glu Phe Leu Thr Ser Thr Gly Pro Thr Pro Glu
 70 75 80 85

ctg tgg gcc tgg gtg ggc gca tat gac cac gtg ttg ttg gca caa atg 403
 Leu Trp Ala Trp Val Gly Ala Tyr Asp His Val Leu Leu Ala Gln Met
 90 95 100

tgg ggc gat atg gcg ggg ctt cct cgg gag atc cct cgt ttt acc cgc 451
 Trp Gly Asp Met Ala Gly Leu Pro Arg Glu Ile Pro Arg Phe Thr Arg
 105 110 115

gag ctt cgc cag tat tgg gac atg gct ggc cgc cca acg ctg cca gag 499
 Glu Leu Arg Gln Tyr Trp Asp Met Ala Gly Arg Pro Thr Leu Pro Glu
 120 125 130

ctg ccg aac ggc aac cac gat gcg ttg att gat gcg cgt cat aat tta 547
 Leu Pro Asn Gly Asn His Asp Ala Leu Ile Asp Ala Arg His Asn Leu
 135 140 145

gcc aag ttc aaa gtg tgc atg gca gcg ctg cct ttg ggt aaa agg gat 595
 Ala Lys Phe Lys Val Cys Met Ala Ala Leu Pro Leu Gly Lys Arg Asp
 150 155 160 165

cgc gtc tct tagtcgatct gctcccatc cat 627
 Arg Val Ser

<210> 2122

<211> 168

<212> PRT

<213> Corynebacterium glutamicum

<400> 2122

Val Arg Tyr Phe Tyr Asp Thr Glu Phe Ile Glu Asp Gly Arg Thr Ile
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Glu Leu Val Ser Ile Gly Ile Val Ala Glu Asp Gly Arg Glu Tyr Tyr
 20 25 30

Ala Val Ser Thr Gln Phe Asp Ser Ser Lys Ala Asn Ala Trp Val Arg
 35 40 45

Ala Asn Val Leu Asp Lys Leu Pro Asn Pro Ser Ser Lys Val Trp Lys
 50 55 60

Ser Ala Asp Thr Ile Lys Arg Glu Val Tyr Glu Phe Leu Thr Ser Thr
 65 70 75 80

Gly Pro Thr Pro Glu Leu Trp Ala Trp Val Gly Ala Tyr Asp His Val
 85 90 95

Leu Leu Ala Gln Met Trp Gly Asp Met Ala Gly Leu Pro Arg Glu Ile
 100 105 110

Pro Arg Phe Thr Arg Glu Leu Arg Gln Tyr Trp Asp Met Ala Gly Arg
 115 120 125

Pro Thr Leu Pro Glu Leu Pro Asn Gly Asn His Asp Ala Leu Ile Asp
 130 135 140

Ala Arg His Asn Leu Ala Lys Phe Lys Val Cys Met Ala Ala Leu Pro
 145 150 155 160

Leu Gly Lys Arg Asp Arg Val Ser
 165

<210> 2123

<211> 2109

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2086)

<223> RXA01177

<400> 2123

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agttccctaa aaaccgctgg atacggatcac actatttttc atg cac ggt gaa aaa 115
 Met His Gly Glu Lys
 1 5

ctt gtg gat ggc act gag gga aat ctc agt caa ttc caa tgg cgc gat 163
 Leu Val Asp Gly Thr Glu Gly Asn Leu Ser Gln Phe Gln Trp Arg Asp
 10 15 20

atg gct aca aat cag acg ctg aga aaa gca ctg tta gtg ctt tct acc 211
 Met Ala Thr Asn Gln Thr Leu Arg Lys Ala Leu Leu Val Leu Ser Thr
 25 30 35

atc gct cta ctc ttg act tta tgg cct tca att ttc aat gtt cgg gcc 259
 Ile Ala Leu Leu Leu Thr Leu Trp Pro Ser Ile Phe Asn Val Arg Ala
 40 45 50

atc gag tct ttt gtt ttc ttc cat att gat act gac gtg tac cgc 307
 Ile Glu Ser Phe Val Phe Phe Phe His Ile Asp Thr Asp Val Tyr Arg
 55 60 65

gcc ggt gct aat gca ttc ttg cat ggc gag aat ctg tat acc cag gac 355
 Ala Gly Ala Asn Ala Phe Leu His Gly Glu Asn Leu Tyr Thr Gln Asp

70	75	80	85
tac caa gtt ggt agc att caa ctt ccc ttc acg tac cca cgc att tct			403
Tyr Gln Val Gly Ser Ile Gln Leu Pro Phe Thr Tyr Pro Pro Ile Ser	90	95	100
gct gcg ctg ttt gtt cca ctt gca atc ctt gca agc agt gta gcc gga			451
Ala Ala Leu Phe Val Pro Leu Ala Ile Leu Ala Ser Ser Val Ala Gly	105	110	115
ata gca tta acg ctt att tcc acg gtg ttg ctg tgg tgg agc gta gct			499
Ile Ala Leu Thr Leu Ile Ser Thr Val Leu Leu Trp Trp Ser Val Ala	120	125	130
atc gtc ttg cgc cga gtg ctc aag ggt ctc acg gat gct gat tcc agg			547
Ile Val Leu Arg Arg Val Leu Lys Gly Leu Thr Asp Ala Asp Ser Arg	135	140	145
ttt gtg tcc tat ttg att ctg cct atg gca ttg tcc acg gaa cct gta			595
Phe Val Ser Tyr Leu Ile Leu Pro Met Ala Leu Ser Thr Glu Pro Val	150	155	160
ttc cag acc ctg cag ttt ggc cag gtc aac atc att ttg atg gcg ctg			643
Phe Gln Thr Leu Gln Phe Gly Gln Val Asn Ile Ile Leu Met Ala Leu	170	175	180
gtt ctc atg gat acc ttc acc aaa aag ccc tgg ttg cca cgt ggt ttt			691
Val Leu Met Asp Thr Phe Thr Lys Lys Pro Trp Leu Pro Arg Gly Phe	185	190	195
tgg att ggt ttg gcg gca tcc atc aag ctg acc ccc gca gtc ttt ggc			739
Trp Ile Gly Leu Ala Ala Ser Ile Lys Leu Thr Pro Ala Val Phe Gly	200	205	210
ctt tac ttc cta gtg aag aag gac tgg aag ggc gct gga gta gca att			787
Leu Tyr Phe Leu Val Lys Lys Asp Trp Lys Gly Ala Gly Val Ala Ile	215	220	225
gct tct ggc gta ggt ttt tcc gcc ttg gcg ttt atc ctc tca cct tca			835
Ala Ser Gly Val Gly Phe Ser Ala Leu Ala Phe Ile Leu Ser Pro Ser	230	235	240
agt tcc aag att tac tgg act gaa aca ctc aac gac cct tct cgc atc			883
Ser Ser Lys Ile Tyr Trp Thr Glu Thr Leu Asn Asp Pro Ser Arg Ile	250	255	260
ggc aac cta tct tat att gct aac caa tct gtg cgt gga acg ctc agc			931
Gly Asn Leu Ser Tyr Ile Ala Asn Gln Ser Val Arg Gly Thr Leu Ser	265	270	275
cga atg atg cat gaa cag cag gat ctc gtc gaa aag ctt tgg ctt gtg			979
Arg Met Met His Glu Gln Gln Asp Leu Val Glu Lys Leu Trp Leu Val	280	285	290
gca gtt gtc ttg tgc ctt gcc gct gtc gcc gtc gcc atg tgg cgc gtg			1027
Ala Val Val Leu Cys Leu Ala Ala Val Ala Val Ala Met Trp Arg Val	295	300	305
gta cgc gcc ggc aac cgc tac ggc gcc gtc atg ctc aac tgg ttg att			1075
Val Arg Ala Gly Asn Pro Tyr Gly Ala Val Met Leu Asn Ser Leu Ile	310	315	320
			325

gct ctg ctg tgc tcc cct gtt tca tgg tct cac cac tgg gta tgg ctg 1123
Ala Leu Leu Cys Ser Pro Val Ser Trp Ser His His Trp Val Trp Leu
330 335 340

att cca atc gct att ggt ttg ggg gca agt gcg tgg aac cag cgg cgg 1171
Ile Pro Ile Ala Ile Gly Leu Gly Ala Ser Ala Trp Asn Gln Arg Arg
345 350 355

act gct cca gga att gcc gcg acg gct gga gtc ttg gcg ctt ctg acc 1219
Thr Ala Pro Gly Ile Ala Ala Thr Ala Gly Val Leu Ala Leu Leu Thr
360 365 370

acg att ccg atg ttc atc aca aca ttt tgg aac atg cca tac gat tca 1267
Thr Ile Pro Met Phe Ile Thr Thr Phe Trp Asn Met Pro Tyr Asp Ser
375 380 385

gag tct tac cca ttt tgg cca ttg att ctg cag ccg tgg gcc aac gcg 1315
Glu Ser Tyr Pro Phe Trp Pro Leu Ile Leu Gln Pro Ser Gly Asn Ala
390 395 400 405

tat gta gta gtg gtc atc gct att ttg atc gtc gcg att gtg aat cca 1363
Tyr Val Val Val Val Ile Ala Ile Leu Ile Val Ala Ile Val Asn Pro
410 415 420

aca gtt ttg gcc agt gcc aat aaa gct gtt tca gcc cag gca gag aag 1411
Thr Val Leu Gly Ser Gly Asn Lys Ala Val Ser Gly Gln Ala Glu Lys
425 430 435

aag tcc tcc cct gcg ttg ctt gtt gtt tta gcg att gcc att ttc tac 1459
Lys Ser Ser Pro Ala Leu Leu Val Val Leu Ala Ile Ala Ile Phe Tyr
440 445 450

ctc ttt gcc aat att tgg ttt aag gga aac aat caa aac aaa gcg ctc 1507
Leu Phe Ala Asn Ile Trp Phe Lys Gly Asn Asn Gln Asn Lys Ala Leu
455 460 465

att cag tac cca ctg cag act atg gaa ggt cgc ggt ctc act gac ttc 1555
Ile Gln Tyr Pro Leu Gln Thr Met Glu Gly Arg Gly Leu Thr Asp Phe
470 475 480 485

ggc gag ctt att ttt gaa ttc gcg gct tcc tcc aac cag ctt gtt tcc 1603
Gly Glu Leu Ile Phe Glu Phe Ala Ala Ser Ser Asn Gln Leu Val Ser
490 495 500

ctc tgg ata atc gcc gcc ctc aac gcc atc gca ttg gct att acc ctg 1651
Leu Trp Ile Ile Gly Ala Leu Asn Ala Ile Ala Leu Ala Ile Thr Leu
505 510 515

tgg ttc ctc ctt cag cgt ttt gct ggg aag aag agc tcc tgg ctg att 1699
Trp Phe Leu Leu Gln Arg Phe Ala Gly Lys Lys Ser Ser Trp Leu Ile
520 525 530

tat ctc agc acc gtg gct gtt gcg ctg atg atg ttc tca gtg cag gat 1747
Tyr Leu Ser Thr Val Ala Val Ala Leu Met Met Phe Ser Val Gln Asp
535 540 545

gcc ttg cag ttt ggt tgc ctg act ctc gtt gca ctc gca ttg atc act 1795
Ala Leu Gln Phe Gly Ser Leu Thr Leu Val Ala Leu Ala Leu Ile Thr
550 555 560 565

gtt gat gtg ttg agt gtc aga gag att ggc cgc cgc ggg ctg ctc aca 1843
Val Asp Val Leu Ser Val Arg Glu Ile Gly Arg Arg Gly Leu Leu Thr
570 575 580

gga ctt gca gca gcc ctg ttt gga tgg cca att ctg att gtt atc gga 1891
Gly Leu Ala Ala Ala Leu Phe Gly Trp Pro Ile Leu Ile Val Ile Gly
585 590 595

ttc ctc att cac cga cgt tat gca gca aca atc aca acc act gtc acc 1939
Phe Leu Ile His Arg Arg Tyr Ala Ala Thr Ile Thr Thr Val Thr
600 605 610

gca gct gtg ctg tgg atc tta gga att ctg ctc aat cca gac gcc ttc 1987
Ala Ala Val Leu Trp Ile Leu Gly Ile Leu Leu Asn Pro Asp Ala Phe
615 620 625

aac ctc aac ctg ctg cgt caa tgg ttc aac ggg cgc gat ggt cgg gac 2035
Asn Leu Asn Leu Leu Arg Gln Trp Phe Asn Gly Arg Asp Gly Arg Asp
630 635 640 645

aat ttg tcc ttc tat gct ttc ctt gcc agg tgg gtc agc gaa tcc cca 2083
Asn Leu Ser Phe Tyr Ala Phe Leu Ala Arg Trp Val Ser Glu Ser Pro
650 655 660

gca tgatgttcgt atggttcatc gtc 2109
Ala

<210> 2124

<211> 662

<212> PRT

<213> Corynebacterium glutamicum

<400> 2124

Met His Gly Glu Lys Leu Val Asp Gly Thr Glu Gly Asn Leu Ser Gln
1 5 10 15

Phe Gln Trp Arg Asp Met Ala Thr Asn Gln Thr Leu Arg Lys Ala Leu
20 25 30

Leu Val Leu Ser Thr Ile Ala Leu Leu Thr Leu Trp Pro Ser Ile
35 40 45

Phe Asn Val Arg Ala Ile Glu Ser Phe Val Phe Phe Phe His Ile Asp
50 55 60

Thr Asp Val Tyr Arg Ala Gly Ala Asn Ala Phe Leu His Gly Glu Asn
65 70 75 80

Leu Tyr Thr Gln Asp Tyr Gln Val Gly Ser Ile Gln Leu Pro Phe Thr
85 90 95

Tyr Pro Pro Ile Ser Ala Ala Leu Phe Val Pro Leu Ala Ile Leu Ala
100 105 110

Ser Ser Val Ala Gly Ile Ala Leu Thr Leu Ile Ser Thr Val Leu Leu
115 120 125

Trp Trp Ser Val Ala Ile Val Leu Arg Arg Val Leu Lys Gly Leu Thr
130 135 140

Asp Ala Asp Ser Arg Phe Val Ser Tyr Leu Ile Leu Pro Met Ala Leu
 145 150 155 160
 Ser Thr Glu Pro Val Phe Gln Thr Leu Gln Phe Gly Gln Val Asn Ile
 165 170 175
 Ile Leu Met Ala Leu Val Leu Met Asp Thr Phe Thr Lys Lys Pro Trp
 180 185 190
 Leu Pro Arg Gly Phe Trp Ile Gly Leu Ala Ala Ser Ile Lys Leu Thr
 195 200 205
 Pro Ala Val Phe Gly Leu Tyr Phe Leu Val Lys Lys Asp Trp Lys Gly
 210 215 220
 Ala Gly Val Ala Ile Ala Ser Gly Val Gly Phe Ser Ala Leu Ala Phe
 225 230 235 240
 Ile Leu Ser Pro Ser Ser Lys Ile Tyr Trp Thr Glu Thr Leu Asn
 245 250 255
 Asp Pro Ser Arg Ile Gly Asn Leu Ser Tyr Ile Ala Asn Gln Ser Val
 260 265 270
 Arg Gly Thr Leu Ser Arg Met Met His Glu Gln Gln Asp Leu Val Glu
 275 280 285
 Lys Leu Trp Leu Val Ala Val Val Leu Cys Leu Ala Val Ala Val
 290 295 300
 Ala Met Trp Arg Val Val Arg Ala Gly Asn Pro Tyr Gly Ala Val Met
 305 310 315 320
 Leu Asn Ser Leu Ile Ala Leu Leu Cys Ser Pro Val Ser Trp Ser His
 325 330 335
 His Trp Val Trp Leu Ile Pro Ile Ala Ile Gly Leu Gly Ala Ser Ala
 340 345 350
 Trp Asn Gln Arg Arg Thr Ala Pro Gly Ile Ala Ala Thr Ala Gly Val
 355 360 365
 Leu Ala Leu Leu Thr Thr Ile Pro Met Phe Ile Thr Thr Phe Trp Asn
 370 375 380
 Met Pro Tyr Asp Ser Glu Ser Tyr Pro Phe Trp Pro Leu Ile Leu Gln
 385 390 395 400
 Pro Ser Gly Asn Ala Tyr Val Val Val Val Ile Ala Ile Leu Ile Val
 405 410 415
 Ala Ile Val Asn Pro Thr Val Leu Gly Ser Gly Asn Lys Ala Val Ser
 420 425 430
 Gly Gln Ala Glu Lys Lys Ser Ser Pro Ala Leu Leu Val Val Leu Ala
 435 440 445
 Ile Ala Ile Phe Tyr Leu Phe Ala Asn Ile Trp Phe Lys Gly Asn Asn
 450 455 460

Gln Asn Lys Ala Leu Ile Gln Tyr Pro Leu Gln Thr Met Glu Gly Arg
465 470 475 480

Gly Leu Thr Asp Phe Gly Glu Leu Ile Phe Glu Phe Ala Ala Ser Ser
485 490 495

Asn Gln Leu Val Ser Leu Trp Ile Ile Gly Ala Leu Asn Ala Ile Ala
500 505 510

Leu Ala Ile Thr Leu Trp Phe Leu Leu Gln Arg Phe Ala Gly Lys Lys
515 520 525

Ser Ser Trp Leu Ile Tyr Leu Ser Thr Val Ala Val Ala Leu Met Met
530 535 540

Phe Ser Val Gln Asp Ala Leu Gln Phe Gly Ser Leu Thr Leu Val Ala
545 550 555 560

Leu Ala Leu Ile Thr Val Asp Val Leu Ser Val Arg Glu Ile Gly Arg
565 570 575

Arg Gly Leu Leu Thr Gly Leu Ala Ala Leu Phe Gly Trp Pro Ile
580 585 590

Leu Ile Val Ile Gly Phe Leu Ile His Arg Arg Tyr Ala Ala Thr Ile
595 600 605

Thr Thr Thr Val Thr Ala Ala Val Leu Trp Ile Leu Gly Ile Leu Leu
610 615 620

Asn Pro Asp Ala Phe Asn Leu Asn Leu Leu Arg Gln Trp Phe Asn Gly
625 630 635 640

Arg Asp Gly Arg Asp Asn Leu Ser Phe Tyr Ala Phe Leu Ala Arg Trp
645 650 655

Val Ser Glu Ser Pro Ala
660

<210> 2125

<211> 573

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(550)

<223> RXA01178

<400> 2125

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tctatgcttt ccttgccagg tgggtcagcg aatccccagc atg atg ttc gta tgg 115
Met Met Phe Val Trp
1 5

ttc atc gtc gcc cta gga ctt ggt gcc tgg gca atc cac cgc acc tgg 163
Phe Ile Val Ala Leu Gly Leu Gly Ala Trp Ala Ile His Arg Thr Trp
10 15 20

tca cat gga ttc aag gac ctc tcc gtt gca ctg agc atc gca cta cca 211
 Ser His Gly Phe Lys Asp Leu Ser Val Ala Leu Ser Ile Ala Leu Pro
 25 30 35

acc ttg gtg ctc ccc ata gtg gaa ctc cac cac ctc gtg cta ctt ctt 259
 Thr Leu Val Leu Pro Ile Val Glu Leu His His Leu Val Leu Leu Leu
 40 45 50

cca ctg atc gca gtg ttg ctt cgt caa gga cgc gtg gca att tcc tac 307
 Pro Leu Ile Ala Val Leu Leu Arg Gln Gly Arg Val Ala Ile Ser Tyr
 55 60 65

ctc atc gga ttt atc tac cta gtc tca tgg act ccg caa cac ctg tcc 355
 Leu Ile Gly Phe Ile Tyr Leu Val Ser Trp Thr Pro Gln His Leu Ser
 70 75 80 85

tac tcc acg gta ttc cca ctt aat gat cca gca cca gaa ggg tac gtc 403
 Tyr Ser Thr Val Phe Pro Leu Asn Asp Pro Ala Pro Glu Gly Tyr Val
 90 95 100

gcc cac ttt gga tgg tat tta ctc gtt gaa cca atg gcg gta gca ccg 451
 Ala His Phe Gly Trp Tyr Leu Leu Val Glu Pro Met Ala Val Ala Pro
 105 110 115

gca gct ata atc ctc gga gca ttt att gcc tgt gct gca acc aca cct 499
 Ala Ala Ile Ile Leu Gly Ala Phe Ile Ala Cys Ala Ala Thr Thr Pro
 120 125 130

aaa aca agt cag ctc gtg cag gtc gac aag tca agc gcg gaa aac acc 547
 Lys Thr Ser Gln Leu Val Gln Val Asp Lys Ser Ser Ala Glu Asn Thr
 135 140 145

aag taagccttac agtccgacag cct 573
 Lys
 150

<210> 2126
 <211> 150
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 2126
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Ile His Arg Thr Trp Ser His Gly Phe Lys Asp Leu Ser Val Ala Leu
 20 25 30

Ser Ile Ala Leu Pro Thr Leu Val Leu Pro Ile Val Glu Leu His His
 35 40 45

Leu Val Leu Leu Leu Pro Leu Ile Ala Val Leu Leu Arg Gln Gly Arg
 50 55 60

Val Ala Ile Ser Tyr Leu Ile Gly Phe Ile Tyr Leu Val Ser Trp Thr
 65 70 75 80

Pro Gln His Leu Ser Tyr Ser Thr Val Phe Pro Leu Asn Asp Pro Ala
 85 90 95

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Pro Glu Gly Tyr Val Ala His Phe Gly Trp Tyr Leu Leu Val Glu Pro
    100                      105                      110

Met Ala Val Ala Pro Ala Ala Ile Ile Leu Gly Ala Phe Ile Ala Cys
    115                      120                      125

Ala Ala Thr Thr Pro Lys Thr Ser Gln Leu Val Gln Val Asp Lys Ser
    130                      135                      140

Ser Ala Glu Asn Thr Lys
    145                      150

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<210> 2127
<211> 1589
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(1573)
<223> RXA01184

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ggcaatagtg atgatgtcgc tgatattctt ttacgccttg atg ggt ttg ttt ggt 115
                                Met Gly Leu Phe Gly
                                1                      5

ttc ggc atc ttt ttg gct ctt ggg ctt ggg caa gac cac atg ggc atc 163
Phe Gly Ile Phe Leu Ala Leu Gly Leu Gly Gln Asp His Met Gly Ile
                        10                      15                      20

ctt gct ggt gtt gtc tcg gtc ggc atg gtg gct tat tgc att gct gcg 211
Leu Ala Gly Val Val Ser Val Gly Met Val Ala Tyr Cys Ile Ala Ala
                        25                      30                      35

ttt atg tgg ccg tca ggt gag ggg cag ctg gat ccg act gca ttt tcc 259
Phe Met Trp Pro Ser Gly Glu Gly Gln Leu Asp Pro Thr Ala Phe Ser
                        40                      45                      50

acc atg ccg cta tcg gcg aag caa tta ttg cct gga ttc gct atc ggt 307
Thr Met Pro Leu Ser Ala Lys Gln Leu Leu Pro Gly Phe Ala Ile Gly
                        55                      60                      65

acg ctc ctg cag tca cgg ggg att att gcg gtg att tgt acg gtg gcg 355
Thr Thr Leu Leu Gln Ser Arg Gly Ile Ile Ala Val Ile Cys Thr Val Ala
                        70                      75                      80                      85

aca tcc att att gct gcg gtg ttt tta cct gtt ggt tcg tgg ccg atg 403
Thr Ser Ile Ile Ala Ala Val Phe Leu Pro Val Gly Ser Trp Pro Met
                        90                      95                      100

atc gtg ttc atg atg gcg gta tcg ctg gtt act acg ttg ctt ttg ggt 451
Ile Val Phe Met Met Ala Val Ser Leu Val Thr Thr Leu Leu Leu Gly
                        105                      110                      115

gag ttg ctt ggg gcg ttg acc tcg ggt tct tct tct agg gtg agt aat 499
Glu Leu Leu Gly Ala Leu Thr Ser Gly Ser Ser Ser Arg Val Ser Asn
                        120                      125                      130

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gat cgc cgt aca gtt ctt act tcc gtt gtc ttc atg gtg ttt gtt gtt 547
 Asp Arg Arg Thr Val Leu Thr Ser Val Val Phe Met Val Phe Val Val
 135 140 145

ggc tat aac atg ctg att ggc gcg gat gga atg agt cga atc gat gcc 595
 Gly Tyr Asn Met Leu Ile Gly Ala Asp Gly Met Ser Arg Ile Asp Ala
 150 155 160 165

att ggg gct tat aca aag tgg aca cca ttt ggg gcg ggt gca ggt gct 643
 Ile Gly Ala Tyr Thr Lys Trp Thr Pro Phe Gly Ala Gly Ala Gly Ala
 170 175 180

att gag gct ttt gct gtt ggt ttg tgg ggt gag gca ggc ctg tta aca 691
 Ile Glu Ala Phe Ala Val Gly Leu Trp Gly Glu Ala Gly Leu Leu Thr
 185 190 195

ttg ctg gct ttt gtt tat gtt gct gct ggt ttc tgg tta tgg tca cag 739
 Leu Leu Ala Phe Val Tyr Val Ala Ala Gly Phe Trp Leu Trp Ser Gln
 200 205 210

ctg att aat cgc gcg ctc act gcg ccg ctg gac caa ggt ggg caa ggg 787
 Leu Ile Asn Arg Ala Leu Thr Ala Pro Leu Asp Gln Gly Gly Gln Gly
 215 220 225

caa agc gct aaa gac agc gcc ggt gaa ggc aag aag gtt ctc ttt ctg 835
 Gln Ser Ala Lys Asp Ser Ala Ala Gly Glu Gly Lys Lys Val Leu Phe Leu
 230 235 240 245

cca ggt att cct tgg tca gtt gga ggt gcc att ttc tgg agg tgg ctg 883
 Pro Gly Ile Pro Trp Ser Val Gly Gly Ala Ile Phe Ser Arg Ser Leu
 250 255 260

cgt tat atg ttc agg gac tcc agg ttg ttg gga tca atg att gtg ttc 931
 Arg Tyr Met Phe Arg Asp Ser Arg Leu Leu Gly Ser Met Ile Val Phe
 265 270 275

ccg ctt ctt ggc gtg ctg ttt att ttc cag agc ttc acc gtt gag ttt 979
 Pro Leu Leu Gly Val Leu Phe Ile Phe Gln Ser Phe Thr Val Glu Phe
 280 285 290

ttc atg atc tat gtt ggg ttg atc atg atg gca gtg ttc gca gga tcc 1027
 Phe Met Ile Tyr Val Gly Leu Ile Met Met Ala Val Phe Ala Gly Ser
 295 300 305

gtt gct acc aat gat ttt ggc tat gac ggc cct tgg ttg tgg cta aat 1075
 Val Ala Thr Asn Asp Phe Gly Tyr Asp Gly Pro Ser Leu Trp Leu Asn
 310 315 320 325

atc gtt gct ggt gtc aaa gcc cga acg ttg ttg atg ccc agg cac tgg 1123
 Ile Val Ala Gly Val Lys Ala Arg Thr Leu Leu Met Pro Arg His Trp
 330 335 340

gca tca atg ctg ccg gga agt gtg tca att gtg gtg ttt atg atc atc 1171
 Ala Ser Met Leu Pro Gly Ser Val Ser Ile Val Val Phe Met Ile Ile
 345 350 355

acc att gtg ctc gcg gag aat aag acc acc gct gtg ctg atc tgt ttt 1219
 Thr Ile Val Leu Ala Glu Asn Lys Thr Thr Ala Val Leu Ile Cys Phe
 360 365 370

att ggc ctg ggg atc ttt atc tcc agt gcg gct gta gcg ttg ttg gtc 1267
 ile gly leu gly ile phe ile ser ser ala ala val ala leu leu val
 375 380 385

acc aca ttt aat ccg tat ccg act tct aag cca ggc acg agt cct tgg 1315
 thr thr phe asn pro tyr pro thr ser lys pro gly thr ser pro trp
 390 395 400 405

ggc gat cga agt ggc tat tcc ggt gct gcg ttc gtg gga gca ttt gcc 1363
 gly asp arg ser gly tyr ser gly ala ala phe val gly ala phe ala
 410 415 420

gca ctg tta ctg gga tgg atc ccg acg att cct act atc gca ttg ggt 1411
 ala leu leu leu gly trp ile pro thr ile pro thr ile ala leu gly
 425 430 435

atc ttt ggt ctg gtt acc gat cag atg tgg atg atc atc ctc gcg gag 1459
 ile phe gly leu val thr asp gln met trp met ile leu ala glu
 440 445 450

gtg ctg gcc att att ctc cca gta gct gtg tac atc ggc gtt gct aag 1507
 val leu ala ile ile leu pro val ala val tyr ile gly val ala lys
 455 460 465

gtg tgt att cgc aag gtg gag aag gat ctt ccg gag atc ttc gac aag 1555
 val cys ile arg lys val glu lys asp leu pro glu ile phe asp lys
 470 475 480 485

gtg aaa act cac gtg aaa tagaaaaatg cggggt 1589
 val lys thr his val lys
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<210> 2128

<211> 491

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2128

Met Gly Leu Phe Gly Phe Gly Ile Phe Leu Ala Leu Gly Leu Gly Gln
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Asp His Met Gly Ile Leu Ala Gly Val Val Ser Val Gly Met Val Ala
 20 25 30

Tyr Cys Ile Ala Ala Phe Met Trp Pro Ser Gly Glu Gly Gln Leu Asp
 35 40 45

Pro Thr Ala Phe Ser Thr Met Pro Leu Ser Ala Lys Gln Leu Leu Pro
 50 55 60

Gly Phe Ala Ile Gly Thr Leu Leu Gln Ser Arg Gly Ile Ile Ala Val
 65 70 75 80

Ile Cys Thr Val Ala Thr Ser Ile Ile Ala Ala Val Phe Leu Pro Val
 85 90 95

Gly Ser Trp Pro Met Ile Val Phe Met Met Ala Val Ser Leu Val Thr
 100 105 110

Thr Leu Leu Leu Gly Glu Leu Leu Gly Ala Leu Thr Ser Gly Ser Ser

115					120					125						
Ser	Arg	Val	Ser	Asn	Asp	Arg	Arg	Thr	Val	Leu	Thr	Ser	Val	Val	Phe	
130					135					140						
Met	Val	Phe	Val	Val	Gly	Tyr	Asn	Met	Leu	Ile	Gly	Ala	Asp	Gly	Met	
145					150					155					160	
Ser	Arg	Ile	Asp	Ala	Ile	Gly	Ala	Tyr	Thr	Lys	Trp	Thr	Pro	Phe	Gly	
165					170					175						
Ala	Gly	Ala	Gly	Ala	Ile	Glu	Ala	Phe	Ala	Val	Gly	Leu	Trp	Gly	Glu	
180					185					190						
Ala	Gly	Leu	Leu	Thr	Leu	Leu	Ala	Phe	Val	Tyr	Val	Ala	Ala	Gly	Phe	
195					200					205						
Trp	Leu	Trp	Ser	Gln	Leu	Ile	Asn	Arg	Ala	Leu	Thr	Ala	Pro	Leu	Asp	
210					215					220						
Gln	Gly	Gly	Gln	Gly	Gln	Ser	Ala	Lys	Asp	Ser	Ala	Gly	Glu	Gly	Lys	
225					230					235					240	
Lys	Val	Leu	Phe	Leu	Pro	Gly	Ile	Pro	Trp	Ser	Val	Gly	Gly	Ala	Ile	
245					250					255						
Phe	Ser	Arg	Ser	Leu	Arg	Tyr	Met	Phe	Arg	Asp	Ser	Arg	Leu	Leu	Gly	
260					265					270						
Ser	Met	Ile	Val	Phe	Pro	Leu	Leu	Gly	Val	Leu	Phe	Ile	Phe	Gln	Ser	
275					280					285						
Phe	Thr	Val	Glu	Phe	Phe	Met	Ile	Tyr	Val	Gly	Leu	Ile	Met	Met	Ala	
290					295					300						
Val	Phe	Ala	Gly	Ser	Val	Ala	Thr	Asn	Asp	Phe	Gly	Tyr	Asp	Gly	Pro	
305					310					315					320	
Ser	Leu	Trp	Leu	Asn	Ile	Val	Ala	Gly	Val	Lys	Ala	Arg	Thr	Leu	Leu	
325					330					335						
Met	Pro	Arg	His	Trp	Ala	Ser	Met	Leu	Pro	Gly	Ser	Val	Ser	Ile	Val	
340					345					350						
Val	Phe	Met	Ile	Ile	Thr	Ile	Val	Leu	Ala	Glu	Asn	Lys	Thr	Thr	Ala	
355					360					365						
Val	Leu	Ile	Cys	Phe	Ile	Gly	Leu	Gly	Ile	Phe	Ile	Ser	Ser	Ala	Ala	
370					375					380						
Val	Ala	Leu	Leu	Val	Thr	Thr	Phe	Asn	Pro	Tyr	Pro	Thr	Ser	Lys	Pro	
385					390					395					400	
Gly	Thr	Ser	Pro	Trp	Gly	Asp	Arg	Ser	Gly	Tyr	Ser	Gly	Ala	Ala	Phe	
405					410					415						
Val	Gly	Ala	Phe	Ala	Ala	Leu	Leu	Leu	Gly	Trp	Ile	Pro	Thr	Ile	Pro	
420					425					430						
Thr	Ile	Ala	Leu	Gly	Ile	Phe	Gly	Leu	Val	Thr	Asp	Gln	Met	Trp	Met	
435					440					445						

Ile Ile Leu Ala Glu Val Leu Ala Ile Ile Leu Pro Val Ala Val Tyr
450 455 460

Ile Gly Val Ala Lys Val Cys Ile Arg Lys Val Glu Lys Asp Leu Pro
465 470 475 480

Glu Ile Phe Asp Lys Val Lys Thr His Val Lys
485 490

<210> 2129

<211> 1221

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1198)

<223> RXA01186

<400> 2129

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agttcaacaa ttacataaca tctgaaagaa tagggacatt atg gct aca cct gta 115
Met Ala Thr Pro Val
1 5

cca ctg gtt ttt aac gca cct aag cgt ggc atg ccc cca acc cac ttt 163
Pro Leu Val Phe Asn Ala Pro Lys Arg Gly Met Pro Pro Thr His Phe
10 15 20

gcg gat ctt aat gat gag gct cgc att gag gct ctt aaa gag ctc ggc 211
Ala Asp Leu Asn Asp Glu Ala Arg Ile Glu Ala Leu Lys Glu Leu Gly
25 30 35

ttg ccc aaa ttc cga ctc aat cag atc gct cga cac tac tat ggt cgc 259
Leu Pro Lys Phe Arg Leu Asn Gln Ile Ala Arg His Tyr Tyr Gly Arg
40 45 50

ctc gag gct gac cca ctc act atg acg gac ctg cct gaa ggt gct cgt 307
Leu Glu Ala Asp Pro Leu Thr Met Thr Asp Leu Pro Glu Gly Ala Arg
55 60 65

caa gaa gtc aag gat gct ctt ttt cca acg ttg atg tct cct ctg cgc 355
Gln Glu Val Lys Asp Ala Leu Phe Pro Thr Leu Met Ser Pro Leu Arg
70 75 80 85

gtc gtc gaa acc gat gac gat aca act cag aag acg tta tgg aag ctc 403
Val Val Glu Thr Asp Asp Thr Thr Gln Lys Thr Leu Trp Lys Leu
90 95 100

cat gat ggc act ttg ctt gag tct gtt ctc atg cgc tat tca gat cgc 451
His Asp Gly Thr Leu Leu Glu Ser Val Leu Met Arg Tyr Ser Asp Arg
105 110 115

tcc acg ctg tgt att tct tcg cag gct ggt tgc ggc atg gcg tgc cca 499
Ser Thr Leu Cys Ile Ser Ser Gln Ala Gly Cys Gly Met Ala Cys Pro
120 125 130

ttc tgt gca act ggt cag ggc ggt ttg gac cgt aac ctt tca atc ggt 547

Phe	Cys	Ala	Thr	Gly	Gln	Gly	Gly	Leu	Asp	Arg	Asn	Leu	Ser	Ile	Gly		
	135					140					145						
gag	atc	gtg	gat	cag	gtt	cgt	aat	gct	gct	gca	acg	atg	cag	tca	gag	595	
Glu	Ile	Val	Asp	Gln	Val	Arg	Asn	Ala	Ala	Ala	Thr	Met	Gln	Ser	Glu		
150				155				160						165			
ggc	ggt	cgt	ctg	tcc	aac	att	gtg	ttc	atg	gga	atg	ggc	gag	cct	ctc	643	
Gly	Gly	Arg	Leu	Ser	Asn	Ile	Val	Phe	Met	Gly	Met	Gly	Glu	Pro	Leu		
			170					175						180			
gct	aac	tac	aag	cgc	gtg	gtg	tcg	gct	gtt	cgt	cag	atc	acg	cag	cca	691	
Ala	Asn	Tyr	Lys	Arg	Val	Val	Ser	Ala	Val	Arg	Gln	Ile	Thr	Gln	Pro		
			185					190					195				
agc	cct	gcg	ggc	ttc	ggc	att	tcc	cag	cgc	agt	gtg	act	gtc	tcc	acc	739	
Ser	Pro	Ala	Gly	Phe	Gly	Ile	Ser	Gln	Arg	Ser	Val	Thr	Val	Ser	Thr		
	200					205						210					
gtg	ggc	ctc	gct	cca	gct	atc	agg	aag	ctt	gcc	gac	gaa	gag	atg	tcc	787	
Val	Gly	Leu	Ala	Pro	Ala	Ile	Arg	Lys	Leu	Ala	Asp	Glu	Glu	Met	Ser		
	215					220					225						
gta	act	ttg	gca	gtt	tcc	ttg	cac	act	cca	gac	gat	gag	ttg	cgt	gac	835	
Val	Thr	Leu	Ala	Val	Ser	Leu	His	Thr	Pro	Asp	Asp	Glu	Leu	Arg	Asp		
230				235				240						245			
act	ctc	gtg	cca	gtc	aac	aat	cgt	tgg	cct	gtc	gct	gag	gta	ctg	gac	883	
Thr	Leu	Val	Pro	Val	Asn	Asn	Arg	Trp	Pro	Val	Ala	Glu	Val	Leu	Asp		
			250					255						260			
gct	gct	cgt	tac	tac	gca	gat	aag	tct	ggc	cgt	cgc	gtc	tcc	atc	gag	931	
Ala	Ala	Arg	Tyr	Tyr	Ala	Asp	Lys	Ser	Gly	Arg	Arg	Val	Ser	Ile	Glu		
			265					270					275				
tat	gcg	ctc	att	cgc	gat	gtg	aat	gac	cag	gat	tgg	cgc	gca	gat	atg	979	
Tyr	Ala	Leu	Ile	Arg	Asp	Val	Asn	Asp	Gln	Asp	Trp	Arg	Ala	Asp	Met		
	280						285					290					
ctg	ggc	gag	aag	ctg	cat	aag	gct	ttg	ggc	tcc	cgt	gtg	cac	gtc	aac	1027	
Leu	Gly	Glu	Lys	Leu	His	Lys	Ala	Leu	Gly	Ser	Arg	Val	His	Val	Asn		
	295					300					305						
ttg	att	cca	ttg	aac	cca	act	cct	ggt	tct	aag	tgg	gat	gct	gca	cca	1075	
Leu	Ile	Pro	Leu	Asn	Pro	Thr	Pro	Gly	Ser	Lys	Trp	Asp	Ala	Ala	Pro		
310				315				320						325			
aag	gct	cgt	cag	gat	gag	ttt	gtg	cgt	cgt	gtg	atc	gcc	aag	ggt	gtt	1123	
Lys	Ala	Arg	Gln	Asp	Glu	Phe	Val	Arg	Arg	Val	Ile	Ala	Lys	Gly	Val		
			330					335						340			
cca	tgc	act	gtg	cgt	gat	acc	aag	gga	caa	gaa	atc	gct	gcg	gct	tgt	1171	
Pro	Cys	Thr	Val	Arg	Asp	Thr	Lys	Gly	Gln	Glu	Ile	Ala	Ala	Ala	Cys		
			345					350					355				
gga	cag	ctt	gct	gcg	gag	gaa	tct	gct	taagccctca	aagctcaaaa						1218	
Gly	Gln	Leu	Ala	Ala	Glu	Glu	Ser	Ala									
		360				365											
gcc																	1221

<210> 2130

<211> 366

<212> PRT

<213> Corynebacterium glutamicum

<400> 2130

Met Ala Thr Pro Val Pro Leu Val Phe Asn Ala Pro Lys Arg Gly Met
1 5 10 15Pro Pro Thr His Phe Ala Asp Leu Asn Asp Glu Ala Arg Ile Glu Ala
20 25 30Leu Lys Glu Leu Gly Leu Pro Lys Phe Arg Leu Asn Gln Ile Ala Arg
35 40 45His Tyr Tyr Gly Arg Leu Glu Ala Asp Pro Leu Thr Met Thr Asp Leu
50 55 60Pro Glu Gly Ala Arg Gln Glu Val Lys Asp Ala Leu Phe Pro Thr Leu
65 70 75 80Met Ser Pro Leu Arg Val Val Glu Thr Asp Asp Asp Thr Thr Gln Lys
85 90 95Thr Leu Trp Lys Leu His Asp Gly Thr Leu Leu Glu Ser Val Leu Met
100 105 110Arg Tyr Ser Asp Arg Ser Thr Leu Cys Ile Ser Ser Gln Ala Gly Cys
115 120 125Gly Met Ala Cys Pro Phe Cys Ala Thr Gly Gln Gly Gly Leu Asp Arg
130 135 140Asn Leu Ser Ile Gly Glu Ile Val Asp Gln Val Arg Asn Ala Ala Ala
145 150 155 160Thr Met Gln Ser Glu Gly Gly Arg Leu Ser Asn Ile Val Phe Met Gly
165 170 175Met Gly Glu Pro Leu Ala Asn Tyr Lys Arg Val Val Ser Ala Val Arg
180 185 190Gln Ile Thr Gln Pro Ser Pro Ala Gly Phe Gly Ile Ser Gln Arg Ser
195 200 205Val Thr Val Ser Thr Val Gly Leu Ala Pro Ala Ile Arg Lys Leu Ala
210 215 220Asp Glu Glu Met Ser Val Thr Leu Ala Val Ser Leu His Thr Pro Asp
225 230 235 240Asp Glu Leu Arg Asp Thr Leu Val Pro Val Asn Asn Arg Trp Pro Val
245 250 255Ala Glu Val Leu Asp Ala Ala Arg Tyr Tyr Ala Asp Lys Ser Gly Arg
260 265 270Arg Val Ser Ile Glu Tyr Ala Leu Ile Arg Asp Val Asn Asp Gln Asp
275 280 285


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Trp Arg Ala Asp Met Leu Gly Glu Lys Leu His Lys Ala Leu Gly Ser
  290                               295                               300

Arg Val His Val Asn Leu Ile Pro Leu Asn Pro Thr Pro Gly Ser Lys
  305                               310                               315                               320

Trp Asp Ala Ala Pro Lys Ala Arg Gln Asp Glu Phe Val Arg Arg Val
                               325                               330                               335

Ile Ala Lys Gly Val Pro Cys Thr Val Arg Asp Thr Lys Gly Gln Glu
                               340                               345                               350

Ile Ala Ala Ala Cys Gly Gln Leu Ala Ala Glu Glu Ser Ala
  355                               360                               365

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<210> 2131

<211> 1221

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1198)

<223> RXA01186

<400> 2131

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agttcaacaa ttacataaca tctgaaagaa tagggacatt atg gct aca cct gta 115
                               Met Ala Thr Pro Val
                               1                               5

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cca ctg gtt ttt aac gca cct aag cgt ggc atg ccc cca acc cac ttt 163
Pro Leu Val Phe Asn Ala Pro Lys Arg Gly Met Pro Pro Thr His Phe
                               10                               15                               20

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gcg gat ctt aat gat gag gct cgc att gag gct ctt aaa gag ctc ggc 211
Ala Asp Leu Asn Asp Glu Ala Arg Ile Glu Ala Leu Lys Glu Leu Gly
                               25                               30                               35

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ttg ccc aaa ttc cga ctc aat cag atc gct cga cac tac tat ggt cgc 259
Leu Pro Lys Phe Arg Leu Asn Gln Ile Ala Arg His Tyr Tyr Gly Arg
                               40                               45                               50

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ctc gag gct gac cca ctc act atg acg gac ctg cct gaa ggt gct cgt 307
Leu Glu Ala Asp Pro Leu Thr Met Thr Asp Leu Pro Glu Gly Ala Arg
                               55                               60                               65

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caa gaa gtc aag gat gct ctt ttt cca acg ttg atg tct cct ctg cgc 355
Gln Glu Val Lys Asp Ala Leu Phe Pro Thr Leu Met Ser Pro Leu Arg
                               70                               75                               80                               85

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gtc gtc gaa acc gat gac gat aca act cag aag acg tta tgg aag ctc 403
Val Val Glu Thr Asp Asp Asp Thr Thr Gln Lys Thr Leu Trp Lys Leu
                               90                               95                               100

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cat gat ggc act ttg ctt gag tct gtt ctc atg cgc tat tca gat cgc 451
His Asp Gly Thr Leu Leu Glu Ser Val Leu Met Arg Tyr Ser Asp Arg
                               105                               110                               115

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tcc acg ctg tgt att tct tcg cag gct ggt tgc ggc atg gcg tgc cca	499
Ser Thr Leu Cys Ile Ser Ser Gln Ala Gly Cys Gly Met Ala Cys Pro	
120 125 130	
ttc tgt gca act ggt cag ggc ggt ttg gac cgt aac ctt tca atc ggt	547
Phe Cys Ala Thr Gly Gln Gly Gly Leu Asp Arg Asn Leu Ser Ile Gly	
135 140 145	
gag atc gtg gat cag gtt cgt aat gct gct gca acg atg cag tca gag	595
Glu Ile Val Asp Gln Val Arg Asn Ala Ala Thr Met Gln Ser Glu	
150 155 160 165	
ggc ggt cgt ctg tcc aac att gtg ttc atg gga atg ggc gag cct ctc	643
Gly Gly Arg Leu Ser Asn Ile Val Phe Met Gly Met Gly Glu Pro Leu	
170 175 180	
gct aac tac aag cgc gtg gtg tcg gct gtt cgt cag atc acg cag cca	691
Ala Asn Tyr Lys Arg Val Val Ser Ala Val Arg Gln Ile Thr Gln Pro	
185 190 195	
agc cct gcg ggc ttc ggc att tcc cag cgc agt gtg act gtc tcc acc	739
Ser Pro Ala Gly Phe Gly Ile Ser Gln Arg Ser Val Thr Val Ser Thr	
200 205 210	
gtg ggc ctc gct cca gct atc agg aag ctt gcc gac gaa gag atg tcc	787
Val Gly Leu Ala Pro Ala Ile Arg Lys Leu Ala Asp Glu Glu Met Ser	
215 220 225	
gta act ttg gca gtt tcc ttg cac act cca gac gat gag ttg cgt gac	835
Val Thr Leu Ala Val Ser Leu His Thr Pro Asp Glu Leu Arg Asp	
230 235 240 245	
act ctc gtg cca gtc aac aat cgt tgg cct gtc gct gag gta ctg gac	883
Thr Leu Val Pro Val Asn Asn Arg Trp Pro Val Ala Glu Val Leu Asp	
250 255 260	
gct gct cgt tac tac gca gat aag tct ggc cgt cgc gtc tcc atc gag	931
Ala Ala Arg Tyr Tyr Ala Asp Lys Ser Gly Arg Arg Val Ser Ile Glu	
265 270 275	
tat gcg ctc att cgc gat gtg aat gac cag gat tgg cgc gca gat atg	979
Tyr Ala Leu Ile Arg Asp Val Asn Asp Gln Asp Trp Arg Ala Asp Met	
280 285 290	
ctg ggc gag aag ctg cat aag gct ttg ggc tcc cgt gtg cac gtc aac	1027
Leu Gly Glu Lys Leu His Lys Ala Leu Gly Ser Arg Val His Val Asn	
295 300 305	
ttg att cca ttg aac cca act cct ggt tct aag tgg gat gct gca cca	1075
Leu Ile Pro Leu Asn Pro Thr Pro Gly Ser Lys Trp Asp Ala Ala Pro	
310 315 320 325	
aag gct cgt cag gat gag ttt gtg cgt cgt gtg atc gcc aag ggt gtt	1123
Lys Ala Arg Gln Asp Glu Phe Val Arg Arg Val Ile Ala Lys Gly Val	
330 335 340	
cca tgc act gtg cgt gat acc aag gga caa gaa atc gct gcg gct tgt	1171
Pro Cys Thr Val Arg Asp Thr Lys Gly Gln Glu Ile Ala Ala Cys	
345 350 355	
gga cag ctt gct gcg gag gaa tct gct taagccctca aagctcaaaa	1218

Gly Gln Leu Ala Ala Glu Glu Ser Ala
 360 365

gcc

1221

<210> 2132

<211> 366

<212> PRT

<213> Corynebacterium glutamicum

<400> 2132

Met Ala Thr Pro Val Pro Leu Val Phe Asn Ala Pro Lys Arg Gly Met
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Pro Pro Thr His Phe Ala Asp Leu Asn Asp Glu Ala Arg Ile Glu Ala
 20 25 30

Leu Lys Glu Leu Gly Leu Pro Lys Phe Arg Leu Asn Gln Ile Ala Arg
 35 40 45

His Tyr Tyr Gly Arg Leu Glu Ala Asp Pro Leu Thr Met Thr Asp Leu
 50 55 60

Pro Glu Gly Ala Arg Gln Glu Val Lys Asp Ala Leu Phe Pro Thr Leu
 65 70 75 80

Met Ser Pro Leu Arg Val Val Glu Thr Asp Asp Asp Thr Thr Gln Lys
 85 90 95

Thr Leu Trp Lys Leu His Asp Gly Thr Leu Leu Glu Ser Val Leu Met
 100 105 110

Arg Tyr Ser Asp Arg Ser Thr Leu Cys Ile Ser Ser Gln Ala Gly Cys
 115 120 125

Gly Met Ala Cys Pro Phe Cys Ala Thr Gly Gln Gly Gly Leu Asp Arg
 130 135 140

Asn Leu Ser Ile Gly Glu Ile Val Asp Gln Val Arg Asn Ala Ala Ala
 145 150 155 160

Thr Met Gln Ser Glu Gly Gly Arg Leu Ser Asn Ile Val Phe Met Gly
 165 170 175

Met Gly Glu Pro Leu Ala Asn Tyr Lys Arg Val Val Ser Ala Val Arg
 180 185 190

Gln Ile Thr Gln Pro Ser Pro Ala Gly Phe Gly Ile Ser Gln Arg Ser
 195 200 205

Val Thr Val Ser Thr Val Gly Leu Ala Pro Ala Ile Arg Lys Leu Ala
 210 215 220

Asp Glu Glu Met Ser Val Thr Leu Ala Val Ser Leu His Thr Pro Asp
 225 230 235 240

Asp Glu Leu Arg Asp Thr Leu Val Pro Val Asn Asn Arg Trp Pro Val
 245 250 255

Ala Glu Val Leu Asp Ala Ala Arg Tyr Tyr Ala Asp Lys Ser Gly Arg

260	265	270
Arg Val Ser Ile Glu Tyr Ala Leu Ile Arg Asp Val Asn Asp Gln Asp		
275	280	285
Trp Arg Ala Asp Met Leu Gly Glu Lys Leu His Lys Ala Leu Gly Ser		
290	295	300
Arg Val His Val Asn Leu Ile Pro Leu Asn Pro Thr Pro Gly Ser Lys		
305	310	315
Trp Asp Ala Ala Pro Lys Ala Arg Gln Asp Glu Phe Val Arg Arg Val		
325	330	335
Ile Ala Lys Gly Val Pro Cys Thr Val Arg Asp Thr Lys Gly Gln Glu		
340	345	350
Ile Ala Ala Ala Cys Gly Gln Leu Ala Ala Glu Glu Ser Ala		
355	360	365

<210> 2133

<211> 573

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(559)

<223> RXA01187

<400> 2133

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gtgattctac	gagttcaatg	gctgtatgag	caacagacct	gtg gat cca ttt gag	115
				Val Asp Pro Phe Glu	
				1 5	

acc aac cca aac gac ctt ccc acc ggt tta gac cca gca tac gaa ggt	163
Thr Asn Pro Asn Asp Leu Pro Thr Gly Leu Asp Pro Ala Tyr Glu Gly	
10 15 20	

aac agt gag tta aac ccg ctt gga gga aaa aat att ccc gac gag cct	211
Asn Ser Glu Leu Asn Pro Leu Gly Gly Lys Asn Ile Pro Asp Glu Pro	
25 30 35	

gag gtg act gca aac aca cct gca gtt caa gaa gaa cct gct tac tcg	259
Glu Val Thr Ala Asn Thr Pro Ala Val Gln Glu Glu Pro Ala Tyr Ser	
40 45 50	

gag cca gaa act gcc gtt gag .tcg aag cgt cag gcg aag cag aac aca	307
Glu Pro Glu Thr Ala Val Glu Ser Lys Arg Gln Ala Lys Gln Asn Thr	
55 60 65	

aag aag tcc gaa cct gtt gtg gct cca aaa caa aca ctt gcc ggt ggc	355
Lys Lys Ser Glu Pro Val Val Ala Pro Lys Gln Thr Leu Ala Gly Gly	
70 75 80 85	

acg tgg gta gct ctc atc gta ggc gca ctt ttg cta atc cta ctg ttg	403
Thr Trp Val Ala Leu Ile Val Gly Ala Leu Leu Leu Ile Leu Leu Leu	
90 95 100	

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gtc ttc atc atg cag aac caa acc acc gta gag ctt aac ctt ttt gcg 451
Val Phe Ile Met Gln Asn Gln Thr Thr Val Glu Leu Asn Leu Phe Ala
      105                      110                      115

tgg acc ttc caa ttc cca gcc gga atc ggt ttc cta cta gca gcc att 499
Trp Thr Phe Gln Phe Pro Ala Gly Ile Gly Phe Leu Leu Ala Ala Ile
      120                      125                      130

acc ggt gca ttg att atg gcg ctt ggt ggt ggc gtg cgc atg ttt gag 547
Thr Gly Ala Leu Ile Met Ala Leu Gly Gly Gly Val Arg Met Phe Glu
      135                      140                      145

tac cgt cgc agt taagaaaaat ccgt 573
Tyr Arg Arg Ser
150

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<210> 2134

<211> 153

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2134

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Val Asp Pro Phe Glu Thr Asn Pro Asn Asp Leu Pro Thr Gly Leu Asp
  1              5              10              15

Pro Ala Tyr Glu Gly Asn Ser Glu Leu Asn Pro Leu Gly Gly Lys Asn
      20              25              30

Ile Pro Asp Glu Pro Glu Val Thr Ala Asn Thr Pro Ala Val Gln Glu
      35              40              45

Glu Pro Ala Tyr Ser Glu Pro Glu Thr Ala Val Glu Ser Lys Arg Gln
      50              55              60

Ala Lys Gln Asn Thr Lys Lys Ser Glu Pro Val Val Ala Pro Lys Gln
      65              70              75              80

Thr Leu Ala Gly Gly Thr Trp Val Ala Leu Ile Val Gly Ala Leu Leu
      85              90              95

Leu Ile Leu Leu Leu Val Phe Ile Met Gln Asn Gln Thr Thr Val Glu
      100             105             110

Leu Asn Leu Phe Ala Trp Thr Phe Gln Phe Pro Ala Gly Ile Gly Phe
      115             120             125

Leu Leu Ala Ala Ile Thr Gly Ala Leu Ile Met Ala Leu Gly Gly Gly
      130             135             140

Val Arg Met Phe Glu Tyr Arg Arg Ser
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<210> 2135

<211> 570

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

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 50 55 60
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 65 70 75 80
 Ala Asp Glu Ala Val Phe Met Ser Gln Gly Leu Lys Ile Leu His Ile
 85 90 95
 Lys Ser Lys Asn Asp Gln Ile Glu Leu Ala Leu Asp Ala His Gly Glu
 100 105 110
 Met Ala Phe Thr Ala Trp Leu Glu Ala Ala Pro Asp Ala Arg Ala Glu
 115 120 125
 His Ser Leu Asn Pro Arg Asp Phe Asn Arg Phe Arg Ala Ser Lys Asp
 130 135 140

Thr Arg Lys Asn Arg
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<210> 2137

<211> 813

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(790)

<223> RXA01196

<400> 2137

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gcaaaaaaccg ctaagtagac gtcattgtta tggtaggggtgc atg cgt tta gtc atc 115
 Met Arg Leu Val Ile
 1 5

gcc cgt tgc tca gtt gat tat gtt ggc cgt ttg gaa gct cat ctt ccg 163
 Ala Arg Cys Ser Val Asp Tyr Val Gly Arg Leu Glu Ala His Leu Pro
 10 15 20

tcc gcc gat cgc ctt ttg atg gtt aag gcg gat ggt tct gta tcc atc 211
 Ser Ala Asp Arg Leu Leu Met Val Lys Ala Asp Gly Ser Val Ser Ile
 25 30 35

cat gcc gat gac cgt gcc tat aag cca ctg aac tgg atg aca cct cca 259
 His Ala Asp Asp Arg Ala Tyr Lys Pro Leu Asn Trp Met Thr Pro Pro
 40 45 50

tgt tct tta gtt gaa act ccc atc act gat gaa gat ggt gaa gca aca 307
 Cys Ser Leu Val Glu Thr Pro Ile Thr Asp Glu Asp Gly Glu Ala Thr
 55 60 65

ggg gaa agc ctg tgg gtg gtg gaa aac aaa aag ggc gag cag ctt cga 355
 Gly Glu Ser Leu Trp Val Val Glu Asn Lys Lys Gly Glu Gln Leu Arg

70	75	80	85	
att act gtg gaa gaa att cat tcg gaa caa aac ttc gat cta ggc caa				403
Ile Thr Val Glu Glu Ile His Ser Glu Gln Asn Phe Asp Leu Gly Gln				
	90	95	100	
gac cca ggt ttg gtg aaa gac gga gtg gaa gat cat ctc caa gag ctt				451
Asp Pro Gly Leu Val Lys Asp Gly Val Glu Asp His Leu Gln Glu Leu				
	105	110	115	
ctt gca gag cac atc act acg ttg ggt gat ggg tac aca ttg att cgt				499
Leu Ala Glu His Ile Thr Thr Leu Gly Asp Gly Tyr Thr Leu Ile Arg				
	120	125	130	
cgg gag tat cca aca gct att ggg cct gtc gat att ttg tgt cgc aac				547
Arg Glu Tyr Pro Thr Ala Ile Gly Pro Val Asp Ile Leu Cys Arg Asn				
	135	140	145	
tct gac ggc gag act gtc gct gtg gag atc aag cgt cgt ggt ggc atc				595
Ser Asp Gly Glu Thr Val Ala Val Glu Ile Lys Arg Arg Gly Gly Ile				
	150	155	160	165
gac ggc gtt gag cag ttg acc agg tat ttg gaa ttg ctc aac cgt gat				643
Asp Gly Val Glu Gln Leu Thr Arg Tyr Leu Glu Leu Leu Asn Arg Asp				
	170	175	180	
gaa ttg ctc aag cct gtt cat gga gtg ttt gca gcc cag gag att aag				691
Glu Leu Leu Lys Pro Val His Gly Val Phe Ala Ala Gln Glu Ile Lys				
	185	190	195	
cct cag gca aag act ctc gcg gag gat cgt ggc atc aag tgc gtg acg				739
Pro Gln Ala Lys Thr Leu Ala Glu Asp Arg Gly Ile Lys Cys Val Thr				
	200	205	210	
ttg gat tat caa cgg ctt cgt ggc att gag tcc aat gag ctg aca ttg				787
Leu Asp Tyr Gln Ala Leu Arg Gly Ile Glu Ser Asn Glu Leu Thr Leu				
	215	220	225	
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Phe				
230				

<210> 2138

<211> 230

<212> PRT

<213> Corynebacterium glutamicum

<400> 2138

Met	Arg	Leu	Val	Ile	Ala	Arg	Cys	Ser	Val	Asp	Tyr	Val	Gly	Arg	Leu
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Glu	Ala	His	Leu	Pro	Ser	Ala	Asp	Arg	Leu	Leu	Met	Val	Lys	Ala	Asp
			20					25					30		

Gly	Ser	Val	Ser	Ile	His	Ala	Asp	Asp	Arg	Ala	Tyr	Lys	Pro	Leu	Asn
		35					40					45			

Trp	Met	Thr	Pro	Pro	Cys	Ser	Leu	Val	Glu	Thr	Pro	Ile	Thr	Asp	Glu
	50						55				60				

Asp Gly Glu Ala Thr Gly Glu Ser Leu Trp Val Val Glu Asn Lys Lys
65 70 75 80

Gly Glu Gln Leu Arg Ile Thr Val Glu Glu Ile His Ser Glu Gln Asn
85 90 95

Phe Asp Leu Gly Gln Asp Pro Gly Leu Val Lys Asp Gly Val Glu Asp
100 105 110

His Leu Gln Glu Leu Leu Ala Glu His Ile Thr Thr Leu Gly Asp Gly
115 120 125

Tyr Thr Leu Ile Arg Arg Glu Tyr Pro Thr Ala Ile Gly Pro Val Asp
130 135 140

Ile Leu Cys Arg Asn Ser Asp Gly Glu Thr Val Ala Val Glu Ile Lys
145 150 155 160

Arg Arg Gly Gly Ile Asp Gly Val Glu Gln Leu Thr Arg Tyr Leu Glu
165 170 175

Leu Leu Asn Arg Asp Glu Leu Leu Lys Pro Val His Gly Val Phe Ala
180 185 190

Ala Gln Glu Ile Lys Pro Gln Ala Lys Thr Leu Ala Glu Asp Arg Gly
195 200 205

Ile Lys Cys Val Thr Leu Asp Tyr Gln Ala Leu Arg Gly Ile Glu Ser
210 215 220

Asn Glu Leu Thr Leu Phe
225 230

<210> 2139

<211> 576

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(553)

<223> RXA01197

<400> 2139

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tcttcaatat tccccacct gctatgccta aaattaagcc atg tct acc gaa cag 115
Met Ser Thr Glu Gln
1 5

tct ttg aat atc ccc cac gaa tac gtc atc tgc ctc gat cat gtt ggc 163
Ser Leu Asn Ile Pro His Glu Tyr Val Ile Cys Leu Asp His Val Gly
10 15 20

atc gcc gtc cct gac ctc gag gaa gcc atc gaa ttt tac cgt tcc gca 211
Ile Ala Val Pro Asp Leu Glu Glu Ala Ile Glu Phe Tyr Arg Ser Ala
25 30 35

ttc ggc tgg gta aac cac cac caa gaa atc aat gag gaa caa ggc att 259
Phe Gly Trp Val Asn His His Gln Glu Ile Asn Glu Glu Gln Gly Ile

40 45 50
 tca gag gcc atg atc ggc ccc aaa gac att aaa agc aca gaa ggc atg 307
 Ser Glu Ala Met Ile Gly Pro Lys Asp Ile Lys Ser Thr Glu Gly Met
 55 60 65
 att cag ctc atc gcg cgc ctc aac gag gac tcc aca atc gcc aaa ttc 355
 Ile Gln Leu Ile Ala Pro Leu Asn Glu Asp Ser Thr Ile Ala Lys Phe
 70 75 80 85
 ctc gaa aag aaa ggt ccc ggc atc cag caa atg tgc ctg cgc acc aac 403
 Leu Glu Lys Lys Gly Pro Gly Ile Gln Gln Met Cys Leu Arg Thr Asn
 90 95 100
 aac atc gat gcg ctc tcc gag cac ctg cgc cgc caa ggc gtg cgc ctg 451
 Asn Ile Asp Ala Leu Ser Glu His Leu Arg Arg Gln Gly Val Arg Leu
 105 110 115
 ctc tac ccc gaa ccc aaa aac ggc acc ggc ggt gcc cgc atc aac ttc 499
 Leu Tyr Pro Glu Pro Lys Asn Gly Thr Gly Gly Ala Arg Ile Asn Phe
 120 125 130
 ctg cac ccc aaa gac gcg ggc ggc gtg ctg ctc gag atc acg cag cct 547
 Leu His Pro Lys Asp Ala Gly Gly Val Leu Leu Glu Ile Thr Gln Pro
 135 140 145
 caa agc taattgctta tcgacgtcc cag 576
 Gln Ser
 150
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 <211> 151
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 2140
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 Leu Asp His Val Gly Ile Ala Val Pro Asp Leu Glu Glu Ala Ile Glu
 20 25 30
 Phe Tyr Arg Ser Ala Phe Gly Trp Val Asn His His Gln Glu Ile Asn
 35 40 45
 Glu Glu Gln Gly Ile Ser Glu Ala Met Ile Gly Pro Lys Asp Ile Lys
 50 55 60
 Ser Thr Glu Gly Met Ile Gln Leu Ile Ala Pro Leu Asn Glu Asp Ser
 65 70 75 80
 Thr Ile Ala Lys Phe Leu Glu Lys Lys Gly Pro Gly Ile Gln Gln Met
 85 90 95
 Cys Leu Arg Thr Asn Asn Ile Asp Ala Leu Ser Glu His Leu Arg Arg
 100 105 110
 Gln Gly Val Arg Leu Leu Tyr Pro Glu Pro Lys Asn Gly Thr Gly Gly
 115 120 125

Ala Arg Ile Asn Phe Leu His Pro Lys Asp Ala Gly Gly Val Leu Leu
 130 135 140

Glu Ile Thr Gln Pro Gln Ser
 145 150

<210> 2141
 <211> 426
 <212> DNA
 <213> *Corynebacterium glutamicum*

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 <221> CDS
 <222> (101)..(403)
 <223> RXA01198

<400> 2141
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 Met Ile Val Ala Phe
 1 5
 tct gta gcc ccg act gtt act gat aat cca gat gct gag atg gcc gat 163
 Ser Val Ala Pro Thr Val Thr Asp Asn Pro Asp Ala Glu Met Ala Asp
 10 15 20
 gcg gtc acg gag gcg att cga atc gtc cgc gca tcg ggt ctg cct aat 211
 Ala Val Thr 25 Ala Ile Arg Ile Val Arg Ala Ser Gly Leu Pro Asn 30 35
 gaa act aac gcg atg ttc acg ctc att gag ggg gag tgg gat gag gtg 259
 Glu Thr Asn Ala Met Phe Thr Leu Ile Glu Gly Glu Trp Asp Glu Val 40 45 50
 atg gcg gtg att aag gag gcc act gag gcg atc tct agg gta tct ccg 307
 Met Ala Val Ile Lys Glu Ala Thr Glu Ala Ile Ser Arg Val Ser Pro 55 60 65
 cgt aca tcg ttg gta att aag gct gat att cgt ccg gga cac act ggc 355
 Arg Thr Ser Leu Val Ile Lys Ala Asp Ile Arg Pro Gly His Thr Gly 70 75 80 85
 caa ttg acg agg aag gtg gag gcg gtg gag gaa cgc cta gct agg gat 403
 Gln Leu Thr Arg Lys Val Glu Ala Val Glu Glu Arg Leu Ala Arg Asp 90 95 100
 tagctttgta cttaaacttg ttg 426

<210> 2142
 <211> 101
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 2142
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 1 5 10 15

Ala Glu Met Ala Asp Ala Val Thr Glu Ala Ile Arg Ile Val Arg Ala

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      35                40                45

Glu Trp Asp Glu Val Met Ala Val Ile Lys Glu Ala Thr Glu Ala Ile
      50                55                60

Ser Arg Val Ser Pro Arg Thr Ser Leu Val Ile Lys Ala Asp Ile Arg
      65                70                75                80

Pro Gly His Thr Gly Gln Leu Thr Arg Lys Val Glu Ala Val Glu Glu
      85                90                95

Arg Leu Ala Arg Asp
      100

<210> 2143
<211> 771
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(748)
<223> RXA01207

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atttttgaac aatccgtaca ccaacttcag gaaaaaaca gtg agc aga atc tat 115
                               Val Ser Arg Ile Tyr
                               1 5

gac tgt gcc gac caa gac tcc cgt gca gca ggc cta aag gcg gct gtc 163
Asp Cys Ala Asp Gln Asp Ser Arg Ala Ala Gly Leu Lys Ala Ala Val
      10                15                20

gat gca gtc aaa gcc ggt cag ctc gtt gtc ctt ccc acg gat acc ctt 211
Asp Ala Val Lys Ala Gly Gln Leu Val Val Leu Pro Thr Asp Thr Leu
      25                30                35

tat gga ctc ggc tgc gac gct ttc aac aac gag gca gta gcc aac ctt 259
Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu Ala Val Ala Asn Leu
      40                45                50

ctg gcc acc aaa cac cgt ggc ccc gat atg ccc gtt cca gtg ctc gtc 307
Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro Val Pro Val Leu Val
      55                60                65

ggc agc tgg gac acc att caa gga ctt gtg cac tcc tat tct gcg cag 355
Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His Ser Tyr Ser Ala Gln
      70                75                80                85

gca aaa gcg ctt gtg gag gcg ttc tgg cct ggt gga ctg tcc atc atc 403
Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly Gly Leu Ser Ile Ile
      90                95                100

gtt ccg cag gca cca agc ctt ccg tgg aac ctt ggc gat acc cgt ggc 451
Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu Gly Asp Thr Arg Gly

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105 110 115
 acc gta atg ctg cgc atg cca ctg cac cca gtt gcc att gaa ttg ctg 499
 Thr Val Met Leu Arg Met Pro Leu His Pro Val Ala Ile Glu Leu Leu
 120 125 130
 cgc caa acc gga cca atg gct gtc tcc tcc gcc aac atc tcc gga cat 547
 Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala Asn Ile Ser Gly His
 135 140 145
 act cct cca acc acc gtg ctg gag gct cgt cag cag ctc aac caa aat 595
 Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln Leu Asn Gln Asn
 150 155 160 165
 gtc gct gtc tac ctc gat ggt ggc gaa tgc gcg ctg gcc acc cct tca 643
 Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala Leu Ala Thr Pro Ser
 170 175 180
 acc atc gtg gat att tca ggc ccc gca cca aag att ttg cgt gag ggt 691
 Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys Ile Leu Arg Glu Gly
 185 190 195
 gcc atc agc gca gaa cgc gtt ggc gaa gta ctt gga gtg tgc gca gaa 739
 Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu Gly Val Ser Ala Glu
 200 205 210
 agc ctg cgc taaatgggag tcggtttcgc ggg 771
 Ser Leu Arg
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 <213> Corynebacterium glutamicum
 <400> 2144
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 20 25 30
 Pro Thr Asp Thr Leu Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu
 35 40 45
 Ala Val Ala Asn Leu Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro
 50 55 60
 Val Pro Val Leu Val Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His
 65 70 75 80
 Ser Tyr Ser Ala Gln Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly
 85 90 95
 Gly Leu Ser Ile Ile Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu
 100 105 110
 Gly Asp Thr Arg Gly Thr Val Met Leu Arg Met Pro Leu His Pro Val
 115 120 125

Ala Ile Glu Leu Leu Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala
 130 135 140

Asn Ile Ser Gly His Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln
 145 150 155 160

Gln Leu Asn Gln Asn Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala
 165 170 175

Leu Ala Thr Pro Ser Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys
 180 185 190

Ile Leu Arg Glu Gly Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu
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Gly Val Ser Ala Glu Ser Leu Arg
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<210> 2145

<211> 1350

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1327)

<223> RXA01213

<400> 2145

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catatcaacc aaacggtgta gttcttctaa gctttcaccc atg aca aat ccc aca 115
 Met Thr Asn Pro Thr
 1 5

gag gag cgc aac gca cgc cgc ctc att tgg gcc aac ggc ctg caa aac 163
 Glu Glu Arg Asn Ala Arg Arg Leu Ile Trp Ala Asn Gly Leu Gln Asn
 10 15 20

atc ggc gat caa atc gtt gcc gcc aaa aca gtc ctg ccc tgg ttg ctg 211
 Ile Gly Asp Gln Ile Val Ala Ala Lys Thr Val Leu Pro Trp Leu Leu
 25 30 35

caa gcc gct ggc gcg ccg gcc ttt ttg ctg gcg ctt ctg gtt cca atc 259
 Gln Ala Ala Gly Ala Pro Gly Phe Leu Leu Ala Leu Leu Val Pro Ile
 40 45 50

cgc gaa gcc gga tcg atg ctg ccg caa gct gcc att act ggc tgg gtg 307
 Arg Glu Ala Gly Ser Met Leu Pro Gln Ala Ala Ile Thr Gly Trp Val
 55 60 65

ctg agg cag acg tcg aga agc aaa gtc tgg gtg att ggc tcg aac ggc 355
 Leu Arg Gln Thr Ser Arg Ser Lys Val Trp Val Ile Gly Ser Asn Gly
 70 75 80 85

cag ttc gtc tcg gcg ctg ggt atc ggc gtg gct gcg ctg ttt ttg cgt 403
 Gln Phe Val Ser Ala Leu Gly Ile Gly Val Ala Ala Leu Phe Leu Arg
 90 95 100

ggg tgg gcg ctg ggc atc acg gtg atc gtg ctg ctt gcg gcg ctg tcg 451

Gly Trp Ala Leu Gly Ile Thr Val Ile Val Leu Leu Ala Ala Leu Ser	
105 110 115	
ctg ttt cga tcg atg tgt tcg att gca tcg aag gat gtt cag ggc aag	499
Leu Phe Arg Ser Met Cys Ser Ile Ala Ser Lys Asp Val Gln Gly Lys	
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gtg att tcc aag ggc aag cgt ggg ctg gta acg ggc cgc gcg acg gtg	547
Val Ile Ser Lys Gly Lys Arg Gly Leu Val Thr Gly Arg Ala Thr Val	
135 140 145	
att ggc ggt gtg atg ggc ctg gtt gca ggc ctg gcg atc gct att ttc	595
Ile Gly Gly Val Met Gly Leu Val Ala Gly Leu Ala Ile Ala Ile Phe	
150 155 160 165	
ttg ggc tcg cat tcc ccg acg agg gtg ctg gcc gca gtg gtg atc cgc	643
Leu Gly Ser His Ser Pro Thr Arg Val Leu Ala Ala Val Val Ile Ala	
170 175 180	
agc tcg ttt agc tgg ctg ttt gcc tcc att gtt ttc gcg cgc atc gaa	691
Ser Ser Phe Ser Trp Leu Phe Ala Ser Ile Val Phe Ala Arg Ile Glu	
185 190 195	
tac gcg aag cca gcg act cca aaa aac gcg cct tcc gca aac ccg tgg	739
Tyr Ala Lys Pro Ala Thr Pro Lys Asn Ala Pro Ser Ala Asn Pro Trp	
200 205 210	
gtg cgt cgc tgc atc gcc gca tta aaa gat gat aaa gct ttt cga cgt	787
Val Arg Arg Cys Ile Ala Ala Leu Lys Asp Asp Lys Ala Phe Arg Arg	
215 220 225	
ttc gtt ctg gtt cgc tca atg atg ctg gtg aca gca ctc tcc acg gct	835
Phe Val Leu Val Arg Ser Met Met Leu Val Thr Ala Leu Ser Thr Ala	
230 235 240 245	
ttc atc gtc gca ctc gcc gct gaa tcc gga aac agc atc gac tcc ttg	883
Phe Ile Val Ala Leu Ala Ala Glu Ser Gly Asn Ser Ile Asp Ser Leu	
250 255 260	
gga ttc ttc ctc atc gcc tcc ggc ttg gcg tcc atg gtt ggt ggc cga	931
Gly Phe Phe Leu Ile Ala Ser Gly Leu Ala Ser Met Val Gly Gly Arg	
265 270 275	
atc tct gga atc tgg tcg gat cat tcc tcc aaa aac gtc atg gcg ggc	979
Ile Ser Gly Ile Trp Ser Asp His Ser Ser Lys Asn Val Met Ala Gly	
280 285 290	
ggt gcc cta ttc ggt tcc atc gtg tta atc ctc gtg gtg ctc agc tcc	1027
Gly Ala Leu Phe Gly Ser Ile Val Leu Ile Leu Val Val Leu Ser Ser	
295 300 305	
gcg ttt gca ccc gcg cag atc aac acg ctg gtg ttc ccg ttg agt ttc	1075
Ala Phe Ala Pro Ala Gln Ile Asn Thr Leu Val Phe Pro Leu Ser Phe	
310 315 320 325	
ttc ctc atc acc ttg gcc cac acc gcc atc cgc gtg gcc cgc aaa act	1123
Phe Leu Ile Thr Leu Ala His Thr Ala Ile Arg Val Ala Arg Lys Thr	
330 335 340	
tat gta atg gac atg gct gaa ggt gat cag cgc acc cgc tat gtt gcc	1171
Tyr Val Met Asp Met Ala Glu Gly Asp Gln Arg Thr Arg Tyr Val Ala	

	345	350	355	
gac gcc aac aca cta atg ggt gta gtt ttg ctc att gtt ggc gca tta				1219
Asp Ala Asn Thr Leu Met Gly Val Val Leu Leu Ile Val Gly Ala Leu				
	360	365	370	
tct ggc ttc att gca att ttc gga aac gaa gcc gca ctg ctc ttc ttg				1267
Ser Gly Phe Ile Ala Ile Phe Gly Asn Glu Ala Ala Leu Leu Phe Leu				
	375	380	385	
gcg gca att ggc ctg ctt gga acc att agc gcc cgt ggc ctc aag gaa				1315
Ala Ala Ile Gly Leu Leu Gly Thr Ile Ser Ala Arg Gly Leu Lys Glu				
	390	395	400	405
gta tcc gcc gga tagttttaca acttttccac cca				1350
Val Ser Ala Gly				

<210> 2146

<211> 409

<212> PRT

<213> Corynebacterium glutamicum

<400> 2146

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20	25	30		

Leu Pro Trp Leu Leu Gln Ala Ala Gly Ala Pro Gly Phe Leu Leu Ala				
35	40	45		

Leu Leu Val Pro Ile Arg Glu Ala Gly Ser Met Leu Pro Gln Ala Ala				
50	55	60		

Ile Thr Gly Trp Val Leu Arg Gln Thr Ser Arg Ser Lys Val Trp Val				
65	70	75	80	

Ile Gly Ser Asn Gly Gln Phe Val Ser Ala Leu Gly Ile Gly Val Ala				
85	90	95		

Ala Leu Phe Leu Arg Gly Trp Ala Leu Gly Ile Thr Val Ile Val Leu				
100	105	110		

Leu Ala Ala Leu Ser Leu Phe Arg Ser Met Cys Ser Ile Ala Ser Lys				
115	120	125		

Asp Val Gln Gly Lys Val Ile Ser Lys Gly Lys Arg Gly Leu Val Thr				
130	135	140		

Gly Arg Ala Thr Val Ile Gly Gly Val Met Gly Leu Val Ala Gly Leu				
145	150	155	160	

Ala Ile Ala Ile Phe Leu Gly Ser His Ser Pro Thr Arg Val Leu Ala				
165	170	175		

Ala Val Val Ile Ala Ser Ser Phe Ser Trp Leu Phe Ala Ser Ile Val				
180	185	190		


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Phe Ala Arg Ile Glu Tyr Ala Lys Pro Ala Thr Pro Lys Asn Ala Pro
    195                      200                      205

Ser Ala Asn Pro Trp Val Arg Arg Cys Ile Ala Ala Leu Lys Asp Asp
    210                      215                      220

Lys Ala Phe Arg Arg Phe Val Leu Val Arg Ser Met Met Leu Val Thr
    225                      230                      235                      240

Ala Leu Ser Thr Ala Phe Ile Val Ala Leu Ala Ala Glu Ser Gly Asn
    245                      250                      255

Ser Ile Asp Ser Leu Gly Phe Phe Leu Ile Ala Ser Gly Leu Ala Ser
    260                      265                      270

Met Val Gly Gly Arg Ile Ser Gly Ile Trp Ser Asp His Ser Ser Lys
    275                      280                      285

Asn Val Met Ala Gly Gly Ala Leu Phe Gly Ser Ile Val Leu Ile Leu
    290                      295                      300

Val Val Leu Ser Ser Ala Phe Ala Pro Ala Gln Ile Asn Thr Leu Val
    305                      310                      315                      320

Phe Pro Leu Ser Phe Phe Leu Ile Thr Leu Ala His Thr Ala Ile Arg
    325                      330                      335

Val Ala Arg Lys Thr Tyr Val Met Asp Met Ala Glu Gly Asp Gln Arg
    340                      345                      350

Thr Arg Tyr Val Ala Asp Ala Asn Thr Leu Met Gly Val Val Leu Leu
    355                      360                      365

Ile Val Gly Ala Leu Ser Gly Phe Ile Ala Ile Phe Gly Asn Glu Ala
    370                      375                      380

Ala Leu Leu Phe Leu Ala Ala Ile Gly Leu Leu Gly Thr Ile Ser Ala
    385                      390                      395                      400

Arg Gly Leu Lys Glu Val Ser Ala Gly
    405

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<210> 2147

<211> 552

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(529)

<223> RXA01218

<400> 2147

ctaaatatgc tagcacgatg gccaaaccta atccaaaaac cggcagtata ctgattgggg 60

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tcacattagc caaaaggcac tttgaggaag tggaactcct atg gca cga ctt cag    115
                Met Ala Arg Leu Gln
                1                      5

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cac gac atg att ttc atc aac cta cca gta tct gac ctt gca gca tct 163

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His Asp Met Ile Phe Ile Asn Leu Pro Val Ser Asp Leu Ala Ala Ser
          10                      15                      20

aag cgt ttt tat gca ggt ctt ggc ttc aaa gaa aac acc gtc ttc agt   211
Lys Arg Phe Tyr Ala Gly Leu Gly Phe Lys Glu Asn Thr Val Phe Ser
          25                      30                      35

gat gag cac act gca tct ttt gag gtc agt gac gcc atc gtg gtg atg   259
Asp Glu His Thr Ala Ser Phe Glu Val Ser Asp Ala Ile Val Val Met
          40                      45                      50

ctt ctg gaa acc gcg cgc ttc agt gat ttc act aag cgc ccc atc gtg   307
Leu Leu Glu Thr Ala Arg Phe Ser Asp Phe Thr Lys Arg Pro Ile Val
          55                      60                      65

gag aag aac ggc tcc cgc gaa gtg ctc aac tgc ctg tct gta tgt tcc   355
Glu Lys Asn Gly Ser Arg Glu Val Leu Asn Cys Leu Ser Val Cys Ser
          70                      75                      80                      85

acc gag gat gcg gat gag ttc gtg cgt cgc gcc cag gaa ttc gga ggc   403
Thr Glu Asp Ala Asp Glu Phe Val Arg Arg Ala Gln Glu Phe Gly Gly
          90                      95                      100

acg atc acc cgt gag ctt gca gcg gaa ggc ccc atg tac ggc gga gct   451
Thr Ile Thr Arg Glu Leu Ala Ala Glu Gly Pro Met Tyr Gly Gly Ala
          105                      110                      115

ttt gat gat cca gat gga cac ggt tgg gag ctg atg tac ttc gat cca   499
Phe Asp Asp Pro Asp Gly His Gly Trp Glu Leu Met Tyr Phe Asp Pro
          120                      125                      130

gag gca ctc gct cag atg atg cct gag ggc taaatattct tcagggtcttc   549
Glu Ala Leu Ala Gln Met Met Pro Glu Gly
          135                      140

tcg                                                                    552

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<210> 2148

<211> 143

<212> PRT

<213> Corynebacterium glutamicum

<400> 2148

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Met Ala Arg Leu Gln His Asp Met Ile Phe Ile Asn Leu Pro Val Ser
  1                      5                      10                      15

Asp Leu Ala Ala Ser Lys Arg Phe Tyr Ala Gly Leu Gly Phe Lys Glu
          20                      25                      30

Asn Thr Val Phe Ser Asp Glu His Thr Ala Ser Phe Glu Val Ser Asp
          35                      40                      45

Ala Ile Val Val Met Leu Leu Glu Thr Ala Arg Phe Ser Asp Phe Thr
          50                      55                      60

Lys Arg Pro Ile Val Glu Lys Asn Gly Ser Arg Glu Val Leu Asn Cys
          65                      70                      75                      80

Leu Ser Val Cys Ser Thr Glu Asp Ala Asp Glu Phe Val Arg Arg Ala
          85                      90                      95

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Gln Glu Phe Gly Gly Thr Ile Thr Arg Glu Leu Ala Ala Glu Gly Pro
100 105 110

Met Tyr Gly Gly Ala Phe Asp Asp Pro Asp Gly His Gly Trp Glu Leu
115 120 125

Met Tyr Phe Asp Pro Glu Ala Leu Ala Gln Met Met Pro Glu Gly
130 135 140

<210> 2149

<211> 507

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(484)

<223> RXA01234

<400> 2149

agaaacaata gccagaccca gaagagcaga ctggagagct tgcaggattt agtgctcctg 60

tgcatttatt cgggtcactt caacgttgaa aagcatagga atg tgg aag ttc atg 115
Met Trp Lys Phe Met
1 5

aag act caa tac gta tgt acc act tat ttc atc gct gca ccc gag gat 163
Lys Thr Gln Tyr Val Cys Thr Thr Tyr Phe Ile Ala Ala Pro Glu Asp
10 15 20

gaa gac gag gcg tac caa act tat cgc agc cga atg aac tct ttg gca 211
Glu Asp Glu Ala Tyr Gln Thr Tyr Arg Ser Arg Met Asn Ser Leu Ala
25 30 35

gca ttg aac ggc gct gac gta gtt tca gtg gca gat ggc cta cgg atg 259
Ala Leu Asn Gly Ala Asp Val Val Ser Val Ala Asp Gly Leu Arg Met
40 45 50

gaa gta gac cag gat att tgg gga agc ctt gct gag cag tat cag att 307
Glu Val Asp Gln Asp Ile Trp Gly Ser Leu Ala Glu Gln Tyr Gln Ile
55 60 65

gag caa gaa ggc ctg tat ccc act ggt cac aac ttg tac ttt gtt gtc 355
Glu Gln Glu Gly Leu Tyr Pro Thr Gly His Asn Leu Tyr Phe Val Val
70 75 80 85

acc gtg gtg aac cta gat gat tca gat gag gtt tat gac cga aca atg 403
Thr Val Val Asn Leu Asp Asp Ser Asp Glu Val Tyr Asp Arg Thr Met
90 95 100

gag cat ctg att atg gat gac cct tat gtg cga gtg gat cgt ttc cca 451
Glu His Leu Ile Met Asp Asp Pro Tyr Val Arg Val Asp Arg Phe Pro
105 110 115

agc act gtc cat gcc agc acc cag atc atg ttg tagaaaaaga aaaagcacca 504
Ser Thr Val His Ala Ser Thr Gln Ile Met Leu
120 125

ccc

507

<210> 2150
 <211> 128
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2150
 Met Trp Lys Phe Met Lys Thr Gln Tyr Val Cys Thr Thr Tyr Phe Ile
 1 5 10 15
 Ala Ala Pro Glu Asp Glu Asp Glu Ala Tyr Gln Thr Tyr Arg Ser Arg
 20 25 30
 Met Asn Ser Leu Ala Ala Leu Asn Gly Ala Asp Val Val Ser Val Ala
 35 40 45
 Asp Gly Leu Arg Met Glu Val Asp Gln Asp Ile Trp Gly Ser Leu Ala
 50 55 60
 Glu Gln Tyr Gln Ile Glu Gln Glu Gly Leu Tyr Pro Thr Gly His Asn
 65 70 75 80
 Leu Tyr Phe Val Val Thr Val Val Asn Leu Asp Asp Ser Asp Glu Val
 85 90 95
 Tyr Asp Arg Thr Met Glu His Leu Ile Met Asp Asp Pro Tyr Val Arg
 100 105 110
 Val Asp Arg Phe Pro Ser Thr Val His Ala Ser Thr Gln Ile Met Leu
 115 120 125

<210> 2151
 <211> 564
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(541)
 <223> RXA01237

<400> 2151
 aaacccaaaa tcacgacgca ttaagtaaca gagacttaaa ttaagaactc cgaacaacaa 60
 cttcggattg tttcattttt gaggatgaaa gagcttttca atg aac gta cag ttt 115
 Met Asn Val Gln Phe
 1 5
 gaa tca gac atg gcc gtc caa cca gga aac acc atg gaa gct acc gtc 163
 Glu Ser Asp Met Ala Val Gln Pro Gly Asn Thr Met Glu Ala Thr Val
 10 15 20
 acc gac att cgt gat gcc aag cgt aaa aca acc cag ctt gat tca gta 211
 Thr Asp Ile Arg Asp Ala Lys Arg Lys Thr Thr Gln Leu Asp Ser Val
 25 30 35

acg ccg ttt aag aag aat tgc ccg agc cgc acc ttg ctc gac acc atc 259
 Thr Pro Phe Lys Lys Asn Cys Pro Ser Arg Thr Leu Asp Thr Ile
 40 45 50

agt gac aag tgg gcg gtg ctg atc ctg ctc agc atg gaa aat ggt cca 307
 Ser Asp Lys Trp Ala Val Leu Ile Leu Leu Ser Met Glu Asn Gly Pro
 55 60 65

cag cgc aat ggt gaa atc aaa gat cag gtc caa gga att acc cca aag 355
 Gln Arg Asn Gly Glu Ile Lys Asp Gln Val Gln Gly Ile Thr Pro Lys
 70 75 80 85

atg ctc acc cag cgt ctt gga gtg ttg gtg gaa gac gga ctg gtc act 403
 Met Leu Thr Gln Arg Leu Gly Val Leu Val Glu Asp Gly Leu Val Thr
 90 95 100

cgc acc tcc cac gca gtt gtg ccg cct cgt gtg gat tat cag ctc acc 451
 Arg Thr Ser His Ala Val Val Pro Arg Val Asp Tyr Gln Leu Thr
 105 110 115

gat ctg ggt gct tct gtc att gag cct tgc cgt gcg atg tat tcc tgg 499
 Asp Leu Gly Ala Ser Val Ile Glu Pro Cys Arg Ala Met Tyr Ser Trp
 120 125 130

gca gtg gag aac att aag caa gtg gag gcc tac cgc tca gca 541
 Ala Val Glu Asn Ile Lys Gln Val Glu Ala Tyr Arg Ser Ala
 135 140 145

taagaacact tggcaaacct cac 564

<210> 2152
 <211> 147
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 2152
 Met Asn Val Gln Phe Glu Ser Asp Met Ala Val Gln Pro Gly Asn Thr
 1 5 10 15

Met Glu Ala Thr Val Thr Asp Ile Arg Asp Ala Lys Arg Lys Thr Thr
 20 25 30

Gln Leu Asp Ser Val Thr Pro Phe Lys Lys Asn Cys Pro Ser Arg Thr
 35 40 45

Leu Leu Asp Thr Ile Ser Asp Lys Trp Ala Val Leu Ile Leu Leu Ser
 50 55 60

Met Glu Asn Gly Pro Gln Arg Asn Gly Glu Ile Lys Asp Gln Val Gln
 65 70 75 80

Gly Ile Thr Pro Lys Met Leu Thr Gln Arg Leu Gly Val Leu Val Glu
 85 90 95

Asp Gly Leu Val Thr Arg Thr Ser His Ala Val Val Pro Pro Arg Val
 100 105 110

Asp Tyr Gln Leu Thr Asp Leu Gly Ala Ser Val Ile Glu Pro Cys Arg
 115 120 125

Ala Met Tyr Ser Trp Ala Val Glu Asn Ile Lys Gln Val Glu Ala Tyr
 130 135 140

Arg Ser Ala
 145

<210> 2153
 <211> 1437
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1414)
 <223> RXA01267

<400> 2153
 tgctagtttt aaagaggcgt tgaggggtag tatcgcgtaa gtttattagt gggttagcgta 60
 gatttttcga attgaagatg tttctgaaag gtatttagat atg tat gca gaa att 115
 Met Tyr Ala Glu Ile
 1 5
 aat ggc ggt ttt att cca gag ggc acc gtg cgg gta agc ggc gca aaa 163
 Asn Gly Gly Phe Ile Pro Glu Gly Thr Val Arg Val Ser Gly Ala Lys
 10 15 20
 aac tct gct act aga ctt ctc gcg gcg gca ctg cta acc gat gag gtg 211
 Asn Ser Ala Thr Arg Leu Leu Ala Ala Ala Leu Leu Thr Asp Glu Val
 25 30 35
 gtg cat ctt ggt aat ttc cca acc aag ctt gtg gat gtt gaa cat aaa 259
 Val His Leu Gly Asn Phe Pro Thr Lys Leu Val Asp Val Glu His Lys
 40 45 50
 att cgc ttt att gaa gag ctt ggc gga aaa gtg cat gtc gac cat gat 307
 Ile Arg Phe Ile Glu Glu Leu Gly Gly Lys Val His Val Asp His Asp
 55 60 65
 gag caa att tta gta gtt gat gct aag gat ctt gca gcg cga gaa atg 355
 Glu Gln Ile Leu Val Val Asp Ala Lys Asp Leu Ala Ala Arg Glu Met
 70 75 80 85
 act act gat gaa ctg aat att ccg att cga act act tat ctc cta gca 403
 Thr Thr Asp Glu Leu Asn Ile Pro Ile Arg Thr Thr Tyr Leu Leu Ala
 90 95 100
 gca gcg cag att ggg cgt ggg gaa att gct cga gtt cct ttt cct ggg 451
 Ala Ala Gln Ile Gly Arg Gly Glu Ile Ala Arg Val Pro Phe Pro Gly
 105 110 115
 ggg tgt gct att gga gga ggt cct gct ggc gga cga gga tat gat ctt 499
 Gly Cys Ala Ile Gly Gly Gly Pro Ala Gly Gly Arg Gly Tyr Asp Leu
 120 125 130
 cat ctt atg gtc tgg gaa cag cta ggt tgt aaa att ctt gaa aaa gat 547
 His Leu Met Val Trp Glu Gln Leu Gly Cys Lys Ile Leu Glu Lys Asp
 135 140 145
 gat cac att gaa gta act gca ccc cag ggc ttt atc ggg gga gtt att 595

Asp His Ile Glu Val Thr Ala Pro Gln Gly Phe Ile Gly Gly Val Ile	
150 155 160 165	
gac ttt cct att tct act gtg gga ggc act gaa aac gcg tta cta tgc	643
Asp Phe Pro Ile Ser Thr Val Gly Gly Thr Glu Asn Ala Leu Leu Cys	
170 175 180	
gca agt att gct tca ggg gat act aaa att gcc aat gct tat att acc	691
Ala Ser Ile Ala Ser Gly Asp Thr Lys Ile Ala Asn Ala Tyr Ile Thr	
185 190 195	
cct gag ata act gat ctt att gaa ctt ctg cga cgt atg ggt gcg gag	739
Pro Glu Ile Thr Asp Leu Ile Glu Leu Leu Arg Arg Met Gly Ala Glu	
200 205 210	
atc act gtc tac ggt acc agc cgt att cat gta aag ggt cga gca ggt	787
Ile Thr Val Tyr Gly Thr Ser Arg Ile His Val Lys Gly Arg Ala Gly	
215 220 225	
ctt ttg cag ggc gca tat atg gac gta atg ccg gat cgt att gag gca	835
Leu Leu Gln Gly Ala Tyr Met Asp Val Met Pro Asp Arg Ile Glu Ala	
230 235 240 245	
ttg acg tgg atc gtg tat gga att att tca ggc gga agg att acc gtc	883
Leu Thr Trp Ile Val Tyr Gly Ile Ile Ser Gly Gly Arg Ile Thr Val	
250 255 260	
gaa ggt gtt cca ttt agc tgc atg gaa gtt cct ttt atc cac ctt gag	931
Glu Gly Val Pro Phe Ser Ser Met Glu Val Pro Phe Ile His Leu Glu	
265 270 275	
aag gct gga gtg gat ctt ttc cgt aat tca agt tcc gta tat att aca	979
Lys Ala Gly Val Asp Leu Phe Arg Asn Ser Ser Ser Val Tyr Ile Thr	
280 285 290	
cca gaa tgc ttg cct tca ggc tca gtt cag cca ttt gag cta gcg tgt	1027
Pro Glu Cys Leu Pro Ser Gly Ser Val Gln Pro Phe Glu Leu Ala Cys	
295 300 305	
gga act cac ccc gga gta att tcg gac atg cag gca ctt ttt gtt ctt	1075
Gly Thr His Pro Gly Val Ile Ser Asp Met Gln Ala Leu Phe Val Leu	
310 315 320 325	
tta gga tta aaa ggt gca gga act tca cgc gtc tat gac tat cga tac	1123
Leu Gly Leu Lys Gly Ala Gly Thr Ser Arg Val Tyr Asp Tyr Arg Tyr	
330 335 340	
cca gaa aga att gca ttt gtt gag gaa ttg aca aat cta gtt tcg ggc	1171
Pro Glu Arg Ile Ala Phe Val Glu Glu Leu Thr Asn Leu Val Ser Gly	
345 350 355	
gac aaa tta agt gca gag gct ggc aag atc act atc cag gga gat gct	1219
Asp Lys Leu Ser Ala Glu Ala Gly Lys Ile Thr Ile Gln Gly Asp Ala	
360 365 370	
act ttc cgg cca gga tat gcg aac tca act gat cta cgt ggt tct atg	1267
Thr Phe Arg Pro Gly Tyr Ala Asn Ser Thr Asp Leu Arg Gly Ser Met	
375 380 385	
gct gtt gtt tta gcg gcg ctt tgc gct gat gga aag tcc acg att aat	1315
Ala Val Val Leu Ala Ala Leu Cys Ala Asp Gly Lys Ser Thr Ile Asn	

390 395 400 405

aac gtc cat atg gcg tta cgt ggg tac aac gag ttg gat aaa aaa ctt 1363
 Asn Val His Met Ala Leu Arg Gly Tyr Asn Glu Leu Asp Lys Lys Leu
 410 415 420

cgt tta ctt ggt gcg gat tta act atc aga gaa ggc gaa gtt cct tca 1411
 Arg Leu Leu Gly Ala Asp Leu Thr Ile Arg Glu Gly Glu Val Pro Ser
 425 430 435

cct taagaacgaa agttttacat tga 1437
 Pro

<210> 2154

<211> 438

<212> PRT

<213> Corynebacterium glutamicum

<400> 2154

Met Tyr Ala Glu Ile Asn Gly Gly Phe Ile Pro Glu Gly Thr Val Arg
 1 5 10 15

Val Ser Gly Ala Lys Asn Ser Ala Thr Arg Leu Leu Ala Ala Ala Leu
 20 25 30

Leu Thr Asp Glu Val Val His Leu Gly Asn Phe Pro Thr Lys Leu Val
 35 40 45

Asp Val Glu His Lys Ile Arg Phe Ile Glu Glu Leu Gly Gly Lys Val
 50 55 60

His Val Asp His Asp Glu Gln Ile Leu Val Val Asp Ala Lys Asp Leu
 65 70 75 80

Ala Ala Arg Glu Met Thr Thr Asp Glu Leu Asn Ile Pro Ile Arg Thr
 85 90 95

Thr Tyr Leu Leu Ala Ala Ala Gln Ile Gly Arg Gly Glu Ile Ala Arg
 100 105 110

Val Pro Phe Pro Gly Gly Cys Ala Ile Gly Gly Gly Pro Ala Gly Gly
 115 120 125

Arg Gly Tyr Asp Leu His Leu Met Val Trp Glu Gln Leu Gly Cys Lys
 130 135 140

Ile Leu Glu Lys Asp Asp His Ile Glu Val Thr Ala Pro Gln Gly Phe
 145 150 155 160

Ile Gly Gly Val Ile Asp Phe Pro Ile Ser Thr Val Gly Gly Thr Glu
 165 170 175

Asn Ala Leu Leu Cys Ala Ser Ile Ala Ser Gly Asp Thr Lys Ile Ala
 180 185 190

Asn Ala Tyr Ile Thr Pro Glu Ile Thr Asp Leu Ile Glu Leu Leu Arg
 195 200 205

Arg Met Gly Ala Glu Ile Thr Val Tyr Gly Thr Ser Arg Ile His Val


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      210              215              220
Lys Gly Arg Ala Gly Leu Leu Gln Gly Ala Tyr Met Asp Val Met Pro
225              230              235              240
Asp Arg Ile Glu Ala Leu Thr Trp Ile Val Tyr Gly Ile Ile Ser Gly
      245              250              255
Gly Arg Ile Thr Val Glu Gly Val Pro Phe Ser Ser Met Glu Val Pro
      260              265              270
Phe Ile His Leu Glu Lys Ala Gly Val Asp Leu Phe Arg Asn Ser Ser
      275              280              285
Ser Val Tyr Ile Thr Pro Glu Cys Leu Pro Ser Gly Ser Val Gln Pro
      290              295              300
Phe Glu Leu Ala Cys Gly Thr His Pro Gly Val Ile Ser Asp Met Gln
305              310              315              320
Ala Leu Phe Val Leu Leu Gly Leu Lys Gly Ala Gly Thr Ser Arg Val
      325              330              335
Tyr Asp Tyr Arg Tyr Pro Glu Arg Ile Ala Phe Val Glu Glu Leu Thr
      340              345              350
Asn Leu Val Ser Gly Asp Lys Leu Ser Ala Glu Ala Gly Lys Ile Thr
      355              360              365
Ile Gln Gly Asp Ala Thr Phe Arg Pro Gly Tyr Ala Asn Ser Thr Asp
      370              375              380
Leu Arg Gly Ser Met Ala Val Val Leu Ala Leu Cys Ala Asp Gly
385              390              395              400
Lys Ser Thr Ile Asn Asn Val His Met Ala Leu Arg Gly Tyr Asn Glu
      405              410              415
Leu Asp Lys Lys Leu Arg Leu Leu Gly Ala Asp Leu Thr Ile Arg Glu
      420              425              430
Gly Glu Val Pro Ser Pro
      435

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<210> 2155

<211> 963

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(940)

<223> RXA01268

<400> 2155

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gctgatagtt ggaactccga aagcttcatt gctgggagtc gtg gca gca cga att 115

Val Ala Ala Arg Ile
1 5

gct cga gtg cca cga att gtc tat gtg gca cat ggg ctg cgc tct gaa 163
 Ala Arg Val Pro Arg Ile Val Tyr Val Ala His Gly Leu Arg Ser Glu
 10 15 20

act gtt tta ggc tta aaa aag aag att cta gtg ttt ttg gaa tat ttg 211
 Thr Val Leu Gly Leu Lys Lys Lys Ile Leu Val Phe Leu Glu Tyr Leu
 25 30 35

acc cag ttg ttt gca cat caa act ttg gct gta agt cat tct ctg aag 259
 Thr Gln Leu Leu Phe Ala His Gln Thr Leu Ala Val Ser His Ser Leu Lys
 40 45 50

aaa gca att gaa gat gcg cac cct cgt ttt aaa gga aga gtg caa gtc 307
 Lys Ala Ile Glu Asp Ala His Pro Arg Phe Lys Gly Arg Val Gln Val
 55 60 65

tta ggt tat ggc agt atg aat gga gtt gag ctt gat cgc ttt aga gtt 355
 Leu Gly Tyr Gly Ser Met Asn Gly Val Glu Leu Asp Arg Phe Arg Val
 70 75 80 85

cca tcc ctt gaa gag aaa tta tct gct cgt aat gct tta aac ctg cct 403
 Pro Ser Leu Glu Glu Lys Leu Ser Ala Arg Asn Ala Leu Asn Leu Pro
 90 95 100

agt aaa tct gtc att gtt ggt ttt gtc ggc aga ata aat aaa gat aag 451
 Ser Lys Ser Val Ile Val Gly Phe Val Gly Arg Ile Asn Lys Asp Lys
 105 110 115

gga gga gat ctt ctc gct gct ctt aca aaa cat gag gct ttt acc cga 499
 Gly Gly Asp Leu Leu Ala Ala Leu Thr Lys His Glu Ala Phe Thr Arg
 120 125 130

ttg cga ctg cat ctc tta att att ggt gaa ttg gaa gac gat gac ttg 547
 Leu Arg Leu His Leu Leu Ile Ile Gly Glu Leu Glu Asp Asp Asp Leu
 135 140 145

cga gaa gca ttc att aaa tta gtt aat gaa ggg cag gtt acg att aca 595
 Arg Glu Ala Phe Ile Lys Leu Val Asn Glu Gly Gln Val Thr Ile Thr
 150 155 160 165

gga tgg att gat ttc cct gaa gaa cca tta gct gca gtt gat gtt ttg 643
 Gly Trp Ile Asp Phe Pro Glu Glu Pro Leu Ala Ala Val Asp Val Leu
 170 175 180

ctt cac cca act cag cga gaa ggt tta ggt atg tct ttg ctg gaa gct 691
 Leu His Pro Thr Gln Arg Glu Gly Leu Gly Met Ser Leu Leu Glu Ala
 185 190 195

cag gct atg gga gtg cct gta ttg acg aat gct gtg act gga aca gtt 739
 Gln Ala Met Gly Val Pro Val Leu Thr Asn Ala Val Thr Gly Thr Val
 200 205 210

gat gca gta aca agt gga gaa ggt ggc ttt ttt gcc gat gac gat tct 787
 Asp Ala Val Thr Ser Gly Glu Gly Gly Phe Phe Ala Asp Asp Asp Ser
 215 220 225

gtt gag tcc tgg gtt tct aag att gat tta tta gtt tcc gat cct aag 835
 Val Glu Ser Trp Val Ser Lys Ile Asp Leu Leu Val Ser Asp Pro Lys
 230 235 240 245

tta aga gac cgg atg gga cgt gct ggt cgc cag ttt gtg tca gct cgt 883
 Leu Arg Asp Arg Met Gly Arg Ala Gly Arg Gln Phe Val Ser Ala Arg
 250 255 260

ttc aat cgt gat gat gtc gca gct cgt ttc agt cat ttc gtg gaa caa 931
 Phe Asn Arg Asp Asp Val Ala Ala Arg Phe Ser His Phe Val Glu Gln
 265 270 275

ttc aaa aaa tagggctcat tcaatttcaa tat 963
 Phe Lys Lys
 280

<210> 2156

<211> 280

<212> PRT

<213> Corynebacterium glutamicum

<400> 2156

Val Ala Ala Arg Ile Ala Arg Val Pro Arg Ile Val Tyr Val Ala His
 1 5 10 15

Gly Leu Arg Ser Glu Thr Val Leu Gly Leu Lys Lys Lys Ile Leu Val
 20 25 30

Phe Leu Glu Tyr Leu Thr Gln Leu Phe Ala His Gln Thr Leu Ala Val
 35 40 45

Ser His Ser Leu Lys Lys Ala Ile Glu Asp Ala His Pro Arg Phe Lys
 50 55 60

Gly Arg Val Gln Val Leu Gly Tyr Gly Ser Met Asn Gly Val Glu Leu
 65 70 75 80

Asp Arg Phe Arg Val Pro Ser Leu Glu Glu Lys Leu Ser Ala Arg Asn
 85 90 95

Ala Leu Asn Leu Pro Ser Lys Ser Val Ile Val Gly Phe Val Gly Arg
 100 105 110

Ile Asn Lys Asp Lys Gly Gly Asp Leu Leu Ala Ala Leu Thr Lys His
 115 120 125

Glu Ala Phe Thr Arg Leu Arg Leu His Leu Leu Ile Ile Gly Glu Leu
 130 135 140

Glu Asp Asp Asp Leu Arg Glu Ala Phe Ile Lys Leu Val Asn Glu Gly
 145 150 155 160

Gln Val Thr Ile Thr Gly Trp Ile Asp Phe Pro Glu Glu Pro Leu Ala
 165 170 175

Ala Val Asp Val Leu Leu His Pro Thr Gln Arg Glu Gly Leu Gly Met
 180 185 190

Ser Leu Leu Glu Ala Gln Ala Met Gly Val Pro Val Leu Thr Asn Ala
 195 200 205

Val Thr Gly Thr Val Asp Ala Val Thr Ser Gly Glu Gly Gly Phe Phe
 210 215 220

Ala Asp Asp Asp Ser Val Glu Ser Trp Val Ser Lys Ile Asp Leu Leu
 225 230 235 240

Val Ser Asp Pro Lys Leu Arg Asp Arg Met Gly Arg Ala Gly Arg Gln
 245 250 255

Phe Val Ser Ala Arg Phe Asn Arg Asp Asp Val Ala Ala Arg Phe Ser
 260 265 270

His Phe Val Glu Gln Phe Lys Lys
 275 280

<210> 2157
 <211> 1935
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1912)
 <223> RXA01271

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 ttggcgaaac ccaatttatt tcaaaagatg gtggacaaaac atg gca ata agc att 115
 Met Ala Ile Ser Ile
 1 5

ggt aaa gca gga cag aac tta aaa ggg tca gtg cct atc gga aaa gtc 163
 Gly Lys Ala Gly Gln Asn Leu Lys Gly Ser Val Pro Ile Gly Lys Val
 10 15 20

ctt ttt ctc att gat gcc ctt gcc tgg att tct gca cta ttt atc ggt 211
 Leu Phe Leu Ile Asp Ala Leu Ala Trp Ile Ser Ala Leu Phe Ile Gly
 25 30 35

gtg gtt ttg cgg tat gaa ttc aat ctg agt tct atc aac tgg agt gcg 259
 Val Val Leu Arg Tyr Glu Phe Asn Leu Ser Ser Ile Asn Trp Ser Ala
 40 45 50

ttt gca tgg ttc ggg ctt gct gca gtt att ttg cag ttt gtt ctc gga 307
 Phe Ala Trp Phe Gly Leu Ala Ala Val Ile Leu Gln Phe Val Leu Gly
 55 60 65

ctt tct ctc cat ctt tac cgc aag gga tta cgt cac ctt ttc ggt agc 355
 Leu Ser Leu His Leu Tyr Arg Lys Gly Leu Arg His Leu Phe Gly Ser
 70 75 80 85

ttc gaa gat aca cta aac gtt tct atc tcg gtc att gtt gtc ggt gtt 403
 Phe Glu Asp Thr Leu Asn Val Ser Ile Ser Val Ile Val Val Gly Val
 90 95 100

gtc ctt tgg atc gcc tca cta ttt gtt ggt cag cgt tgg aaa atc tca 451
 Val Leu Trp Ile Ala Ser Leu Phe Val Gly Gln Arg Trp Lys Ile Ser
 105 110 115

cgc ggt gtc atg ctg cta gtt atc ccg ctt gct ctc gta ttc gta ttg 499
 Arg Gly Val Met Leu Leu Val Ile Pro Leu Ala Leu Val Phe Val Leu
 120 125 130

gca gtg cgt tat ctc gcg cgt atg cga gtt gag cgt ttt cgt cgt ccg 547
 Ala Val Arg Tyr Leu Ala Arg Met Arg Val Glu Arg Phe Arg Arg Pro
 135 140 145

gct gcg gat tcc aca cca gca ttg att ctt ggt ggt gga tac atc ggt 595
 Ala Ala Asp Ser Thr Pro Ala Leu Ile Leu Gly Gly Gly Tyr Ile Gly
 150 155 160 165

acc aac ctg atc cag tgg atg atg tcc gat cct aag tcg cct ttc cgc 643
 Thr Asn Leu Ile Gln Trp Met Met Ser Asp Pro Lys Ser Pro Phe Arg
 170 175 180

cca gtc ggc gtt att gat gat aac cct gaa tta gca tgc caa cgc gta 691
 Pro Val Gly Val Ile Asp Asp Asn Pro Glu Leu Ala Cys Gln Arg Val
 185 190 195

cgt ggt gtg ccg gtt ctt ggc aag ttt gat gat atc gcc caa gtt gca 739
 Arg Gly Val Pro Val Leu Gly Lys Phe Asp Asp Ile Ala Gln Val Ala
 200 205 210

tca gac act ggc gca gaa ctt ctt atc gtt gct att ggt gat gcc gac 787
 Ser Asp Thr Gly Ala Glu Leu Leu Ile Val Ala Ile Gly Asp Ala Asp
 215 220 225

tct gca ctt tta agg cgt gtc caa gat acc gct aat aaa aat ggt ctt 835
 Ser Ala Leu Leu Arg Arg Val Gln Asp Thr Ala Asn Lys Asn Gly Leu
 230 235 240 245

tca gta aag gta atg ccg gct att gac cgc gtc gtt tct aag ggc gtt 883
 Ser Val Lys Val Met Pro Ala Ile Asp Arg Val Val Ser Lys Gly Val
 250 255 260

cgt gga aac gat ttg cgt gat ctc tct att gaa gat ttg ctt gga cgt 931
 Arg Gly Asn Asp Leu Arg Asp Leu Ser Ile Glu Asp Leu Leu Gly Arg
 265 270 275

caa cct gtt gaa acc aat gtt tca gaa att act ggc tat cta aca ggt 979
 Gln Pro Val Glu Thr Asn Val Ser Glu Ile Thr Gly Tyr Leu Thr Gly
 280 285 290

aag cgt gtt ctt gtt acc ggt gca ggt ggg tca att ggt tcc cag cta 1027
 Lys Arg Val Leu Val Thr Gly Ala Gly Ser Ile Gly Ser Gln Leu
 295 300 305

tgt acg gaa att gcc aaa tac gga cct gct gag ctt atg atg ctt gat 1075
 Cys Thr Glu Ile Ala Lys Tyr Gly Pro Ala Glu Leu Met Met Leu Asp
 310 315 320 325

cgc gat gag act ggt ttg cag cag gtt ctg att aac gtt gct ggt aac 1123
 Arg Asp Glu Thr Gly Leu Gln Gln Val Leu Ile Asn Val Ala Gly Asn
 330 335 340

ggt ttg ttg gat acg gat gct gtg gtt ctt gcg gat atc cgc gaa gca 1171
 Gly Leu Leu Asp Thr Asp Ala Val Val Leu Ala Asp Ile Arg Glu Ala
 345 350 355

gac gcg atg aaa gag att ttt ctc aag cgt aaa cca gaa gtt gtc ttc 1219
 Asp Ala Met Lys Glu Ile Phe Leu Lys Arg Lys Pro Glu Val Val Phe
 360 365 370

cat gca gca gca tta aag cac ttg cca atg ctg gag cag tat cca gat 1267
His Ala Ala Ala Leu Lys His Leu Pro Met Leu Glu Gln Tyr Pro Asp
375 380 385

gag ggc tgg aaa aca aac gtt cta gga act ctt aac gtt ctt gct gcc 1315
Glu Gly Trp Lys Thr Asn Val Leu Gly Thr Leu Asn Val Leu Ala Ala
390 395 400 405

gca gaa gct gtt ggt gtt gag act ttc gtc aat att tcc acc gat aag 1363
Ala Glu Ala Val Gly Val Glu Thr Phe Val Asn Ile Ser Thr Asp Lys
410 415 420

gca gct aat cca acc agc gtc tta ggg cac tca aag cga gtc gct gaa 1411
Ala Ala Asn Pro Thr Ser Val Leu Gly His Ser Lys Arg Val Ala Glu
425 430 435

aag ctg act gcc tgg tat gga cag aat tcc acc agc aag tac cta tcg 1459
Lys Leu Thr Ala Trp Tyr Gly Gln Asn Ser Thr Ser Lys Tyr Leu Ser
440 445 450

gtt cga ttt gga aac gtc att ggt agc cgt gga tcg atg ctc ccg act 1507
Val Arg Phe Gly Asn Val Ile Gly Ser Arg Gly Ser Met Leu Pro Thr
455 460 465

ttc acc agg cta atc atg gaa gat aaa ccg cta aca gtg acg cac ccg 1555
Phe Thr Arg Leu Ile Met Glu Asp Lys Pro Leu Thr Val Thr His Pro
470 475 480 485

gat gtc act agg ttc ttc atg aca att cct gaa gct tgc caa ttg gtc 1603
Asp Val Thr Arg Phe Phe Met Thr Ile Pro Glu Ala Cys Gln Leu Val
490 495 500

ctg caa gcc ggt ggt att gga cgt tcc gcc gag gtt ctc atc ctt gac 1651
Leu Gln Ala Gly Gly Ile Gly Arg Ser Gly Glu Val Leu Ile Leu Asp
505 510 515

atg ggt gag cct gta agc atc ctt gaa att gca cag cgc atg atc gca 1699
Met Gly Glu Pro Val Ser Ile Leu Glu Ile Ala Gln Arg Met Ile Ala
520 525 530

atg tcc ggt aaa gat att gac atc gtg ttc acc gcc ctt cgc gag gcc 1747
Met Ser Gly Lys Asp Ile Asp Ile Val Phe Thr Gly Leu Arg Glu Gly
535 540 545

gaa aag atg cac gaa gag ctg gtt ggt gat ggt gaa acc gaa gat cgt 1795
Glu Lys Met His Glu Glu Leu Val Gly Asp Gly Glu Thr Glu Asp Arg
550 555 560 565

cca ttc cac tca aag att tcg cat gca cat gca gaa agc ctc gct cct 1843
Pro Phe His Ser Lys Ile Ser His Ala His Ala Glu Ser Leu Ala Pro
570 575 580

aat aat ctc gat aga gat cga ttt atg caa cgt gct gga aaa cta gct 1891
Asn Asn Leu Asp Arg Asp Arg Phe Met Gln Arg Ala Gly Lys Leu Ala
585 590 595

tca aca gat tcg gag atc atc taaatgacta atgaacgaat ttt 1935
Ser Thr Asp Ser Glu Ile Ile
600

<210> 2158

<211> 604

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2158

Met Ala Ile Ser Ile Gly Lys Ala Gly Gln Asn Leu Lys Gly Ser Val
 1 5 10 15

Pro Ile Gly Lys Val Leu Phe Leu Ile Asp Ala Leu Ala Trp Ile Ser
 20 25 30

Ala Leu Phe Ile Gly Val Val Leu Arg Tyr Glu Phe Asn Leu Ser Ser
 35 40 45

Ile Asn Trp Ser Ala Phe Ala Trp Phe Gly Leu Ala Ala Val Ile Leu
 50 55 60

Gln Phe Val Leu Gly Leu Ser Leu His Leu Tyr Arg Lys Gly Leu Arg
 65 70 75 80

His Leu Phe Gly Ser Phe Glu Asp Thr Leu Asn Val Ser Ile Ser Val
 85 90 95

Ile Val Val Gly Val Val Leu Trp Ile Ala Ser Leu Phe Val Gly Gln
 100 105 110

Arg Trp Lys Ile Ser Arg Gly Val Met Leu Leu Val Ile Pro Leu Ala
 115 120 125

Leu Val Phe Val Leu Ala Val Arg Tyr Leu Ala Arg Met Arg Val Glu
 130 135 140

Arg Phe Arg Arg Pro Ala Ala Asp Ser Thr Pro Ala Leu Ile Leu Gly
 145 150 155 160

Gly Gly Tyr Ile Gly Thr Asn Leu Ile Gln Trp Met Met Ser Asp Pro
 165 170 175

Lys Ser Pro Phe Arg Pro Val Gly Val Ile Asp Asp Asn Pro Glu Leu
 180 185 190

Ala Cys Gln Arg Val Arg Gly Val Pro Val Leu Gly Lys Phe Asp Asp
 195 200 205

Ile Ala Gln Val Ala Ser Asp Thr Gly Ala Glu Leu Leu Ile Val Ala
 210 215 220

Ile Gly Asp Ala Asp Ser Ala Leu Leu Arg Arg Val Gln Asp Thr Ala
 225 230 235 240

Asn Lys Asn Gly Leu Ser Val Lys Val Met Pro Ala Ile Asp Arg Val
 245 250 255

Val Ser Lys Gly Val Arg Gly Asn Asp Leu Arg Asp Leu Ser Ile Glu
 260 265 270

Asp Leu Leu Gly Arg Gln Pro Val Glu Thr Asn Val Ser Glu Ile Thr
 275 280 285

Gly Tyr Leu Thr Gly Lys Arg Val Leu Val Thr Gly Ala Gly Gly Ser

290

295

300

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Ile Gly Ser Gln Leu Cys Thr Glu Ile Ala Lys Tyr Gly Pro Ala Glu
305                      310                      315                      320

Leu Met Met Leu Asp Arg Asp Glu Thr Gly Leu Gln Gln Val Leu Ile
                      325                      330                      335

Asn Val Ala Gly Asp Asn Gly Leu Leu Asp Thr Asp Ala Val Val Leu Ala
                      340                      345                      350

Asp Ile Arg Glu Ala Asp Ala Met Lys Glu Ile Phe Leu Lys Arg Lys
                      355                      360                      365

Pro Glu Val Val Phe His Ala Ala Ala Leu Lys His Leu Pro Met Leu
                      370                      375                      380

Glu Gln Tyr Pro Asp Glu Gly Trp Lys Thr Asn Val Leu Gly Thr Leu
385                      390                      395                      400

Asn Val Leu Ala Ala Ala Glu Ala Val Gly Val Glu Thr Phe Val Asn
                      405                      410                      415

Ile Ser Thr Asp Lys Ala Ala Asn Pro Thr Ser Val Leu Gly His Ser
                      420                      425                      430

Lys Arg Val Ala Glu Lys Leu Thr Ala Trp Tyr Gly Gln Asn Ser Thr
                      435                      440                      445

Ser Lys Tyr Leu Ser Val Arg Phe Gly Asn Val Ile Gly Ser Arg Gly
                      450                      455                      460

Ser Met Leu Pro Thr Phe Thr Arg Leu Ile Met Glu Asp Lys Pro Leu
465                      470                      475                      480

Thr Val Thr His Pro Asp Val Thr Arg Phe Phe Met Thr Ile Pro Glu
                      485                      490                      495

Ala Cys Gln Leu Val Leu Gln Ala Gly Gly Ile Gly Arg Ser Gly Glu
                      500                      505                      510

Val Leu Ile Leu Asp Met Gly Glu Pro Val Ser Ile Leu Glu Ile Ala
                      515                      520                      525

Gln Arg Met Ile Ala Met Ser Gly Lys Asp Ile Asp Ile Val Phe Thr
                      530                      535                      540

Gly Leu Arg Glu Gly Glu Lys Met His Glu Glu Leu Val Gly Asp Gly
545                      550                      555                      560

Glu Thr Glu Asp Arg Pro Phe His Ser Lys Ile Ser His Ala His Ala
                      565                      570                      575

Glu Ser Leu Ala Pro Asn Asn Leu Asp Arg Asp Arg Phe Met Gln Arg
                      580                      585                      590

Ala Gly Lys Leu Ala Ser Thr Asp Ser Glu Ile Ile
                      595                      600

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<211> 1557
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1534)
<223> RXA01273

<400> 2159
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tctattgggt aaaaattgat ctgcaagagg actgcaaaat atg gaa tta agg gaa 115
               Met Glu Leu Arg Glu
               1               5

tac gcg aca atc ctg atg aag aat tgg gtg ttg atc gtt atc gca tcc 163
Tyr Ala Thr Ile Leu Met Lys Asn Trp Val Leu Ile Val Ile Ala Ser
               10               15               20

att ctt gga att gca gcg ggc gct ggt ttt tcc ctt cta gct aca ccg 211
Ile Leu Gly Ile Ala Ala Gly Ala Gly Phe Ser Leu Leu Ala Thr Pro
               25               30               35

gag tat cag tca cgt act cag ttg tat gta tcg gtg cgg tcg ggg gct 259
Glu Tyr Gln Ser Arg Thr Gln Leu Tyr Val Ser Val Arg Ser Gly Ala
               40               45               50

ggg aca acc tct gac atg gtt cag ggt gct aac ttt tcg cgt cag att 307
Gly Thr Thr Ser Asp Met Val Gln Gly Ala Asn Phe Ser Arg Gln Ile
               55               60               65

gtg aat agt tat gtt gat gtc att aag acg ggt gtt gtt cta gag ccg 355
Val Asn Ser Tyr Val Asp Val Ile Lys Thr Gly Val Val Leu Glu Pro
               70               75               80               85

gtt gtt gat gag ctt ggt ctg gag ttg acg gct aac cag ttg agt tct 403
Val Val Asp Glu Leu Gly Leu Glu Leu Thr Ala Asn Gln Leu Ser Ser
               90               95               100

cat atc agt gcg gct tct cct gct gat act gcg ttg atc aac atc act 451
His Ile Ser Ala Ala Ser Pro Ala Asp Thr Ala Leu Ile Asn Ile Thr
               105               110               115

gct tct agt cct tct cct cag cag gcg gct gag atc gcc aat gca gtg 499
Ala Ser Ser Pro Ser Pro Gln Gln Ala Ala Glu Ile Ala Asn Ala Val
               120               125               130

ggg gag agt ttc aag aat gtg att cag act gaa ttg gaa cca gac tcc 547
Gly Glu Ser Phe Lys Asn Val Ile Gln Thr Glu Leu Glu Pro Asp Ser
               135               140               145

ggc gat ggc atg agc ccg att aac ctg act act act cag gtg gct ctg 595
Gly Asp Gly Met Ser Pro Ile Asn Leu Thr Thr Thr Gln Val Ala Leu
               150               155               160               165

gaa cca tct tct ccg gtc agt cct aat gtg atg atg aat atc ctc ctc 643
Glu Pro Ser Ser Pro Val Ser Pro Asn Val Met Met Asn Ile Leu Leu
               170               175               180

ggc cta ctt gta ggt ctt gca ata ggt gtt ggt att gca gtg ctt cgc 691

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Gly Leu Leu Val Gly Leu Ala Ile Gly Val Gly Ile Ala Val Leu Arg	
185 190 195	
gcg gct ttg gat act cgt att cat tcc ttg cgc gat att gaa gag gtt	739
Ala Ala Leu Asp Thr Arg Ile His Ser Leu Arg Asp Ile Glu Glu Val	
200 205 210	
act gat aag cca ctt ttg ggc gga atc att cgc gat tct gaa gtt gag	787
Thr Asp Lys Pro Leu Leu Gly Gly Ile Ile Ala Asp Ser Glu Val Glu	
215 220 225	
aag cac ccg ttg atc att aag cac aag ccg cat agt cct att cgc gag	835
Lys His Pro Leu Ile Ile Lys His Lys Pro His Ser Pro Ile Ala Glu	
230 235 240 245	
tcc ttt cgt gcg tta cgt act aac ctg cag ttc ctt aac gtc ggc ggc	883
Ser Phe Arg Ala Leu Arg Thr Asn Leu Gln Phe Leu Asn Val Gly Gly	
250 255 260	
tca tct tca gta ttt gtt atc tcc tct gct aat cct ggt gag ggt aag	931
Ser Ser Ser Val Phe Val Ile Ser Ser Ala Asn Pro Gly Glu Lys	
265 270 275	
tca acc act tct gta aac cta gct ttg gcg ctt gca gag gcc ggc tcc	979
Ser Thr Thr Ser Val Asn Leu Ala Leu Ala Leu Ala Glu Ala Gly Ser	
280 285 290	
cgt gta gcg ctg atc gaa gct gat ctt cgc ttg cca cga gtg agc aag	1027
Arg Val Ala Leu Ile Glu Ala Asp Leu Arg Leu Pro Arg Val Ser Lys	
295 300 305	
tac ctc gga gtt gag ggc aac gca ggt ctg act gac att ctc att ggc	1075
Tyr Leu Gly Val Glu Gly Asn Ala Gly Leu Thr Asp Ile Leu Ile Gly	
310 315 320 325	
aag gcc gag gtt aat gat gtg ttg cag cgt tgg ggt agg act cag ttg	1123
Lys Ala Glu Val Asn Asp Val Leu Gln Arg Trp Gly Arg Thr Gln Leu	
330 335 340	
tac tat ctc ccg gca ggg cgc att ccg ccg aac ccg agt gag ttg ctt	1171
Tyr Tyr Leu Pro Ala Gly Arg Ile Pro Pro Asn Pro Ser Glu Leu Leu	
345 350 355	
ggt tca gct gag atg gac aag gtc att gcg gag ctt gag gaa agc ttt	1219
Gly Ser Ala Glu Met Asp Lys Val Ile Ala Glu Leu Glu Glu Ser Phe	
360 365 370	
gat tat gtg atc atc gat gcc cct ccg gcg ttg gcg gtt acc gat gct	1267
Asp Tyr Val Ile Ile Asp Ala Pro Pro Ala Leu Ala Val Thr Asp Ala	
375 380 385	
gca gtt att ggt cat ggc aag gct ggc atc ctg att gcg gtc tcc gca	1315
Ala Val Ile Gly His Gly Lys Lys Ala Gly Ile Leu Ile Ala Val Ser Ala	
390 395 400 405	
ggt tct aca aag aag cct gag ttg gaa gct acg ctg tcc acg ctt gag	1363
Gly Ser Thr Lys Lys Pro Glu Leu Glu Ala Thr Leu Ser Thr Leu Glu	
410 415 420	
aat gcg gat gcc aat gtt gtt ggc gtt gtc gct acg atg ctc ccg cct	1411
Asn Ala Asp Ala Asn Val Val Gly Val Val Ala Thr Met Leu Pro Pro	

425 430 435
 aag tct gtg gct ggt tat ggc tac gga aat tac ggc tac ggc gac acc 1459
 Lys Ser Val Ala Gly Tyr Gly Tyr Gly Asn Tyr Gly Tyr Gly Asp Thr
 440 445 450
 tcc aaa atc aat gcc cct aag ccc gac aac acc gaa cta acc acc acc 1507
 Ser Lys Ile Asn Ala Pro Lys Pro Asp Asn Thr Glu Leu Thr Thr Thr
 455 460 465
 gat gct tcc aag gcc aac aat gag caa tagcttcact attctcactg 1554
 Asp Ala Ser Lys Ala Asn Asn Glu Gln
 470 475
 tct 1557

 <210> 2160
 <211> 478
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 2160
 Met Glu Leu Arg Glu Tyr Ala Thr Ile Leu Met Lys Asn Trp Val Leu
 1 5 10 15
 Ile Val Ile Ala Ser Ile Leu Gly Ile Ala Ala Gly Ala Gly Phe Ser
 20 25 30
 Leu Leu Ala Thr Pro Glu Tyr Gln Ser Arg Thr Gln Leu Tyr Val Ser
 35 40 45
 Val Arg Ser Gly Ala Gly Thr Ser Asp Met Val Gln Gly Ala Asn
 50 55 60
 Phe Ser Arg Gln Ile Val Asn Ser Tyr Val Asp Val Ile Lys Thr Gly
 65 70 75 80
 Val Val Leu Glu Pro Val Val Asp Glu Leu Gly Leu Glu Leu Thr Ala
 85 90 95
 Asn Gln Leu Ser Ser His Ile Ser Ala Ala Ser Pro Ala Asp Thr Ala
 100 105 110
 Leu Ile Asn Ile Thr Ala Ser Ser Pro Ser Pro Gln Gln Ala Ala Glu
 115 120 125
 Ile Ala Asn Ala Val Gly Glu Ser Phe Lys Asn Val Ile Gln Thr Glu
 130 135 140
 Leu Glu Pro Asp Ser Gly Asp Gly Met Ser Pro Ile Asn Leu Thr Thr
 145 150 155 160
 Thr Gln Val Ala Leu Glu Pro Ser Ser Pro Val Ser Pro Asn Val Met
 165 170 175
 Met Asn Ile Leu Leu Gly Leu Leu Val Gly Leu Ala Ile Gly Val Gly
 180 185 190
 Ile Ala Val Leu Arg Ala Ala Leu Asp Thr Arg Ile His Ser Leu Arg
 195 200 205

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Asp Ile Glu Glu Val Thr Asp Lys Pro Leu Leu Gly Gly Ile Ile Ala
210                215                220

Asp Ser Glu Val Glu Lys His Pro Leu Ile Ile Lys His Lys Pro His
225                230                235                240

Ser Pro Ile Ala Glu Ser Phe Arg Ala Leu Arg Thr Asn Leu Gln Phe
                245                250                255

Leu Asn Val Gly Gly Ser Ser Ser Val Phe Val Ile Ser Ser Ala Asn
260                265                270

Pro Gly Glu Gly Lys Ser Thr Thr Ser Val Asn Leu Ala Leu Ala Leu
275                280                285

Ala Glu Ala Gly Ser Arg Val Ala Leu Ile Glu Ala Asp Leu Arg Leu
290                295                300

Pro Arg Val Ser Lys Tyr Leu Gly Val Glu Gly Asn Ala Gly Leu Thr
305                310                315                320

Asp Ile Leu Ile Gly Lys Ala Glu Val Asn Asp Val Leu Gln Arg Trp
                325                330                335

Gly Arg Thr Gln Leu Tyr Tyr Leu Pro Ala Gly Arg Ile Pro Pro Asn
340                345                350

Pro Ser Glu Leu Leu Gly Ser Ala Glu Met Asp Lys Val Ile Ala Glu
355                360                365

Leu Glu Glu Ser Phe Asp Tyr Val Ile Ile Asp Ala Pro Pro Ala Leu
370                375                380

Ala Val Thr Asp Ala Ala Val Ile Gly His Gly Lys Ala Gly Ile Leu
385                390                395                400

Ile Ala Val Ser Ala Gly Ser Thr Lys Lys Pro Glu Leu Glu Ala Thr
405                410                415

Leu Ser Thr Leu Glu Asn Ala Asp Ala Asn Val Val Gly Val Val Ala
420                425                430

Thr Met Leu Pro Pro Lys Ser Val Ala Gly Tyr Gly Tyr Gly Asn Tyr
435                440                445

Gly Tyr Gly Asp Thr Ser Lys Ile Asn Ala Pro Lys Pro Asp Asn Thr
450                455                460

Glu Leu Thr Thr Thr Asp Ala Ser Lys Ala Asn Asn Glu Gln
465                470                475

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<210> 2161

<211> 903

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(880)

caggatgggt	cggaacgtc	cgctcgtttg	cggtgtgggt	ctgggtcatt	tggtgggcag	60										
cggtaggaaa	tacaaaaagc	ccactctaaag	atggcagggt	atg	gat	gag	ctg	ctc	115							
				Met	Asp	Glu	Leu	Leu	5							
aaa	cag	gaa	gtc	aag	gat	ttc	ctc	acc	acc	agg	cgt	gca	cgg	att	acg	163
Lys	Gln	Glu	Val	Lys	Asp	Phe	Leu	Thr	Thr	Arg	Arg	Ala	Arg	Ile	Thr	10
																15
ccg	gcc	gct	gcg	gga	cta	gaa	acg	cag	ccg	tgg	agt	gat	cgt	cgg	gtg	211
Pro	Ala	Ala	Ala	Gly	Leu	Glu	Thr	Gln	Pro	Trp	Ser	Asp	Arg	Arg	Val	25
																30
ccg	ggg	ctt	cgg	cgg	gaa	gaa	gtc	gcg	gat	ctg	gcg	ggc	att	tct	ttg	259
Pro	Gly	Leu	Arg	Arg	Glu	Glu	Val	Ala	Asp	Leu	Ala	Gly	Ile	Ser	Leu	40
																45
gag	tat	tac	atc	cgg	ttt	gag	cgc	gga	aat	ctc	aag	ggt	gca	tcg	cct	307
Glu	Tyr	Tyr	Ile	Arg	Phe	Glu	Arg	Gly	Asn	Leu	Lys	Gly	Ala	Ser	Pro	55
																60
gaa	ata	ttg	caa	tcg	ttg	gct	aag	gct	ctc	caa	ctg	agc	cca	att	gag	355
Glu	Ile	Leu	Gln	Ser	Leu	Ala	Lys	Ala	Leu	Gln	Leu	Ser	Pro	Ile	Glu	70
																75
cgc	gaa	cac	ctt	cac	aat	ttg	gct	tat	cgc	gcc	gac	cat	ccg	cgc	aac	403
Arg	Glu	His	Leu	His	Asn	Leu	Ala	Tyr	Arg	Ala	Asp	His	Pro	Arg	Asn	90
																95
cta	cct	agt	gca	gag	acc	cca	acg	gca	ccc	ctc	cag	gac	atc	gtt	gat	451
Leu	Pro	Ser	Ala	Glu	Thr	Pro	Thr	Ala	Pro	Leu	Gln	Asp	Ile	Val	Asp	105
																110
gcg	gtc	aca	gat	aaa	ccg	gcg	tgg	atc	cgc	aac	gag	cag	atg	gat	att	499
Ala	Val	Thr	Asp	Lys	Pro	Ala	Trp	Ile	Arg	Asn	Glu	Gln	Met	Asp	Ile	120
																125
ttg	gct	aca	aat	cgg	ctc	tgc	gcg	gaa	ctt	tac	gcc	ccg	att	ttc	aag	547
Leu	Ala	Thr	Asn	Arg	Leu	Cys	Ala	Glu	Leu	Tyr	Ala	Pro	Ile	Phe	Lys	135
																140
gat	ctg	ccc	gat	cgg	ccc	aac	act	gcg	cgg	cat	tgc	ttt	atc	ggc	gca	595
Asp	Leu	Pro	Asp	Arg	Pro	Asn	Thr	Ala	Arg	His	Cys	Phe	Ile	Gly	Ala	150
																155
aca	gcc	tcc	gag	ttc	tgg	gtg	gac	cgg	gat	cag	ttc	agt	gcg	gag	ttc	643
Thr	Ala	Ser	Glu	Phe	Trp	Val	Asp	Arg	Asp	Gln	Phe	Ser	Ala	Glu	Phe	170
																175
gct	gcc	aaa	cta	cgc	ctc	gag	tac	gcc	cgg	cgc	ccc	agc	gtg	cca	ggt	691
Ala	Ala	Lys	Leu	Arg	Leu	Glu	Tyr	Ala	Arg	Arg	Pro	Ser	Val	Pro	Gly	185
																190
tta	aag	gag	ctt	atc	gac	gag	ctc	cat	cag	aaa	agt	tct	gtt	ttc	cgc	739
Leu	Lys	Glu	Leu													

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gat aat tgg gcg tct gct gat gtt ttg tca ttc ggc tct ggc atc aaa 787
Asp Asn Trp Ala Ser Ala Asp Val Leu Ser Phe Gly Ser Gly Ile Lys
215 220 225

cgt ttc agg cac cca aca ctg ggg gag cgg gtc tat gaa tac gag acg 835
Arg Phe Arg His Pro Thr Leu Gly Glu Arg Val Tyr Glu Tyr Glu Thr
230 235 240 245

ttt aat ctc aat agt gca cgg ggg tat gtg ttg agc att tac ttt 880
Phe Asn Leu Asn Ser Ala Pro Gly Tyr Val Leu Ser Ile Tyr Phe
250 255 260

taggtggtgg aggggcgcgt cga 903

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<210> 2162

<211> 260

<212> PRT

<213> Corynebacterium glutamicum

<400> 2162

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Met Asp Glu Leu Leu Lys Gln Glu Val Lys Asp Phe Leu Thr Thr Arg
1 5 10 15

Arg Ala Arg Ile Thr Pro Ala Ala Ala Gly Leu Glu Thr Gln Pro Trp
20 25 30

Ser Asp Arg Arg Val Pro Gly Leu Arg Arg Glu Glu Val Ala Asp Leu
35 40 45

Ala Gly Ile Ser Leu Glu Tyr Tyr Ile Arg Phe Glu Arg Gly Asn Leu
50 55 60

Lys Gly Ala Ser Pro Glu Ile Leu Gln Ser Leu Ala Lys Ala Leu Gln
65 70 75 80

Leu Ser Pro Ile Glu Arg Glu His Leu His Asn Leu Ala Tyr Arg Ala
85 90 95

Asp His Pro Arg Asn Leu Pro Ser Ala Glu Thr Pro Thr Ala Pro Leu
100 105 110

Gln Asp Ile Val Asp Ala Val Thr Asp Lys Pro Ala Trp Ile Arg Asn
115 120 125

Glu Gln Met Asp Ile Leu Ala Thr Asn Arg Leu Cys Ala Glu Leu Tyr
130 135 140

Ala Pro Ile Phe Lys Asp Leu Pro Asp Arg Pro Asn Thr Ala Arg His
145 150 155 160

Cys Phe Ile Gly Ala Thr Ala Ser Glu Phe Trp Val Asp Arg Asp Gln
165 170 175

Phe Ser Ala Glu Phe Ala Ala Lys Leu Arg Leu Glu Tyr Ala Arg Arg
180 185 190

Pro Ser Val Pro Gly Leu Lys Glu Leu Ile Asp Glu Leu His Gln Lys
195 200 205

Ser Ser Val Phe Arg Asp Asn Trp Ala Ser Ala Asp Val Leu Ser Phe

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ccg aat tgg caa gtc cca gca gcg tgt gaa tgg ctc ggc tgc atg aat 547
 Pro Asn Trp Gln Val Pro Ala Ala Cys Glu Trp Leu Gly Cys Met Asn
 135 140 145

gtt ggt gaa cca ttt gaa atg tca cac gta ctt agg gtg tgg cag aac 595
 Val Gly Glu Pro Phe Glu Met Ser His Val Leu Arg Val Trp Gln Asn
 150 155 160 165

agt tgg ggc gtc gag gcc ctg gct ttt ggt ggt gaa gaa gac gac gcg 643
 Ser Trp Gly Val Glu Ala Leu Ala Phe Gly Gly Glu Glu Asp Asp Ala
 170 175 180

gat ctg ctg ctt cga gtc cct gaa gaa agc gaa gag cta ctg aag gct 691
 Asp Leu Leu Leu Arg Val Pro Glu Glu Ser Glu Glu Leu Leu Lys Ala
 185 190 195

ctc gca gtc gct tct gac caa gtc act acc tac aag cat gaa gat ctg 739
 Leu Ala Val Ala Ser Asp Gln Val Thr Thr Tyr Lys His Glu Asp Leu
 200 205 210

gga ttc tta gct agt ctt tgg ttt gac taactacaat caatgtcatg 786
 Gly Phe Leu Ala Ser Leu Trp Phe Asp
 215 220

acc 789

<210> 2164
 <211> 222
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2164
 Met Ser Thr Ile Pro Asp Val Phe Thr Ser Glu Val Phe Pro Glu Ile
 1 5 10 15

Ser Gly Thr Lys Glu Phe Arg Gly Leu Thr Tyr Met Phe Phe Asp Gln
 20 25 30

Phe Thr Leu Pro Thr Ala Glu Gln Leu Glu Gln Ala Lys Ala Ala Gly
 35 40 45

Trp Ser Leu Ile Thr Trp Gly Trp Trp Asn Ser Asp Thr Asp Leu Glu
 50 55 60

Asp Val Glu Leu Glu Asp Ile Thr Asn Glu Gly Asp Ser Leu Pro Lys
 65 70 75 80

Leu Thr Asp Glu Phe Ala Val Ser Ser Leu Ser Thr Phe Asp Leu Asn
 85 90 95

Ser Gln Gly Leu Pro Asn Asp Asp Arg Glu Pro Gln Pro Ile Glu Glu
 100 105 110

Ala Asp Ser Leu Asp Asp Ile Phe Ser Glu Glu Glu Gly Trp Gly Leu
 115 120 125

Met Ala Ile Asn Cys Pro Asn Trp Gln Val Pro Ala Ala Cys Glu Trp
 130 135 140

Leu Gly Cys Met Asn Val Gly Glu Pro Phe Glu Met Ser His Val Leu

145		150		155		160
Arg Val Trp Gln Asn Ser Trp Gly Val Glu Ala Leu Ala Phe Gly Gly						
	165			170		175
Glu Glu Asp Asp Ala Asp Leu Leu Leu Arg Val Pro Glu Glu Ser Glu						
	180			185		190
Glu Leu Leu Lys Ala Leu Ala Val Ala Ser Asp Gln Val Thr Thr Tyr						
	195			200		205
Lys His Glu Asp Leu Gly Phe Leu Ala Ser Leu Trp Phe Asp						
	210			215		220

<210> 2165

<211> 1098

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1075)

<223> RXA01295

<400> 2165

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ttcttggtgt taccctcggg taattgtaaa aaattcattg attaaaaacg atcagccaat 60
tgccatgctc agactccttg tgaagaaagt gacagtttcg atg acc gaa aat ctt 115
                                     Met Thr Glu Asn Leu
                                     1                               5
gat aat gcg ttg cta tcc atg cgg atg aaa cct gta caa atg gcg ctt 163
Asp Asn Ala Leu Leu Ser Met Arg Met Lys Pro Val Gln Met Ala Leu
                               10                               20
atg aca ctg ggc tac aac cat gac atg gcg gtg acc gat tcc ggt atg 211
Met Thr Leu Gly Tyr Asn His Asp Met Ala Val Thr Asp Ser Gly Met
                               25                               30                               35
gaa ctt ata gtg cgc cgc cca ggg ctg acc gtg aac ttc aac ttg gat 259
Glu Leu Ile Val Arg Arg Pro Gly Leu Thr Val Asn Phe Asn Leu Asp
                               40                               45                               50
tcg gtc acc ttg tgc atc gtc gct gat ttc atg tgg cat ggc tgt gtc 307
Ser Val Thr Leu Cys Ile Val Ala Asp Phe Met Trp His Gly Cys Val
                               55                               60                               65
cct gca aag aaa cag gca gag tac ctg cgg gcc gct aat gaa ttc aac 355
Pro Ala Lys Lys Gln Ala Glu Tyr Leu Arg Ala Ala Asn Glu Phe Asn
                               70                               75                               80                               85
agg cca acc cgt gat ctg cag gtg gtt tta gat gaa gct gat tca aag 403
Arg Pro Thr Arg Asp Leu Gln Val Val Leu Asp Glu Ala Asp Ser Lys
                               90                               95                               100
aac atg act gtg cga ggt cgt gaa ttc ttc ttc tca agc gtc ggc gca 451
Asn Met Thr Val Arg Gly Arg Glu Phe Phe Phe Ser Ser Val Gly Ala
                               105                               110                               115
acg tgg gaa cag tcg gca gag ttc gtg cac tac tgc atg aat gat gtg 499

```

Thr	Trp	Glu	Gln	Ser	Ala	Glu	Phe	Val	His	Tyr	Cys	Met	Asn	Asp	Val		
		120					125					130					
gca	acg	act	ttc	gtg	tct	tgg	tgc	gaa	caa	atc	tgg	ccg	aag	ttt	tcc	547	
Ala	Thr	Thr	Phe	Val	Ser	Trp	Cys	Glu	Gln	Ile	Trp	Pro	Lys	Phe	Ser		
	135					140				145							
cct	gaa	cgc	gta	gag	ttc	aac	gca	act	cct	cca	gat	gtg	gat	ttc	gag	595	
Pro	Glu	Arg	Val	Glu	Phe	Asn	Ala	Thr	Pro	Pro	Asp	Val	Asp	Phe	Glu		
	150				155				160					165			
ttc	tct	gaa	gat	caa	ctc	aaa	gaa	ggc	aat	ccc	ttc	ggg	ctg	att	gac	643	
Phe	Ser	Glu	Asp	Gln	Leu	Lys	Glu	Gly	Asn	Pro	Phe	Gly	Leu	Ile	Asp		
			170					175					180				
gaa	ccc	acc	ccg	ctg	gtt	tct	ttg	gat	cgt	atc	tac	caa	caa	tac	gaa	691	
Glu	Pro	Thr	Pro	Leu	Val	Ser	Leu	Asp	Arg	Ile	Tyr	Gln	Gln	Tyr	Glu		
		185				190						195					
tta	atg	ggg	gcg	gat	caa	ctc	aag	atg	ggg	gag	gac	ttc	gtt	gag	tat	739	
Leu	Met	Gly	Ala	Asp	Gln	Leu	Lys	Met	Gly	Glu	Asp	Phe	Val	Glu	Tyr		
	200					205					210						
ctg	cat	atg	ggg	caa	cgt	gtc	agt	gca	tgg	ttg	acc	gat	ggc	aac	aac	787	
Leu	His	Met	Gly	Gln	Arg	Val	Ser	Ala	Trp	Leu	Thr	Asp	Gly	Asn	Asn		
	215					220				225							
ggc	agc	gat	cga	aaa	acc	cta	gcg	gtg	tct	tcc	ggg	aca	ggg	gtg	aaa	835	
Gly	Ser	Asp	Arg	Lys	Thr	Leu	Ala	Val	Ser	Ser	Gly	Thr	Gly	Val	Lys		
	230				235				240					245			
atc	aaa	aac	aag	aag	caa	ctt	cag	gaa	ctt	ctt	gga	ctg	tgc	aac	ctg	883	
Ile	Lys	Asn	Lys	Lys	Gln	Leu	Gln	Glu	Leu	Gly	Leu	Cys	Asn	Leu			
			250					255					260				
tac	tcg	aaa	gaa	cat	gta	ctg	gtc	aca	gta	ttt	gcg	gaa	gag	atc	gaa	931	
Tyr	Ser	Lys	Glu	His	Val	Leu	Val	Thr	Val	Phe	Ala	Glu	Glu	Ile	Glu		
		265				270						275					
aac	ggc	gca	agg	tgg	ggg	att	ttc	gcc	gaa	gca	cgc	atc	gat	cta	ccg	979	
Asn	Gly	Ala	Arg	Trp	Gly	Ile	Phe	Ala	Glu	Ala	Arg	Ile	Asp	Leu	Pro		
		280				285						290					
gca	ggg	tta	aac	gat	cat	cag	ttg	tgg	gta	ttc	ctc	gcc	aac	tcc	agc	1027	
Ala	Gly	Leu	Asn	Asp	His	Gln	Leu	Trp	Val	Phe	Leu	Ala	Asn	Ser	Ser		
	295					300				305							
aaa	tgg	act	gca	gag	gtg	tgc	ctg	acc	gtg	gca	cac	cga	ctg	cag	aac	1075	
Lys	Trp	Thr	Ala	Glu	Val	Cys	Leu	Thr	Val	Ala	His	Arg	Leu	Gln	Asn		
	310				315					320				325			
taaaggcaga	acttaagcgt	tca														1098	

<210> 2166

<211> 325

<212> PRT

<213> Corynebacterium glutamicum

<400> 2166

Met Thr Glu Asn Leu Asp Asn Ala Leu Leu Ser Met Arg Met Lys Pro

1 5 10 15
 Val Gln Met Ala Leu Met Thr Leu Gly Tyr Asn His Asp Met Ala Val
 20 25 30
 Thr Asp Ser Gly Met Glu Leu Ile Val Arg Arg Pro Gly Leu Thr Val
 35 40 45
 Asn Phe Asn Leu Asp Ser Val Thr Leu Cys Ile Val Ala Asp Phe Met
 50 55 60
 Trp His Gly Cys Val Pro Ala Lys Lys Gln Ala Glu Tyr Leu Arg Ala
 65 70 75 80
 Ala Asn Glu Phe Asn Arg Pro Thr Arg Asp Leu Gln Val Val Leu Asp
 85 90 95
 Glu Ala Asp Ser Lys Asn Met Thr Val Arg Gly Arg Glu Phe Phe Phe
 100 105 110
 Ser Ser Val Gly Ala Thr Trp Glu Gln Ser Ala Glu Phe Val His Tyr
 115 120 125
 Cys Met Asn Asp Val Ala Thr Thr Phe Val Ser Trp Cys Glu Gln Ile
 130 135 140
 Trp Pro Lys Phe Ser Pro Glu Arg Val Glu Phe Asn Ala Thr Pro Pro
 145 150 155 160
 Asp Val Asp Phe Glu Phe Ser Glu Asp Gln Leu Lys Glu Gly Asn Pro
 165 170 175
 Phe Gly Leu Ile Asp Glu Pro Thr Pro Leu Val Ser Leu Asp Arg Ile
 180 185 190
 Tyr Gln Gln Tyr Glu Leu Met Gly Ala Asp Gln Leu Lys Met Gly Glu
 195 200 205
 Asp Phe Val Glu Tyr Leu His Met Gly Gln Arg Val Ser Ala Trp Leu
 210 215 220
 Thr Asp Gly Asn Asn Gly Ser Asp Arg Lys Thr Leu Ala Val Ser Ser
 225 230 235 240
 Gly Thr Gly Val Lys Ile Lys Asn Lys Lys Gln Leu Gln Glu Leu Leu
 245 250 255
 Gly Leu Cys Asn Leu Tyr Ser Lys Glu His Val Leu Val Thr Val Phe
 260 265 270
 Ala Glu Glu Ile Glu Asn Gly Ala Arg Trp Gly Ile Phe Ala Glu Ala
 275 280 285
 Arg Ile Asp Leu Pro Ala Gly Leu Asn Asp His Gln Leu Trp Val Phe
 290 295 300
 Leu Ala Asn Ser Ser Lys Trp Thr Ala Glu Val Cys Leu Thr Val Ala
 305 310 315 320
 His Arg Leu Gln Asn
 325

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<210> 2167
<211> 609
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(586)
<223> RXA01304

<400> 2167
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tgaaaaaggg gattaattac cccacttga ggagaaattg atg ccc gca cag aac 115
                               Met Pro Ala Gln Asn
                               1           5

aaa aac ctc cca gga tcc gtc atc gtt gtg tct gat cgg att aaa tcg 163
Lys Asn Leu Pro Gly Ser Val Ile Val Val Ser Asp Arg Ile Lys Ser
                        10                      15                      20

gga gaa aga att gat aaa gca gga ccc gta gca gta gac ctt ctt cag 211
Gly Glu Arg Ile Asp Lys Ala Gly Pro Val Ala Val Asp Leu Leu Gln
                        25                      30                      35

gaa tca ggc gtg gag att tcc aca ttc acc gtc gtg gag gag ggc ttt 259
Glu Ser Gly Val Glu Ile Ser Thr Phe Thr Val Val Glu Glu Gly Phe
                        40                      45                      50

gaa cct gtc cat caa gaa ttg gtt aag gcg ttg gcg cgc cgg gat cgc 307
Glu Pro Val His Gln Glu Leu Val Lys Ala Leu Ala Arg Arg Asp Arg
                        55                      60                      65

gtc atc atc acc atc ggc gga acg ggc gtg ggg cct aga aat cgg acg 355
Val Ile Ile Thr Ile Gly Gly Thr Gly Val Gly Pro Arg Asn Arg Thr
                        70                      75                      80                      85

ccg gag gcc aca gaa ccg cac atc gat acg cta ctg ccg ggt ctg atg 403
Pro Glu Ala Thr Glu Pro His Ile Asp Thr Leu Leu Pro Gly Leu Met
                        90                      95                      100

acg cag att ttg ttc tct gga ctg tcc aat acc gcg cag gcg ggg tta 451
Thr Gln Ile Leu Phe Ser Gly Leu Ser Asn Thr Ala Gln Ala Gly Leu
                        105                      110                      115

tct cgg ggg ctg gtg ggc ttg agt gct cgc gat tcc acg gcc gcg ctc 499
Ser Arg Gly Leu Val Gly Leu Ser Ala Arg Asp Ser Thr Ala Ala Leu
                        120                      125                      130

atc gtc aac gcg ccg agt tct tcc ggg ggc gtg cgc gac gcg ctc ggg 547
Ile Val Asn Ala Pro Ser Ser Ser Gly Gly Val Arg Asp Ala Leu Gly
                        135                      140                      145

gtg gtc tgc ccg ctt ttc ggt tcc att ttt gag cgt ctt taaaagattt 596
Val Val Cys Pro Leu Phe Gly Ser Ile Phe Glu Arg Leu
                        150                      155                      160

ttgcttatcg acg 609

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<210> 2168

<211> 162

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2168

Met Pro Ala Gln Asn Lys Asn Leu Pro Gly Ser Val Ile Val Val Ser
 1 5 10 15

Asp Arg Ile Lys Ser Gly Glu Arg Ile Asp Lys Ala Gly Pro Val Ala
 20 25 30

Val Asp Leu Leu Gln Glu Ser Gly Val Glu Ile Ser Thr Phe Thr Val
 35 40 45

Val Glu Glu Gly Phe Glu Pro Val His Gln Glu Leu Val Lys Ala Leu
 50 55 60

Ala Arg Arg Asp Arg Val Ile Ile Thr Ile Gly Thr Gly Val Gly
 65 70 75 80

Pro Arg Asn Arg Thr Pro Glu Ala Thr Glu Pro His Ile Asp Thr Leu
 85 90 95

Leu Pro Gly Leu Met Thr Gln Ile Leu Phe Ser Gly Leu Ser Asn Thr
 100 105 110

Ala Gln Ala Gly Leu Ser Arg Gly Leu Val Gly Leu Ser Ala Arg Asp
 115 120 125

Ser Thr Ala Ala Leu Ile Val Asn Ala Pro Ser Ser Ser Gly Gly Val
 130 135 140

Arg Asp Ala Leu Gly Val Val Cys Pro Leu Phe Gly Ser Ile Phe Glu
 145 150 155 160

Arg Leu

<210> 2169

<211> 450

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(427)

<223> RXA01310

<400> 2169

aaggaacgtg cgcgtgcagc tttccgaggc aaagacgact agtctttaat ccaagtaagt 60

accgggttcag acagttaaac cagaaagacg agtgaacacc atg tcc tcc gcg aaa 115
 Met Ser Ser Ala Lys
 1 5

aag aaa ccc gca ccg gag cgt atg cac tac atc aag ggc tat gta cct 163
 Lys Lys Pro Ala Pro Glu Arg Met His Tyr Ile Lys Gly Tyr Val Pro
 10 15 20

gtg gcg tat agc tct cca cac tca tcc ctc gag cgc agc gca acc tgg 211
Val Ala Tyr Ser Ser Pro His Ser Ser Leu Glu Arg Ser Ala Thr Trp
25 30 35

ttg ggc atg gga ttc ctc ctc act gct ctg gca ggc gtt ggc gca gtc 259
Leu Gly Met Gly Phe Leu Leu Thr Ala Leu Ala Gly Val Gly Ala Val
40 45 50

ctc ttc gca gtc ggc gca aac agc gtt ggc cag cag cag gaa cac tgg 307
Leu Phe Ala Val Gly Ala Asn Ser Val Gly Gln Gln Gln Glu His Trp
55 60 65

gtc ctc tac agc atc atc ggt gtt gta ttc gcc gtt gtc tgc aca gtt 355
Val Leu Tyr Ser Ile Ile Gly Val Val Phe Ala Val Val Cys Thr Val
70 75 80 85

ttg ggc acc gtc ctg atc atc aag ggc cga gca cct tac aac cgt tac 403
Leu Gly Thr Val Leu Ile Ile Lys Gly Arg Ala Pro Tyr Asn Arg Tyr
90 95 100

gtc aag gaa acc ggc cgt acg cag tagtttctgt atgcaggttc ttt 450
Val Lys Glu Thr Gly Arg Thr Gln
105

<210> 2170

<211> 109

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2170

Met Ser Ser Ala Lys Lys Lys Pro Ala Pro Glu Arg Met His Tyr Ile
1 5 10 15

Lys Gly Tyr Val Pro Val Ala Tyr Ser Ser Pro His Ser Ser Leu Glu
20 25 30

Arg Ser Ala Thr Trp Leu Gly Met Gly Phe Leu Leu Thr Ala Leu Ala
35 40 45

Gly Val Gly Ala Val Leu Phe Ala Val Gly Ala Asn Ser Val Gly Gln
50 55 60

Gln Gln Glu His Trp Val Leu Tyr Ser Ile Ile Gly Val Val Phe Ala
65 70 75 80

Val Val Cys Thr Val Leu Gly Thr Val Leu Ile Ile Lys Gly Arg Ala
85 90 95

Pro Tyr Asn Arg Tyr Val Lys Glu Thr Gly Arg Thr Gln
100 105

<210> 2171

<211> 968

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1) .. (945)

<223> RXA01313

<400> 2171

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gcc cta cgc ctc att tca cag ctg ctt gca cca tct gcg cgc ttg aat 48
Ala Leu Arg Leu Ile Ser Gln Leu Leu Ala Pro Ser Ala Ala Leu Asn
1 5 10 15

```

```

ttt aag tcc gag cgc aat gcc gtc gac gtg gca aaa cac atg ctc gcc 96
Phe Lys Ser Glu Arg Asn Ala Val Asp Val Ala Lys His Met Leu Ala
20 25 30

```

```

agc cag gcc caa caa cgc ggt tcc gca ctc gtt gcg cta gac acc cgc 144
Ser Gln Ala Gln Gln Arg Gly Ser Ala Leu Val Ala Leu Asp Thr Arg
35 40 45

```

```

tcg gaa aac gcc gac gcc gcc acg gca tta aga aag tca ctg ctc atc 192
Ser Glu Asn Ala Asp Ala Ala Thr Ala Leu Arg Lys Ser Leu Leu Ile
50 55 60

```

```

cgc agc tgg acg cag cgc gcc acc cac caa ata ctt gcc gcc gaa gac 240
Arg Ser Trp Thr Gln Arg Gly Thr His Gln Ile Leu Ala Ala Glu Asp
65 70 75 80

```

```

gtc cgc tgg atg acg cta cta tgc tcc cca cgc atc ctg gct gct tca 288
Val Arg Trp Met Thr Leu Leu Cys Ser Pro Arg Ile Leu Ala Ala Ser
85 90 95

```

```

gcc aag cgc cgc tcc agc ctt tcg ctt gat agc gcc gca gtc cag cgc 336
Ala Lys Arg Arg Ser Ser Leu Ser Leu Asp Ser Ala Ala Val Gln Arg
100 105 110

```

```

gcc cgc gac gca cta aca acc gcc gcc gaa aaa tcc ccc gta tcc aga 384
Ala Arg Asp Ala Leu Thr Thr Ala Ala Glu Lys Ser Pro Val Ser Arg
115 120 125

```

```

acc cag gcc tac gaa att ttc cga tcc gta gac gtt gac ccc gcc gag 432
Thr Gln Ala Tyr Glu Ile Phe Arg Ser Val Asp Val Asp Pro Gly Glu
130 135 140

```

```

cac aga gcc caa cat tta ctc cgg cat ttc ggt gcc gaa ggt gac atc 480
His Arg Gly Gln His Leu Leu Arg His Phe Gly Gly Glu Gly Asp Ile
145 150 155 160

```

```

gta caa gcc ccg ccc atc gga acg gaa gat tcc ttt gtg ctt ctc gat 528
Val Gln Gly Pro Pro Ile Gly Thr Glu Asp Ser Phe Val Leu Leu Asp
165 170 175

```

```

tcc atc tgc ccc ctt tcc cta gca ctt aac gcc gac gaa gcg ctc aca 576
Ser Ile Cys Pro Leu Ser Leu Ala Leu Asn Gly Asp Glu Ala Leu Thr
180 185 190

```

```

gag atg acc cgt cgc tac ttc cac tcc cgt ggt gct gcc act gtg aaa 624
Glu Met Thr Arg Arg Tyr Phe His Ser Arg Gly Ala Ala Thr Val Lys
195 200 205

```

```

gat ctg gtg tgg tgg acc gga ctg act gtg cgt gat gta aag aaa gcc 672
Asp Leu Val Trp Trp Thr Gly Leu Thr Val Arg Asp Val Lys Lys Gly
210 215 220

```

```

atc gct gcc gtg tct tcg gat gga ctg att cac tct gtt gaa gcc ccg 720

```

```

Ile Ala Ala Val Ser Ser Asp Gly Leu Ile His Ser Val Glu Gly Pro
225                230                235                240

aat ggt gaa gaa atg tgg atc cct acc tgg gca gat gat gtc aca gac   768
Asn Gly Glu Glu Met Trp Ile Pro Thr Trp Ala Asp Asp Val Thr Asp
                245                250                255

gca gag gtt tct gat gca cta gcg ttg gaa cta acc ctc ccc gcc ttt   816
Ala Glu Val Ser Asp Ala Leu Ala Leu Glu Leu Thr Leu Pro Ala Phe
                260                265                270

gat gaa tac cta ctt tcc tac acc gac cgc agc cac gtc atg gat ccc   864
Asp Glu Tyr Leu Leu Ser Tyr Thr Asp Arg Ser His Val Met Asp Pro
                275                280                285

gag cac ctt ttc agc atc ggt ccc ggc aaa aac ggt gtg ttc aaa ccc   912
Glu His Leu Phe Ser Ile Gly Pro Gly Lys Asn Gly Val Phe Lys Pro
                290                295                300

ttc aaa gta gtt cag ggt gag gca ctg ccg gtt tagcccgca aaatcttcac 965
Phe Lys Val Val Gln Gly Glu Ala Leu Pro Val
305                310                315

ttg                                                    968

<210> 2172
<211> 315
<212> PRT
<213> Corynebacterium glutamicum

<400> 2172
Ala Leu Arg Leu Ile Ser Gln Leu Leu Ala Pro Ser Ala Ala Leu Asn
 1                5                10                15

Phe Lys Ser Glu Arg Asn Ala Val Asp Val Ala Lys His Met Leu Ala
                20                25                30

Ser Gln Ala Gln Gln Arg Gly Ser Ala Leu Val Ala Leu Asp Thr Arg
                35                40                45

Ser Glu Asn Ala Asp Ala Ala Thr Ala Leu Arg Lys Ser Leu Leu Ile
 50                55                60

Arg Ser Trp Thr Gln Arg Gly Thr His Gln Ile Leu Ala Ala Glu Asp
 65                70                75                80

Val Arg Trp Met Thr Leu Leu Cys Ser Pro Arg Ile Leu Ala Ala Ser
                85                90                95

Ala Lys Arg Arg Ser Ser Leu Ser Leu Asp Ser Ala Ala Val Gln Arg
100                105                110

Ala Arg Asp Ala Leu Thr Thr Ala Ala Glu Lys Ser Pro Val Ser Arg
115                120                125

Thr Gln Ala Tyr Glu Ile Phe Arg Ser Val Asp Val Asp Pro Gly Glu
130                135                140

His Arg Gly Gln His Leu Leu Arg His Phe Gly Gly Glu Gly Asp Ile
145                150                155                160

```


Val Gln Gly Pro Pro Ile Gly Thr Glu Asp Ser Phe Val Leu Leu Asp
165 170 175

Ser Ile Cys Pro Leu Ser Leu Ala Leu Asn Gly Asp Glu Ala Leu Thr
180 185 190

Glu Met Thr Arg Arg Tyr Phe His Ser Arg Gly Ala Ala Thr Val Lys
195 200 205

Asp Leu Val Trp Trp Thr Gly Leu Thr Val Arg Asp Val Lys Lys Gly
210 215 220

Ile Ala Ala Val Ser Ser Asp Gly Leu Ile His Ser Val Glu Gly Pro
225 230 235 240

Asn Gly Glu Glu Met Trp Ile Pro Thr Trp Ala Asp Asp Val Thr Asp
245 250 255

Ala Glu Val Ser Asp Ala Leu Ala Leu Glu Leu Thr Leu Pro Ala Phe
260 265 270

Asp Glu Tyr Leu Leu Ser Tyr Thr Asp Arg Ser His Val Met Asp Pro
275 280 285

Glu His Leu Phe Ser Ile Gly Pro Gly Lys Asn Gly Val Phe Lys Pro
290 295 300

Phe Lys Val Val Gln Gly Glu Ala Leu Pro Val
305 310 315

<210> 2173

<211> 774

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(751)

<223> RXA01315

<400> 2173

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aatattgcac tgagtgcgaag ttacactag gtttacttca gtg gat att gaa gag 115
Val Asp Ile Glu Glu 5

cag ccc tcg tta aga gaa atc aag cgc caa atg acc ctg gaa gcg ata 163
Gln Pro Ser Leu Arg Glu Ile Lys Arg Gln Met Thr Leu Glu Ala Ile 10 15 20

gaa gat aac gca acc agg ctc att ctg gag cgt ggc ttc gac aat gtc 211
Glu Asp Asn Ala Thr Arg Leu Ile Leu Glu Arg Gly Phe Asp Asn Val 25 30 35

aca atc gaa gac atc tgc gca gag gca ggg ata tcc aag cgc aca ttc 259
Thr Ile Glu Asp Ile Cys Ala Glu Ala Gly Ile Ser Lys Arg Thr Phe 40 45 50

ttt aac tac gtg gag tcc aaa gag tct gtg gcc atc ggg cac aca gcc 307
 Phe Asn Tyr Val Glu Ser Lys Glu Ser Val Ala Ile Gly His Thr Ala
 55 60 65
 aag ctc cca acg gat gaa gaa cgt gaa gca ttc ctg gct acg cgt cat 355
 Lys Leu Pro Thr Asp Glu Glu Arg Glu Ala Phe Leu Ala Thr Arg His
 70 75 80 85
 gaa aat att atc gat act gta ttt gac ctg gta atc aac ctc ttt ggc 403
 Glu Asn Ile Ile Asp Thr Val Phe Asp Leu Val Ile Asn Leu Phe Gly
 90 95 100
 aac cac gac aac tcc aag tct gga gtt gca ggc gac att atg cgt cga 451
 Asn His Asp Asn Ser Lys Ser Gly Val Ala Gly Asp Ile Met Arg Arg
 105 110 115
 cgc aaa gag atc cgg gtg aag cat cca gaa ctg gca gtg caa cat ttc 499
 Arg Lys Glu Ile Arg Val Lys His Pro Glu Leu Ala Val Gln His Phe
 120 125 130
 gcc agg ttc cac caa gca cgc gaa ggg cta gaa cac cta att gtt gag 547
 Ala Arg Phe His Gln Ala Arg Glu Gly Leu Glu His Leu Ile Val Glu
 135 140 145
 tac ttc gaa aaa tgg cca ggc tcc caa cat cta gat gag cct gca gat 595
 Tyr Phe Glu Lys Trp Pro Gly Ser Gln His Leu Asp Glu Pro Ala Asp
 150 155 160 165
 cga gaa gca atc gcc ata gtt ggc ctg ctg atc tcg gtc atg ctt caa 643
 Arg Glu Ala Ile Ala Ile Val Gly Leu Leu Ile Ser Val Met Leu Gln
 170 175 180
 ggt tct cgt gaa tgg cac gac atg cca caa ggc acg caa gct gat ttc 691
 Gly Ser Arg Glu Trp His Asp Met Pro Gln Gly Thr Gln Ala Asp Phe
 185 190 195
 caa gcc tgc tgt cgc aaa gca att aaa aat act ttt ctt ctt aga ggt 739
 Gln Ala Cys Cys Arg Lys Ala Ile Lys Asn Thr Phe Leu Leu Arg Gly
 200 205 210
 gga ttt tca gaa tgacatcaca ggtaagccg gac 774
 Gly Phe Ser Glu
 215

<210> 2174

<211> 217

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2174

Val Asp Ile Glu Glu Gln Pro Ser Leu Arg Glu Ile Lys Arg Gln Met
 1 5 10 15
 Thr Leu Glu Ala Ile Glu Asp Asn Ala Thr Arg Leu Ile Leu Glu Arg
 20 25 30
 Gly Phe Asp Asn Val Thr Ile Glu Asp Ile Cys Ala Glu Ala Gly Ile
 35 40 45
 Ser Lys Arg Thr Phe Phe Asn Tyr Val Glu Ser Lys Glu Ser Val Ala

50

55

60

Ile Gly His Thr Ala Lys Leu Pro Thr Asp Glu Glu Arg Glu Ala Phe
65 70 75 80

Leu Ala Thr Arg His Glu Asn Ile Ile Asp Thr Val Phe Asp Leu Val
85 90 95

Ile Asn Leu Phe Gly Asn His Asp Asn Ser Lys Ser Gly Val Ala Gly
100 105 110

Asp Ile Met Arg Arg Arg Lys Glu Ile Arg Val Lys His Pro Glu Leu
115 120 125

Ala Val Gln His Phe Ala Arg Phe His Gln Ala Arg Glu Gly Leu Glu
130 135 140

His Leu Ile Val Glu Tyr Phe Glu Lys Trp Pro Gly Ser Gln His Leu
145 150 155 160

Asp Glu Pro Ala Asp Arg Glu Ala Ile Ala Ile Val Gly Leu Leu Ile
165 170 175

Ser Val Met Leu Gln Gly Ser Arg Glu Trp His Asp Met Pro Gln Gly
180 185 190

Thr Gln Ala Asp Phe Gln Ala Cys Cys Arg Lys Ala Ile Lys Asn Thr
195 200 205

Phe Leu Leu Arg Gly Gly Phe Ser Glu
210 215

<210> 2175

<211> 426

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(403)

<223> RXA01316

<400> 2175

aaagcgcaag gctaagaagg attccccaga accaggcgat gacgatatca tcgatggaga 60

agtaattcct ccgcagaatt aaggaagtcg gtttcacccc atg gat att tcc atg 115
Met Asp Ile Ser Met
1 5

ctc aac gta ata acg agc tac acc att tgg gcc att ttt gcc atc atc 163
Leu Asn Val Ile Thr Ser Tyr Thr Ile Trp Ala Ile Phe Ala Ile Ile
10 15 20

ggc atc tgc gga ttc gtt ggt gcc ttc ttg gca gcc acc acc aga gaa 211
Gly Ile Cys Gly Phe Val Gly Ala Phe Leu Ala Ala Thr Thr Arg Glu
25 30 35

gat gcc ttt gag gtt gct gat cgc caa aag aaa atg gtg tgg gta gca 259
Asp Ala Phe Glu Val Ala Asp Arg Gln Lys Lys Met Val Trp Val Ala
40 45 50

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atc ctt atc gca tcc gga ttt gtc ctc acc gcg cta ggt cca tcg att 307
Ile Leu Ile Ala Ser Gly Phe Val Leu Thr Ala Leu Gly Pro Ser Ile
    55                      60                      65

ccg atc ctg cca tgg gtc gcc atc atc atg atc ggc ctg tac tgg ttt 355
Pro Ile Leu Pro Trp Val Ala Ile Ile Met Ile Gly Leu Tyr Trp Phe
    70                      75                      80                      85

gat gtt cgc ccg caa atc aag agc atc ctt gaa ggt gcc ggc ggc tgg 403
Asp Val Arg Pro Gln Ile Lys Ser Ile Leu Glu Gly Ala Gly Gly Trp
    90                      95                      100

taaaagctcc ctgaactgcg aaa 426

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<210> 2176
<211> 101
<212> PRT
<213> Corynebacterium glutamicum

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<400> 2176
Met Asp Ile Ser Met Leu Asn Val Ile Thr Ser Tyr Thr Ile Trp Ala
 1          5          10          15

Ile Phe Ala Ile Ile Gly Ile Cys Gly Phe Val Gly Ala Phe Leu Ala
 20          25          30

Ala Thr Thr Arg Glu Asp Ala Phe Glu Val Ala Asp Arg Gln Lys Lys
 35          40          45

Met Val Trp Val Ala Ile Leu Ile Ala Ser Gly Phe Val Leu Thr Ala
 50          55          60

Leu Gly Pro Ser Ile Pro Ile Leu Pro Trp Val Ala Ile Ile Met Ile
 65          70          75          80

Gly Leu Tyr Trp Phe Asp Val Arg Pro Gln Ile Lys Ser Ile Leu Glu
 85          90          95

Gly Ala Gly Gly Trp
100

```

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<210> 2177
<211> 543
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(520)
<223> RXA01317

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<400> 2177
atacatccgc cttaatggca caattgtagg tgcattagca ggaactggcca tttagcgtat 60

ttcccatatc ctcttcggag cttaactagg agtaaccatc atg tcc gat gca aaa 115
Met Ser Asp Ala Lys
    1          5

```

gac gat tcc atc ttg tcc aag tgg agc aat gca gct tcc gag ctc agc 163
 Asp Asp Ser Ile Leu Ser Lys Trp Ser Asn Ala Ala Ser Glu Leu Ser
 10 15 20

ggt gcc gtc agt gga gta gcg aag aag ctc cgt gaa gaa ctc tct gag 211
 Gly Ala Val Ser Gly Val Ala Lys Lys Leu Arg Glu Glu Leu Ser Glu
 25 30 35

aag gaa acc ttc agc aag ctt aaa acc gaa gcc agc gaa gcc gtc gat 259
 Lys Glu Thr Phe Ser Lys Leu Lys Thr Glu Ala Ser Glu Ala Val Asp
 40 45 50

caa gca aag tcc ggc tcc tac cta gat gcc ggt aag gaa ttc gcc cgc 307
 Gln Ala Lys Ser Gly Ser Tyr Leu Asp Ala Gly Lys Glu Phe Ala Arg
 55 60 65

gac gcc gga tcc atc atc aaa gat gca gcc aaa acc gtc aaa ggt gcc 355
 Asp Ala Gly Ser Ile Ile Lys Asp Ala Ala Lys Thr Val Lys Gly Ala
 70 75 80 85

gtc agt gat tcc gat aaa aac gac gtg aaa tcc gcc ttc ggt aac gcc 403
 Val Ser Asp Ser Asp Lys Asn Asp Val Lys Ser Ala Phe Gly Asn Ala
 90 95 100

gtg gaa gct tcc cgc gac aag ttc gat gac acc ctc gaa aag cgc aag 451
 Val Glu Ala Ser Arg Asp Lys Phe Asp Asp Thr Leu Glu Lys Arg Lys
 105 110 115

gct aag aag gat tcc cca gaa cca gcc gat gac gat atc atc gat gga 499
 Ala Lys Lys Asp Ser Pro Glu Pro Gly Asp Asp Asp Ile Ile Asp Gly
 120 125 130

gaa gta att cct ccg cag aat taaggaagtc gggttcaccc cat 543
 Glu Val Ile Pro Pro Gln Asn
 135 140

<210> 2178

<211> 140

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2178

Met Ser Asp Ala Lys Asp Asp Ser Ile Leu Ser Lys Trp Ser Asn Ala
 1 5 10 15

Ala Ser Glu Leu Ser Gly Ala Val Ser Gly Val Ala Lys Lys Leu Arg
 20 25 30

Glu Glu Leu Ser Glu Lys Glu Thr Phe Ser Lys Leu Lys Thr Glu Ala
 35 40 45

Ser Glu Ala Val Asp Gln Ala Lys Ser Gly Ser Tyr Leu Asp Ala Gly
 50 55 60

Lys Glu Phe Ala Arg Asp Ala Gly Ser Ile Ile Lys Asp Ala Ala Lys
 65 70 75 80

Thr Val Lys Gly Ala Val Ser Asp Ser Asp Lys Asn Asp Val Lys Ser
 85 90 95

Ala Phe Gly Asn Ala Val Glu Ala Ser Arg Asp Lys Phe Asp Asp Thr
 100 105 110

Leu Glu Lys Arg Lys Ala Lys Lys Asp Ser Pro Glu Pro Gly Asp Asp
 115 120 125

Asp Ile Ile Asp Gly Glu Val Ile Pro Pro Gln Asn
 130 135 140

<210> 2179

<211> 1425

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1402)

<223> RXA01318

<400> 2179

ggacgcgttc cagagaaaag tgcaggcdata acccctaataa taccctgatc ttcccccggtg 60

tcctgcccc gtgtccaccc ctgcgtacat aataggacgc atg gga aaa cat gag 115
 Met Gly Lys His Glu
 1 5

gtt gct cag cag acg gtt ccg ggt cct tgc ccg gaa atg gaa gcg cag 163
 Val Ala Gln Gln Thr Val Pro Gly Pro Ser Pro Glu Met Glu Ala Gln
 10 15 20

cggt cgt aaa gag ttg cgc aag cac aag gcc att gcc act ggc ctg ttg 211
 Arg Arg Lys Glu Leu Arg Lys His Lys Ala Ile Ala Thr Gly Leu Leu
 25 30 35

att ttt gct gcc gct gta tat ttt ctt tgc cgt ttc gtg gag acc cgt 259
 Ile Phe Ala Ala Val Tyr Phe Leu Cys Arg Phe Val Glu Thr Arg
 40 45 50

ccg ggt gaa act gca gcg tgg gta ggt ttt gtg cgc gct gcg gca gag 307
 Pro Gly Glu Thr Ala Ala Trp Val Gly Phe Val Arg Ala Ala Ala Glu
 55 60 65

gcc gga atg att ggc ggg ttg gcc gac tgg ttc gcg gtc acc gcg ctg 355
 Ala Gly Met Ile Gly Gly Leu Ala Asp Trp Phe Ala Val Thr Ala Leu
 70 75 80 85

ttc cgt cat cca ttg tgg ctg cct att ccg cac act gcg att atc ccg 403
 Phe Arg His Pro Leu Trp Leu Pro Ile Pro His Thr Ala Ile Ile Pro
 90 95 100

cggt aag aaa gac cag tta ggt gag gcc tta agc ggg ttt gtg ggg gat 451
 Arg Lys Lys Asp Gln Leu Gly Glu Ala Leu Ser Gly Phe Val Gly Asp
 105 110 115

aac ttc cta aat gcc cag ctc att acg gaa aaa gtc tct cag gcg cgg 499
 Asn Phe Leu Asn Ala Gln Leu Ile Thr Glu Lys Val Ser Gln Ala Arg
 120 125 130

atc cca gag gcg gcc ggg gag tgg ctc gcc cag ccg gaa aac ggg gag 547
 Ile Pro Glu Arg Ala Gly Glu Trp Leu Ala Gln Pro Glu Asn Gly Glu

135	140	145	
aaa gtt tgc cgc gaa gtc ggc aaa ttg acc gct aat att gtg cgc gca			595
Lys Val Ser Arg Glu Val Gly Lys Leu Thr Ala Asn Ile Val Arg Ala			
150	155	160	165
atc gat ccg tca gat gct gaa gcg gtg att aaa tct gcg gtg atc gac			643
Ile Asp Pro Ser Asp Ala Glu Ala Val Ile Lys Ser Ala Val Ile Asp			
170	175		180
aag ctt gcg gaa ccc acc tgg ggc cca cca gct ggg cgg ttg ctg gaa			691
Lys Leu Ala Glu Pro Thr Trp Gly Pro Pro Ala Gly Arg Leu Leu Glu			
185	190		195
caa ctc ctc gcc gaa ggc aaa gcc gaa cca gtt gtc cag gaa ctc gcg			739
Gln Leu Leu Ala Glu Gly Lys Ala Glu Pro Val Val Gln Glu Leu Ala			
200	205		210
cag tgg ctg cac aaa aag gcg ttg ggc tcc gag ccg ctg att gat cgc			787
Gln Trp Leu His Lys Lys Ala Leu Gly Ser Glu Pro Leu Ile Asp Arg			
215	220		225
ctg ctc aac gag cgc cgc ccg att tgg gcg ccg aaa ttc act gcg cag			835
Leu Leu Asn Glu Arg Arg Pro Ile Trp Ala Pro Lys Phe Thr Ala Gln			
230	235		240
ctg gtc agc ggc aaa gtc tat gac gag gtc ata aaa ttc act gaa gcc			883
Leu Val Ser Gly Lys Val Tyr Asp Glu Val Ile Lys Phe Thr Glu Ala			
250	255		260
gtc gct gcc gat cct aac cac gag gcc cgc aaa tcg ctg cgc cga ttc			931
Val Ala Ala Asp Pro Asn His Glu Ala Arg Lys Ser Leu Arg Arg Phe			
265	270		275
ctt aat aaa ttg gcg caa gac ctg cag cat gac cca ggc atg att att			979
Leu Asn Lys Leu Ala Gln Asp Leu Gln His Asp Pro Gly Met Ile Ile			
280	285		290
aaa gtt gaa gaa atc aaa cgc gac atc atg ggc tcc ggc gcc atc gcg			1027
Lys Val Glu Glu Ile Lys Arg Asp Ile Met Gly Ser Gly Ala Ile Ala			
295	300		305
caa gcc gcg cca acc atc tgg gcg tca gcc tcc gag tcg ctc att gaa			1075
Gln Ala Ala Pro Thr Ile Trp Ala Ser Ala Ser Glu Ser Leu Ile Glu			
310	315		320
tcc gca gaa gat gag tca tca att ctg cgt cgc aaa att gcc gaa gca			1123
Ser Ala Glu Asp Glu Ser Ser Ile Leu Arg Arg Lys Ile Ala Glu Ala			
330	335		340
gct acc agc tgg ggt caa aga ttg ctt gtc gac gac tcc ctc cgg cat			1171
Ala Thr Ser Trp Gly Gln Arg Leu Leu Val Asp Asp Ser Leu Arg His			
345	350		355
tca ctc gac acc cgg att acc ggc gcc gct gct ttc ctc gcc gac aat			1219
Ser Leu Asp Thr Arg Ile Thr Gly Ala Ala Ala Phe Leu Ala Asp Asn			
360	365		370
tac gcc ccc gaa gtc acc ggc att atc tcc gaa acc att gaa cga tgg			1267
Tyr Ala Pro Glu Val Thr Gly Ile Ile Ser Glu Thr Ile Glu Arg Trp			
375	380		385

gac gct gaa gaa gct tca gag aaa atc gaa ctc atg gtg ggc aaa gac 1315
 Asp Ala Glu Glu Ala Ser Glu Lys Ile Glu Leu Met Val Gly Lys Asp
 390 395 400 405

ctc caa tac atc cgc ctt aat ggc aca att gta ggt gca tta gca gga 1363
 Leu Gln Tyr Ile Arg Leu Asn Gly Thr Ile Val Gly Ala Leu Ala Gly
 410 415 420

ctg gcc att tac gct att tcc cat atc ctc ttc gga gct taactaggag 1412
 Leu Ala Ile Tyr Ala Ile Ser His Ile Leu Phe Gly Ala
 425 430

taaccatcat gtc 1425

<210> 2180

<211> 434

<212> PRT

<213> Corynebacterium glutamicum

<400> 2180

Met Gly Lys His Glu Val Ala Gln Gln Thr Val Pro Gly Pro Ser Pro
 1 5 10 15

Glu Met Glu Ala Gln Arg Arg Lys Glu Leu Arg Lys His Lys Ala Ile
 20 25 30

Ala Thr Gly Leu Leu Ile Phe Ala Ala Val Tyr Phe Leu Cys Arg
 35 40 45

Phe Val Glu Thr Arg Pro Gly Glu Thr Ala Ala Trp Val Gly Phe Val
 50 55 60

Arg Ala Ala Ala Glu Ala Gly Met Ile Gly Gly Leu Ala Asp Trp Phe
 65 70 75 80

Ala Val Thr Ala Leu Phe Arg His Pro Leu Trp Leu Pro Ile Pro His
 85 90 95

Thr Ala Ile Ile Pro Arg Lys Lys Asp Gln Leu Gly Glu Ala Leu Ser
 100 105 110

Gly Phe Val Gly Asp Asn Phe Leu Asn Ala Gln Leu Ile Thr Glu Lys
 115 120 125

Val Ser Gln Ala Arg Ile Pro Glu Arg Ala Gly Glu Trp Leu Ala Gln
 130 135 140

Pro Glu Asn Gly Glu Lys Val Ser Arg Glu Val Gly Lys Leu Thr Ala
 145 150 155 160

Asn Ile Val Arg Ala Ile Asp Pro Ser Asp Ala Glu Ala Val Ile Lys
 165 170 175

Ser Ala Val Ile Asp Lys Leu Ala Glu Pro Thr Trp Gly Pro Pro Ala
 180 185 190

Gly Arg Leu Leu Glu Gln Leu Leu Ala Glu Gly Lys Ala Glu Pro Val
 195 200 205

Val Gln Glu Leu Ala Gln Trp Leu His Lys Lys Ala Leu Gly Ser Glu
 210 215 220
 Pro Leu Ile Asp Arg Leu Asn Glu Arg Arg Pro Ile Trp Ala Pro
 225 230 235 240
 Lys Phe Thr Ala Gln Leu Val Ser Gly Lys Val Tyr Asp Glu Val Ile
 245 250 255
 Lys Phe Thr Glu Ala Val Ala Ala Asp Pro Asn His Glu Ala Arg Lys
 260 265 270
 Ser Leu Arg Arg Phe Leu Asn Lys Leu Ala Gln Asp Leu Gln His Asp
 275 280 285
 Pro Gly Met Ile Ile Lys Val Glu Glu Ile Lys Arg Asp Ile Met Gly
 290 295 300
 Ser Gly Ala Ile Ala Gln Ala Ala Pro Thr Ile Trp Ala Ser Ala Ser
 305 310 315 320
 Glu Ser Leu Ile Glu Ser Ala Glu Asp Glu Ser Ser Ile Leu Arg Arg
 325 330 335
 Lys Ile Ala Glu Ala Ala Thr Ser Trp Gly Gln Arg Leu Leu Val Asp
 340 345 350
 Asp Ser Leu Arg His Ser Leu Asp Thr Arg Ile Thr Gly Ala Ala Ala
 355 360 365
 Phe Leu Ala Asp Asn Tyr Ala Pro Glu Val Thr Gly Ile Ile Ser Glu
 370 375 380
 Thr Ile Glu Arg Trp Asp Ala Glu Glu Ala Ser Glu Lys Ile Glu Leu
 385 390 395 400
 Met Val Gly Lys Asp Leu Gln Tyr Ile Arg Leu Asn Gly Thr Ile Val
 405 410 415
 Gly Ala Leu Ala Gly Leu Ala Ile Tyr Ala Ile Ser His Ile Leu Phe
 420 425 430
 Gly Ala

<210> 2181

<211> 579

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(556)

<223> RXA01330

<400> 2181

ccgtccggttt tcttggtggg tcggcccccgc atccagccct agaaatatcg gagagctgct 60

 cggttgaggcc caatgaaatg cctccgaaac agaaacaggc atg tgg aaa gac tta 115
 Met Trp Lys Asp Leu

1

5

acc gaa ccg ctg ccc gaa gct tgc gct gag ggc tta gag atc cgg gtg 163
 Thr Glu Pro Leu Pro Glu Ala Cys Ala Glu Gly Leu Glu Ile Arg Val
 10 15 20

gtt aaa tct ccc gaa gag ctg gca gat tac gct gca gtt ctt tct gcg 211
 Val Lys Ser Pro Glu Glu Leu Ala Asp Tyr Ala Ala Val Leu Ser Ala
 25 30 35

aat tgg aat cca ccc gcc gaa act gtg cag cgt ttc tat acc gaa gca 259
 Asn Trp Asn Pro Pro Ala Glu Thr Val Gln Arg Phe Tyr Thr Glu Ala
 40 45 50

gct gaa tac gca ctg aga aag aac tcg ccc gca ctt tat ctg gtg ggt 307
 Ala Glu Tyr Ala Leu Arg Lys Asn Ser Pro Ala Leu Tyr Leu Val Gly
 55 60 65

tat gcg ggc aac cgc gca gtg tgt tct gcg gaa gca ttc ata cac gcg 355
 Tyr Ala Gly Asn Arg Ala Val Cys Ser Ala Glu Ala Phe Ile His Ala
 70 75 80 85

agc gta gtt gga atc tac aat atc tcc acc ctt gag cac aaa cgc gcg 403
 Ser Val Val Gly Ile Tyr Asn Ile Ser Thr Leu Glu His Lys Arg Arg
 90 95 100

cgt ggc tac ggc gga gcc atc acc tta gcc acg ttg cat acc gca cgt 451
 Arg Gly Tyr Gly Gly Ala Ile Thr Leu Ala Thr Leu His Thr Ala Arg
 105 110 115

aac gca ggg tgt gac acc gcc gtg ttg caa gct tcc gaa gat ggt gag 499
 Asn Ala Gly Cys Asp Thr Ala Val Leu Gln Ala Ser Glu Asp Gly Glu
 120 125 130

ccc gtt tat cgc aaa cta gga ttc acc gac tgc ggt cga ttt act gaa 547
 Pro Val Tyr Arg Lys Leu Gly Phe Thr Asp Cys Gly Arg Phe Thr Glu
 135 140 145

tac tct ttg tgattagtta gggaccgtat gcg 579
 Tyr Ser Leu
 150

<210> 2182

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 2182

Met Trp Lys Asp Leu Thr Glu Pro Leu Pro Glu Ala Cys Ala Glu Gly
 1 5 10 15

Leu Glu Ile Arg Val Val Lys Ser Pro Glu Glu Leu Ala Asp Tyr Ala
 20 25 30

Ala Val Leu Ser Ala Asn Trp Asn Pro Pro Ala Glu Thr Val Gln Arg
 35 40 45

Phe Tyr Thr Glu Ala Ala Glu Tyr Ala Leu Arg Lys Asn Ser Pro Ala
 50 55 60

Leu Tyr Leu Val Gly Tyr Ala Gly Asn Arg Ala Val Cys Ser Ala Glu
65 70 75 80

Ala Phe Ile His Ala Ser Val Val Gly Ile Tyr Asn Ile Ser Thr Leu
85 90 95

Glu His Lys Arg Arg Arg Gly Tyr Gly Gly Ala Ile Thr Leu Ala Thr
100 105 110

Leu His Thr Ala Arg Asn Ala Gly Cys Asp Thr Ala Val Leu Gln Ala
115 120 125

Ser Glu Asp Gly Glu Pro Val Tyr Arg Lys Leu Gly Phe Thr Asp Cys
130 135 140

Gly Arg Phe Thr Glu Tyr Ser Leu
145 150

<210> 2183

<211> 1128

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1105)

<223> RXA01333

<400> 2183

cgccctttaa ggcccgtaaa gcactccaca acacttcacg gcaggccgta atttccctgt 60

gaggtacttt cttgcaagtt gtagcgacc gccgatacca atg cct ggc ggg tgc 115
Met Pro Gly Gly Cys
1 5

tcc ggt aac atc gtc cgc atg ctg cct aaa tcc cgg att ttc tcc gca 163
Ser Gly Asn Ile Val Arg Met Leu Pro Lys Ser Arg Ile Phe Ser Ala
10 15 20

atc ttg ctc gga att ggt gtg gca ctt gtg gtc tgg ggt ctg gtg gct 211
Ile Leu Leu Gly Ile Gly Val Ala Leu Val Val Trp Gly Leu Val Ala
25 30 35

ccg cgc ttt gtg cac gct gat ggc cgt ttg cct ctt gat ttg gag gcg 259
Pro Arg Phe Val His Ala Asp Gly Arg Leu Pro Leu Asp Leu Glu Ala
40 45 50

acg acg tac gtt ctc cat gac tct gac gct cag acc act att aat tct 307
Thr Thr Tyr Val Leu His Asp Ser Asp Ala Gln Thr Thr Ile Asn Ser
55 60 65

gat ccg ttg gcc ggt gtg gtg act acg ccg gtg act cgt cag ttg cat 355
Asp Pro Leu Ala Gly Val Val Thr Thr Pro Val Thr Arg Gln Leu His
70 75 80 85

ttt gag gtg atg gat cct gcg agt gct gat gat gcc act att cgt att 403
Phe Glu Val Met Asp Pro Ala Ser Ala Asp Asp Ala Thr Ile Arg Ile
90 95 100

ggg gat tcg atg ttg cgt ggt aat cct gat act cag ggt ttt gag cag 451

Gly Asp Ser Met Leu Arg Gly Asn Pro Asp Thr Gln Gly Phe Glu Gln	
105 110 115	
gaa cgg ctc ctg tca gcg act gtg tcg agt ttc cgc att gat cgc acc	499
Glu Arg Leu Leu Ser Ala Thr Val Ser Ser Phe Arg Ile Asp Arg Thr	
120 125 130	
tct ggt gag gtt ttg tcc gat att gcg ctg act aat cag ttg gcg agc	547
Ser Gly Glu Val Leu Ser Asp Ile Ala Leu Thr Asn Gln Leu Ala Ser	
135 140 145	
cct acg gtg cag tat tcg gtg gat ggc att tgg ttg aag ttc cca act	595
Pro Thr Val Gln Tyr Ser Val Asp Gly Ile Trp Leu Lys Phe Pro Thr	
150 155 160 165	
gac gcg cag gag acc act tac aac gtg gtg gat ccg gtg ctg agg tct	643
Asp Ala Gln Glu Thr Thr Tyr Asn Val Val Asp Pro Val Leu Arg Ser	
170 175 180	
gcg ctg cgc gcg gat ttt gtg gag tcc acg gag atc gat ggc cgt gag	691
Ala Leu Pro Ala Asp Phe Val Glu Ser Thr Glu Ile Asp Gly Arg Glu	
185 190 195	
gtg ctg cat tac cgt cag gtg att gat aac gtg aat gtg gcg gag tat	739
Val Leu His Tyr Arg Gln Val Ile Asp Asn Val Asn Val Ala Glu Tyr	
200 205 210	
ttc gcg gat gcc aac aac acc acc acg ttg act aaa gag gat ggc ggt	787
Phe Ala Asp Ala Asn Asn Thr Thr Thr Leu Thr Lys Glu Asp Gly Gly	
215 220 225	
acc acg acg ggc tat ttt tat cac aat gtg act cgt gat ttt tgg gtg	835
Thr Thr Thr Gly Tyr Phe Tyr His Asn Val Thr Arg Asp Phe Trp Val	
230 235 240 245	
gat cag cgt acc ggt ttg gtt gtc gat cta gct gaa aat att gat gat	883
Asp Gln Arg Thr Gly Leu Val Val Asp Leu Ala Glu Asn Ile Asp Asp	
250 255 260	
ttt tac ggc gac cgc agc ggc cag aag tac gaa cag aaa ttg ctt ttc	931
Phe Tyr Gly Asp Arg Ser Gly Gln Lys Tyr Glu Gln Lys Leu Leu Phe	
265 270 275	
gac gcc tcc ctc gac gat gca gct gtc tct aag ctg gtt gca cag gcc	979
Asp Ala Ser Leu Asp Asp Ala Val Ser Lys Leu Val Ala Gln Ala	
280 285 290	
gaa agc atc cct gat gga gat gtg agc aaa atc gca aat acc gta ggt	1027
Glu Ser Ile Pro Asp Gly Asp Val Ser Lys Ile Ala Asn Thr Val Gly	
295 300 305	
att gtg atc ggt gcg gta ttg gct ctc gtg ggc ctg gcc ggg tgt ttt	1075
Ile Val Ile Gly Ala Val Leu Ala Leu Val Gly Leu Ala Gly Cys Phe	
310 315 320 325	
ggg gcg ttt ggg aag aaa cgt cga gaa gct taacctgctg ttcaaataga	1125
Gly Ala Phe Gly Lys Lys Arg Arg Glu Ala	
330 335	
ttt	1128

<210> 2184

<211> 335

<212> PRF

<213> *Corynebacterium glutamicum*

<400> 2184

Met	Pro	Gly	Gly	Cys	Ser	Gly	Asn	Ile	Val	Arg	Met	Leu	Pro	Lys	Ser
1				5					10					15	
Arg	Ile	Phe	Ser	Ala	Ile	Leu	Leu	Gly	Ile	Gly	Val	Ala	Leu	Val	Val
			20					25					30		
Trp	Gly	Leu	Val	Ala	Pro	Arg	Phe	Val	His	Ala	Asp	Gly	Arg	Leu	Pro
		35					40					45			
Leu	Asp	Leu	Glu	Ala	Thr	Thr	Tyr	Val	Leu	His	Asp	Ser	Asp	Ala	Gln
	50					55					60				
Thr	Thr	Ile	Asn	Ser	Asp	Pro	Leu	Ala	Gly	Val	Val	Thr	Thr	Pro	Val
	65				70					75					80
Thr	Arg	Gln	Leu	His	Phe	Glu	Val	Met	Asp	Pro	Ala	Ser	Ala	Asp	Asp
				85					90					95	
Ala	Thr	Ile	Arg	Ile	Gly	Asp	Ser	Met	Leu	Arg	Gly	Asn	Pro	Asp	Thr
			100					105					110		
Gln	Gly	Phe	Glu	Gln	Glu	Arg	Leu	Leu	Ser	Ala	Thr	Val	Ser	Ser	Phe
		115					120					125			
Arg	Ile	Asp	Arg	Thr	Ser	Gly	Glu	Val	Leu	Ser	Asp	Ile	Ala	Leu	Thr
	130					135					140				
Asn	Gln	Leu	Ala	Ser	Pro	Thr	Val	Gln	Tyr	Ser	Val	Asp	Gly	Ile	Trp
	145			150						155				160	
Leu	Lys	Phe	Pro	Thr	Asp	Ala	Gln	Glu	Thr	Thr	Tyr	Asn	Val	Val	Asp
			165						170					175	
Pro	Val	Leu	Arg	Ser	Ala	Leu	Pro	Ala	Asp	Phe	Val	Glu	Ser	Thr	Glu
		180						185					190		
Ile	Asp	Gly	Arg	Glu	Val	Leu	His	Tyr	Arg	Gln	Val	Ile	Asp	Asn	Val
	195					200						205			
Asn	Val	Ala	Glu	Tyr	Phe	Ala	Asp	Ala	Asn	Asn	Thr	Thr	Thr	Leu	Thr
	210					215					220				
Lys	Glu	Asp	Gly	Gly	Thr	Thr	Thr	Gly	Tyr	Phe	Tyr	His	Asn	Val	Thr
	225				230					235				240	
Arg	Asp	Phe	Trp	Val	Asp	Gln	Arg	Thr	Gly	Leu	Val	Val	Asp	Leu	Ala
			245					250						255	
Glu	Asn	Ile	Asp	Asp	Phe	Tyr	Gly	Asp	Arg	Ser	Gly	Gln	Lys	Tyr	Glu
		260					265						270		
Gln	Lys	Leu	Leu	Phe	Asp	Ala	Ser	Leu	Asp	Asp	Ala	Ala	Val	Ser	Lys
	275						280						285		

Leu Val Ala Gln Ala Glu Ser Ile Pro Asp Gly Asp Val Ser Lys Ile
290 295 300

Ala Asn Thr Val Gly Ile Val Ile Gly Ala Val Leu Ala Leu Val Gly
305 310 315 320

Leu Ala Gly Cys Phe Gly Ala Phe Gly Lys Lys Arg Arg Glu Ala
325 330 335

<210> 2185

<211> 726

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(703)

<223> RXA01336

<400> 2185

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agcgcaagcc gttttagcag atcacaggta gaattgcgac atg gag ccc acc gta 115
Met Glu Pro Thr Val 5

aaa gcc agc gcg cgc cac acc atc cac gtc acc gcc gac acc tgg cgc 163
Lys Ala Ser Ala Arg His Thr Ile His Val Thr Ala Asp Thr Trp Arg 10 15 20

atc cgc ctg agt gcc tca gcc cac tca cac ccc aac gac gcg tac gcg 211
Ile Arg Leu Ser Ala Ser Ala His Ser His Pro Asn Asp Ala Tyr Ala 25 30 35

cgc cgg gct acg gca att tcc gcc ata ggc agc gtg ctt atc gac gtc 259
Arg Arg Ala Thr Ala Ile Ser Ala Ile Gly Ser Val Leu Ile Asp Val 40 45 50

ccc ctc caa ggc gaa cgc atc tct gaa tcc act gca tac gac gcc caa 307
Pro Leu Gln Gly Glu Arg Ile Ser Glu Ser Thr Ala Tyr Asp Gly Gln 55 60 65

atc aac gcc gac tgg aac gca gaa gtc acc ggc acc gat gtg aac atc 355
Ile Asn Ala Asp Trp Asn Ala Glu Val Thr Gly Thr Asp Val Asn Ile 70 75 80 85

gca cgc gac atc atc tcc cgg ctc gca gcg gtg cca gac gtt caa gtc 403
Ala Arg Asp Ile Ile Ser Arg Leu Ala Ala Val Pro Asp Val Gln Val 90 95 100

gac ggc cgg ttg tgg tcc ttg agt gac agt ttg gct gca gag gct gct 451
Asp Gly Pro Leu Trp Ser Leu Ser Asp Ser Leu Ala Ala Glu Ala Ala 105 110 115

gtg gag gca ttg caa ggt gct gcc gac act gcg cgg aac acc gcg acc 499
Val Glu Ala Leu Gln Gly Ala Ala Asp Thr Ala Arg Asn Thr Ala Thr 120 125 130

gcc atc gca gaa tcc ctc gcc ggg cag cta ggt gca ctt ctc tac gca 547
Ala Ile Ala Glu Ser Leu Gly Gly Gln Leu Gly Ala Leu Leu Tyr Ala

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135              140              145
aca acc gac acc cac agc tcc aca ccg ata cca gca cgc gca gaa atg 595
Thr Thr Asp Thr His Ser Ser Thr Pro Ile Pro Ala Arg Ala Glu Met
150              155              160
atg gca gca aaa gcc tcc ata cca ccg cgc aca ctc gac cta gaa ctc 643
Met Ala Ala Lys Ala Ser Ile Pro Pro Arg Thr Leu Asp Leu Glu Leu
170              175              180
gcc ccc tct gac atc gaa gtc acc aaa gaa atc gcc gtg acc ttt gaa 691
Ala Pro Ser Asp Ile Glu Val Thr Lys Glu Ile Ala Val Thr Phe Glu
185              190              195
ttc ctt gca ggc taaaccgca tttgtattt cgg 726
Phe Leu Ala Gly
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<210> 2186
<211> 201
<212> PRT
<213> Corynebacterium glutamicum

<400> 2186
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Asn Asp Ala Tyr Ala Arg Arg Ala Thr Ala Ile Ser Ala Ile Gly Ser
35 40 45
Val Leu Ile Asp Val Pro Leu Gln Gly Glu Arg Ile Ser Glu Ser Thr
50 55 60
Ala Tyr Asp Gly Gln Ile Asn Ala Asp Trp Asn Ala Glu Val Thr Gly
65 70 75 80
Thr Asp Val Asn Ile Ala Arg Asp Ile Ile Ser Arg Leu Ala Ala Val
85 90 95
Pro Asp Val Gln Val Asp Gly Pro Leu Trp Ser Leu Ser Asp Ser Leu
100 105 110
Ala Ala Glu Ala Ala Val Glu Ala Leu Gln Gly Ala Ala Asp Thr Ala
115 120 125
Arg Asn Thr Ala Thr Ala Ile Ala Glu Ser Leu Gly Gly Gln Leu Gly
130 135 140
Ala Leu Leu Tyr Ala Thr Thr Asp Thr His Ser Ser Thr Pro Ile Pro
145 150 155 160
Ala Arg Ala Glu Met Met Ala Ala Lys Ala Ser Ile Pro Pro Arg Thr
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Leu Asp Leu Glu Leu Ala Pro Ser Asp Ile Glu Val Thr Lys Glu Ile
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Ala Val Thr Phe Glu Phe Leu Ala Gly
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<210> 2187

<211> 1635

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1612)

<223> RXA01342

<400> 2187

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Met Glu Thr Pro Thr
1 5

caa gac atg gat gtc cgc tgg tta tac acc caa agc cag ctc aaa ctc 163
Gln Asp Met Asp Val Arg Trp Leu Tyr Thr Gln Ser Gln Leu Lys Leu
10 15 20

cgc gaa att ctc ccc aca aac aaa acc ttc gat gtc atc caa atc agc 211
Arg Glu Ile Leu Pro Thr Asn Lys Thr Phe Asp Val Ile Gln Ile Ser
25 30 35

gaa ctc gtt gac ccc acc gac ttc atc agg ccc aac agc gtg gtc tta 259
Glu Leu Val Asp Pro Thr Asp Phe Ile Arg Pro Asn Ser Val Val Leu
40 45 50

tcc gtt ggc atc gcc ttc gca gaa acg ccc gac ggg ctt cgc gat tgg 307
Ser Val Gly Ile Ala Phe Ala Glu Thr Pro Asp Gly Leu Arg Asp Trp
55 60 65

gca cac cga ctc gcc gac gca ggg gtc atc gcg atc ggg ttc ggc tcc 355
Ala His Arg Leu Ala Asp Ala Gly Val Ile Ala Ile Gly Phe Gly Ser
70 75 80 85

ggc ctc acc ttc cca cag gtt ccg cag gcg ctt atc gac gcc tcc ctc 403
Gly Leu Thr Phe Pro Gln Val Pro Gln Ala Leu Ile Asp Ala Ser Leu
90 95 100

cac ctt ggc ctc ggc ctc ttt gaa gtc ccc cgt gaa att cca ttt atc 451
His Leu Gly Leu Gly Leu Phe Glu Val Pro Arg Glu Ile Pro Phe Ile
105 110 115

tcg atc acc tcc agc gtg cgt gat gag caa acc cgc cgt gcc ggc cgc 499
Ser Ile Thr Ser Ser Val Arg Asp Glu Gln Thr Arg Arg Ala Gly Arg
120 125 130

ctg caa caa gaa ctc ctc ctg gaa cag gaa cgg ctt aac tcc atc gcc 547
Leu Gln Gln Glu Leu Leu Leu Glu Gln Glu Arg Leu Asn Ser Ile Ala
135 140 145

atc tcc ggt ggc atc gaa gcc ctg tgc cgt gct gcc gcc gac tat ttg 595
Ile Ser Gly Gly Ile Glu Ala Leu Cys Arg Ala Ala Ala Asp Tyr Leu
150 155 160 165

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Gly Gly Ala Val Thr Ile Val Asp Ser Asp Gly Arg Val Ala Cys Ser	
170 175 180	
att acc acc gat gac cta gac gca ctc ccc caa gct gtc tgc cgc ctg	691
Ile Thr Thr Asp Asp Leu Asp Ala Leu Pro Gln Ala Val Ser Arg Leu	
185 190 195	
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Asn Gly Ser Ser Gln Ala Leu Thr Asp Ala Thr Asn Phe Gly Phe Ile	
200 205 210	
cac cgc atg acc cgc tac ggc gac cgc cac cac gtg ctc tca gtc ctt	787
His Arg Met Thr Arg Tyr Gly Asp Arg His His Val Leu Ser Val Leu	
215 220 225	
atg ccc acc cgc ccc aca gac caa cac cgc gcg ctg atc aga cac tgc	835
Met Pro Thr Arg Pro Thr Asp Gln His Arg Ala Leu Ile Arg His Cys	
230 235 240 245	
gca ggc ctt gcc gat att ttg ctc caa cgc ccc gaa gcc atg cgc gac	883
Ala Gly Leu Ala Asp Ile Leu Leu Gln Arg Pro Glu Ala Met Arg Asp	
250 255 260	
cga gaa atc gaa gtg cga tca ctt gcc atg tca cta ctt ctg ggt cga	931
Arg Glu Ile Glu Val Arg Ser Leu Ala Met Ser Leu Leu Leu Gly Arg	
265 270 275	
agc gac gac ctg gcc acc att cac cgc gtg ttc gct gac atc act gat	979
Ser Asp Asp Leu Ala Thr Ile His Arg Val Phe Ala Asp Ile Thr Asp	
280 285 290	
gct tcc gga aat atc cgc ccc atc ctc atc acc ggc aac aca ccc caa	1027
Ala Ser Gly Asn Ile Arg Pro Ile Leu Ile Thr Gly Asn Thr Pro Gln	
295 300 305	
tca gta cga aaa gca ctc tcc agt gtc gcc acc gca ctg tac aaa cag	1075
Ser Val Arg Lys Ala Leu Ser Ser Val Ala Thr Ala Leu Tyr Lys Gln	
310 315 320 325	
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Glu Arg Ala Leu Ala His Leu Arg Leu Ala Glu Ser Thr Glu Leu Leu	
330 335 340	
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Phe Leu Arg Gly Ser Arg Ser Val His Asn Ile Val Gln Leu Phe Gly	
345 350 355	
act gcc gca agc gga gtt cgc ctc tgc att ggt ctg ccc acc cga gcg	1219
Thr Ala Ala Ser Gly Val Arg Leu Cys Ile Gly Leu Pro Thr Arg Ala	
360 365 370	
gaa aac atc gat aag aaa ctc atc cgc gaa ctc act gcc acc gca aaa	1267
Glu Asn Ile Asp Lys Lys Leu Ile Arg Glu Leu Thr Ala Thr Ala Lys	
375 380 385	
acc cta caa ctt gga acc cac gcc gaa ccc cgt gac gcc acc ttg ctg	1315
Thr Leu Gln Leu Gly Thr His Ala Glu Pro Arg Asp Gly Thr Leu Leu	
390 395 400 405	
tgg ctc caa aac ccc gag ctg cgc aaa atc ctt aag atc cga tcc cgc	1363

Trp Leu Gln Asn Pro Glu Leu Arg Lys Ile Leu Lys Ile Arg Ser Arg
 410 415 420

gac acc tac gac cgt ctc ctc gac cac gac cgc acc aac aac acc gag 1411
 Asp Thr Tyr Asp Arg Leu Leu Asp His Asp Arg Thr Asn Asn Thr Glu
 425 430 435

ctc gcc ccc acc ttg gtg tct ttt act cag cac agc gga cat ata ggc 1459
 Leu Ala Pro Thr Leu Val Ser Phe Thr Gln His Ser Gly His Ile Gly
 440 445 450

gac acc gcc aaa gaa ctg ggc atc cac cgc cac acc gtg cgc acc cgc 1507
 Asp Thr Ala Lys Glu Leu Gly Ile His Arg His Thr Val Arg Thr Arg
 455 460 465

atg atc cgc att gaa gag atc tgc gaa atc gac ctc aat gat cca ctg 1555
 Met Ile Arg Ile Glu Glu Ile Cys Glu Ile Asp Leu Asn Asp Pro Leu
 470 475 480 485

acc aga gcg gag ctg ctc tta gtg atc gca acg aag gag gga gac gtc 1603
 Thr Arg Ala Glu Leu Leu Val Ile Ala Thr Lys Glu Gly Asp Val
 490 495 500

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 Glu Lys Gln

<210> 2188
 <211> 504
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2188
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Val Ile Gln Ile Ser Glu Leu Val Asp Pro Thr Asp Phe Ile Arg Pro
 35 40 45

Asn Ser Val Val Leu Ser Val Gly Ile Ala Phe Ala Glu Thr Pro Asp
 50 55 60

Gly Leu Arg Asp Trp Ala His Arg Leu Ala Asp Ala Gly Val Ile Ala
 65 70 75 80

Ile Gly Phe Gly Ser Gly Leu Thr Phe Pro Gln Val Pro Gln Ala Leu
 85 90 95

Ile Asp Ala Ser Leu His Leu Gly Leu Gly Leu Phe Glu Val Pro Arg
 100 105 110

Glu Ile Pro Phe Ile Ser Ile Thr Ser Ser Val Arg Asp Glu Gln Thr
 115 120 125

Arg Arg Ala Gly Arg Leu Gln Gln Glu Leu Leu Leu Glu Gln Glu Arg
 130 135 140

Leu Asn Ser Ile Ala Ile Ser Gly Gly Ile Glu Ala Leu Cys Arg Ala
 145 150 155 160
 Ala Ala Asp Tyr Leu Gly Gly Ala Val Thr Ile Val Asp Ser Asp Gly
 165 170 175
 Arg Val Ala Cys Ser Ile Thr Thr Asp Asp Leu Asp Ala Leu Pro Gln
 180 185 190
 Ala Val Ser Arg Leu Asn Gly Ser Ser Gln Ala Leu Thr Asp Ala Thr
 195 200 205
 Asn Phe Gly Phe Ile His Arg Met Thr Arg Tyr Gly Asp Arg His His
 210 215 220
 Val Leu Ser Val Leu Met Pro Thr Arg Pro Thr Asp Gln His Arg Ala
 225 230 235 240
 Leu Ile Arg His Cys Ala Gly Leu Ala Asp Ile Leu Leu Gln Arg Pro
 245 250 255
 Glu Ala Met Arg Asp Arg Glu Ile Glu Val Arg Ser Leu Ala Met Ser
 260 265 270
 Leu Leu Leu Gly Arg Ser Asp Asp Leu Ala Thr Ile His Arg Val Phe
 275 280 285
 Ala Asp Ile Thr Asp Ala Ser Gly Asn Ile Arg Pro Ile Leu Ile Thr
 290 295 300
 Gly Asn Thr Pro Gln Ser Val Arg Lys Ala Leu Ser Ser Val Ala Thr
 305 310 315 320
 Ala Leu Tyr Lys Gln Glu Arg Ala Leu Ala His Leu Arg Leu Ala Glu
 325 330 335
 Ser Thr Glu Leu Leu Phe Leu Arg Gly Ser Arg Ser Val His Asn Ile
 340 345 350
 Val Gln Leu Phe Gly Thr Ala Ala Ser Gly Val Arg Leu Cys Ile Gly
 355 360 365
 Leu Pro Thr Arg Ala Glu Asn Ile Asp Lys Lys Leu Ile Arg Glu Leu
 370 375 380
 Thr Ala Thr Ala Lys Thr Leu Gln Leu Gly Thr His Ala Glu Pro Arg
 385 390 395 400
 Asp Gly Thr Leu Leu Trp Leu Gln Asn Pro Glu Leu Arg Lys Ile Leu
 405 410 415
 Lys Ile Arg Ser Arg Asp Thr Tyr Asp Arg Leu Leu Asp His Asp Arg
 420 425 430
 Thr Asn Asn Thr Glu Leu Ala Pro Thr Leu Val Ser Phe Thr Gln His
 435 440 445
 Ser Gly His Ile Gly Asp Thr Ala Lys Glu Leu Gly Ile His Arg His
 450 455 460
 Thr Val Arg Thr Arg Met Ile Arg Ile Glu Glu Ile Cys Glu Ile Asp

gcg ttt aaa gtg ctt gcc tat gag ggg cag att gca cgc gct cag gca 547
Ala Phe Lys Val Leu Ala Tyr Glu Gly Gln Ile Ala Arg Ala Gln Ala
135 140 145

gag att gaa tgg gcg gaa aag ggc ttg aaa cta ctc gat acc ctt 592
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<210> 2190

<211> 164

<212> PRT

<213> Corynebacterium glutamicum

<400> 2190

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 20 25 30

Gly Ser Lys Gly Ala Thr Lys Thr Glu Tyr Ala Leu Ser Glu Lys Gly
 35 40 45

Trp Glu Ala Leu Arg Lys Ala Trp Tyr Glu Pro Val Thr Tyr Gly Pro
 50 55 60

Thr Arg Asp Pro Ala Arg Leu Lys Ala Ala Tyr Phe Glu Val Gly Thr
 65 70 75 80

Asn Gly Asp Ala Arg Arg His Leu Arg Ala His Ile Ala His Phe Glu
 85 90 95

Gln Gln Lys Ile Gln Ser Glu Ser Met Ile Asp Glu Leu Lys Ala Lys
 100 105 110

Thr His Pro Thr Leu Ala Arg Arg Leu Glu Arg Ser Pro Lys Lys Glu
 115 120 125

His Glu Arg Ile Val Ala Phe Lys Val Leu Ala Tyr Glu Gly Gln Ile
 130 135 140

Ala Arg Ala Gln Ala Glu Ile Glu Trp Ala Glu Lys Gly Leu Lys Leu
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Leu Asp Thr Leu

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<211> 900

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(877)

<223> RXA01349

<400> 2191

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aattcacgtt ttctcggttac ccgaaaggaa ttgatcgatt atg gcg aca tca cgt 115
Met Ala Thr Ser Arg
1 5

cga gat gcc gaa aac ata gac cag gcc ggt agc gaa ttc att gaa tct 163
Arg Asp Ala Glu Asn Ile Asp Gln Ala Gly Ser Glu Phe Ile Glu Ser
10 15 20

gat tca gga cac acc gca acc cct gaa gag gta gta gcc acc gct ctg 211
Asp Ser Gly His Thr Ala Thr Pro Glu Val Val Ala Thr Ala Leu
25 30 35

aca ttt ttt gca gag gat ggt ttt agc gaa acc aaa ttg gag aaa atc 259
Thr Phe Phe Ala Glu Asp Gly Phe Ser Glu Thr Lys Leu Glu Lys Ile
40 45 50

gcg aag gca tct ggc atg tcc aag cgc atg atc cac tat cac ttt ggc 307
Ala Lys Ala Ser Gly Met Ser Lys Arg Met Ile His Tyr His Phe Gly
55 60 65

gat aag aaa ggc ctg tac atc aag gct gtt tcc tac gcg ttg cga ttg 355
Asp Lys Lys Gly Leu Tyr Ile Lys Ala Val Ser Tyr Ala Leu Arg Leu
70 75 80 85

ctg cgc cca gag gct gaa gcg atg caa ctt gat tcc gcg gta cca gtt 403
Leu Arg Pro Glu Ala Glu Ala Met Gln Leu Asp Ser Ala Val Pro Val
90 95 100

gat ggt gtc cgc aaa atc gtc gag gct tta tat acc tgc atc acc aag 451
Asp Gly Val Arg Lys Ile Val Glu Ala Leu Tyr Thr Cys Ile Thr Lys
105 110 115

cac cca gaa gca gtg cgc ctg cta ttg atg gaa aac ctg cat agc caa 499
His Pro Glu Ala Val Arg Leu Leu Leu Met Glu Asn Leu His Ser Gln
120 125 130

gac agc gtg gat tcc acc gcg gca tat tcc gat gaa tcc aat gtg ctg 547
Asp Ser Val Asp Ser Thr Ala Ala Tyr Ser Asp Glu Ser Asn Val Leu
135 140 145

ctc aac ctg gat aag ctg ctc atg ctt ggc cag gat gcc ggc gcc ttc 595
Leu Asn Leu Asp Lys Leu Leu Met Leu Gly Gln Asp Ala Gly Ala Phe
150 155 160 165

cgt cct gga atc tcc gca gaa gac gta ctg gtt ctt att agc tcc ctg 643
Arg Pro Gly Ile Ser Ala Glu Asp Val Leu Val Leu Ile Ser Ser Leu
170 175 180

gcc tac ttc cgc gta tcc aac aag gtc acg ttg aag aac ctc tac tcc 691
Ala Tyr Phe Arg Val Ser Asn Lys Val Thr Leu Lys Asn Leu Tyr Ser
185 190 195

ctt gat ttg gaa tca gag gcc aat att gaa ggc atg aag cgc atc gtc 739
Leu Asp Leu Glu Ser Glu Ala Asn Ile Glu Gly Met Lys Arg Ile Val
200 205 210

gtt gac acg gtg ctg gca ttc ttg acc tca aat att caa aat tct ggc 787
Val Asp Thr Val Leu Ala Phe Leu Thr Ser Asn Ile Gln Asn Ser Gly
215 220 225

aac tcc agc tac ctg gtt gtt ggt ggc aag act gca gaa cca gaa act 835

Asn Ser Ser Tyr Leu Val Val Gly Gly Lys Thr Ala Glu Pro Glu Thr
230 235 240 245

gat gac agc gtc tac agc ttt gat acg gac gtg ttc gaa aac 877
Asp Asp Ser Val Tyr Ser Phe Asp Thr Asp Val Phe Glu Asn
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taaagggtat cgagtagttt caa 900

<210> 2192

<211> 259

<212> PRT

<213> Corynebacterium glutamicum

<400> 2192

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Val Ala Thr Ala Leu Thr Phe Phe Ala Glu Asp Gly Phe Ser Glu Thr
35 40 45

Lys Leu Glu Lys Ile Ala Lys Ala Ser Gly Met Ser Lys Arg Met Ile
50 55 60

His Tyr His Phe Gly Asp Lys Lys Gly Leu Tyr Ile Lys Ala Val Ser
65 70 75 80

Tyr Ala Leu Arg Leu Leu Arg Pro Glu Ala Glu Ala Met Gln Leu Asp
85 90 95

Ser Ala Val Pro Val Asp Gly Val Arg Lys Ile Val Glu Ala Leu Tyr
100 105 110

Thr Cys Ile Thr Lys His Pro Glu Ala Val Arg Leu Leu Met Glu
115 120 125

Asn Leu His Ser Gln Asp Ser Val Asp Ser Thr Ala Ala Tyr Ser Asp
130 135 140

Glu Ser Asn Val Leu Leu Asn Leu Asp Lys Leu Met Leu Gly Gln
145 150 155 160

Asp Ala Gly Ala Phe Arg Pro Gly Ile Ser Glu Asp Val Leu Val
165 170 175

Leu Ile Ser Ser Leu Ala Tyr Phe Arg Val Ser Asn Lys Val Thr Leu
180 185 190

Lys Asn Leu Tyr Ser Leu Asp Leu Glu Ser Glu Ala Asn Ile Glu Gly
195 200 205

Met Lys Arg Ile Val Val Asp Thr Val Leu Ala Phe Leu Thr Ser Asn
210 215 220

Ile Gln Asn Ser Gly Asn Ser Ser Tyr Leu Val Val Gly Gly Lys Thr
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Ala Glu Pro Glu Thr Asp Asp Ser Val Tyr Ser Phe Asp Thr Asp Val
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Phe Glu Asn

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 <211> 426
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(403)
 <223> RXA01357

<400> 2193
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ggctacacgc tgcagataat gacacgacgg aagggtggagc atg agc gct gaa gaa 115
 Met Ser Ala Glu Glu
 1 5

ctc gac aac tac gaa gca gag gtt gaa ctc tct ctt tac cgc gaa tac 163
 Leu Asp Asn Tyr Glu Ala Glu Val Glu Leu Ser Leu Tyr Arg Glu Tyr
 10 15 20

cgc gac gta gtc agc cag ttt tcc tat gtt gta gaa act gaa cgt cgc 211
 Arg Asp Val Val Ser Gln Phe Ser Tyr Val Val Glu Thr Glu Arg Arg
 25 30 35

ttc tac tta gca aat gca gtg cag ctt att cca cac aac agc gga aac 259
 Phe Tyr Leu Ala Asn Ala Val Gln Leu Ile Pro His Asn Ser Gly Asn
 40 45 50

gat gtc tac tac gaa gtc cgc atg tct gac gcc tgg gta tgg gac atg 307
 Asp Val Tyr Tyr Glu Val Arg Met Ser Asp Ala Trp Val Trp Asp Met
 55 60 65

tac cgc tca gca cgc ttc gtt cgc tac gtc cga gtg atc acc tac aag 355
 Tyr Arg Ser Ala Arg Phe Val Arg Tyr Val Arg Val Ile Thr Tyr Lys
 70 75 80 85

gac gtc aac atc gaa gaa tta gat aag cct gac atc atc atg cct gag 403
 Asp Val Asn Ile Glu Glu Leu Asp Lys Pro Asp Ile Ile Met Pro Glu
 90 95 100

tagttcttag gtttaaatac gct 426

<210> 2194
 <211> 101
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 <213> Corynebacterium glutamicum

<400> 2194
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	20		25		30	
Glu Thr Glu Arg Arg Phe Tyr Leu Ala Asn Ala Val Gln Leu Ile Pro	35	40	45			
His Asn Ser Gly Asn Asp Val Tyr Tyr Glu Val Arg Met Ser Asp Ala	50	55	60			
Trp Val Trp Asp Met Tyr Arg Ser Ala Arg Phe Val Arg Tyr Val Arg	65	70	75	80		
Val Ile Thr Tyr Lys Asp Val Asn Ile Glu Glu Leu Asp Lys Pro Asp	85	90	95			
Ile Ile Met Pro Glu	100					

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<211> 1305

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1282)

<223> RXA01359

<400> 2195

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ccatggagct tgcgggcact acatacagtg aggtagcagc atg att gac tcc cgc	115
Met Ile Asp Ser Arg	
1 5	

ttg ctg gca tgg gcg tat ctc tca aaa gtg gtg gag ggt ccc aat gca	163
Leu Leu Ala Trp Ala Tyr Leu Ser Lys Val Val Glu Gly Pro Asn Ala	
10 15 20	

cac ctg caa aag ctc ctg aaa gaa ggt cat gat gta gag cgg atc gca	211
His Leu Gln Lys Leu Leu Lys Glu Gly His Asp Val Glu Arg Ile Ala	
25 30 35	

ttt ggt att aaa cac cgc gaa gag tgg att ggc gaa ggt ctg ctg aaa	259
Phe Gly Ile Lys His Arg Glu Glu Trp Ile Gly Glu Gly Leu Leu Lys	
40 45 50	

aac acc gat tcc cgg tac tgc att gat acc gcg caa act gat ctg gaa	307
Asn Thr Asp Ser Arg Tyr Ser Ile Asp Thr Ala Gln Thr Asp Leu Glu	
55 60 65	

act atc gcc aaa ctc ggt ggg cgg ctc atc aca cct gaa gac gac gaa	355
Thr Ile Ala Lys Leu Gly Gly Arg Leu Ile Thr Pro Glu Asp Asp Glu	
70 75 80 85	

tgg cgg atg gaa gaa tta gac cat gct ttt gga ttt gcc gct tct ggc	403
Trp Pro Met Glu Glu Leu Asp His Ala Phe Gly Phe Ala Ala Ser Gly	
90 95 100	

atg agt gat cat gtg cgt acc tat caa gat gat gcg ctg cca cgg cat	451
Met Ser Asp His Val Arg Thr Tyr Gln Asp Asp Ala Leu Pro Pro His	

	105	110	115	
	gcg ttg tgg att agg gga gga aat ctc aga aca ctc agt gca cag tcc			499
	Ala Leu Trp Ile Arg Gly Gly Asn Leu Arg Thr Leu Ser Ala Gln Ser			
	120	125	130	
	gtc aca ctc gtg ggc acc agg gca ata agc caa tat ggc acg gaa gta			547
	Val Thr Leu Val Gly Thr Arg Ala Ile Ser Gln Tyr Gly Thr Glu Val			
	135	140	145	
	act cgg gaa ttc acc caa aac ctt gtg tct cat cag tgg aca atc atc			595
	Thr Arg Glu Phe Thr Gln Asn Leu Val Ser His Gln Trp Thr Ile Ile			
	150	155	160	165
	tca ggt ggt gcc ttg gga gtt gat agc gtc gcc cat agt gaa gcc gta			643
	Ser Gly Gly Ala Leu Gly Val Asp Ser Val Ala His Ser Glu Ala Val			
	170	175	180	
	cgt gca caa ggc tcc acc atc gcg atc gca gca tgc gga ttg gat cgc			691
	Arg Ala Gln Gly Ser Thr Ile Ala Ile Ala Ala Cys Gly Leu Asp Arg			
	185	190	195	
	tcg tac ccc agc cac aat cga gat ctg ttc aac cag att gcc aaa tcc			739
	Ser Tyr Pro Ser His Asn Arg Asp Leu Phe Asn Gln Ile Ala Lys Ser			
	200	205	210	
	gga aag ggg gcg ttg gtg agt gaa tat cca ccg gga act cca cct caa			787
	Gly Lys Gly Ala Leu Val Ser Glu Tyr Pro Pro Gly Thr Pro Pro Gln			
	215	220	225	
	cgc cac cgc ttt ctc act cgc aat cgt ctc gtt gct gct cta tct caa			835
	Arg His Arg Phe Leu Thr Arg Asn Arg Leu Val Ala Ala Leu Ser Gln			
	230	235	240	245
	gga act gtc gtg gtg gag gca gcc tgg agg tca ggc gcg cta aac act			883
	Gly Thr Val Val Val Glu Ala Ala Trp Arg Ser Gly Ala Leu Asn Thr			
	250	255	260	
	ttg agc tgg tgt gct ggt tta ggc agg att gct atg gcg gtc cct ggg			931
	Leu Ser Trp Cys Ala Gly Leu Gly Arg Ile Ala Met Ala Val Pro Gly			
	265	270	275	
	ccg gta aat act gct gga tca ctt ggg tgc cac gaa agg att cga aac			979
	Pro Val Asn Thr Ala Gly Ser Leu Gly Cys His Glu Arg Ile Arg Asn			
	280	285	290	
	ggc agc gca caa atg gtc acc agt gcg gat gac gtt cgg tca ctt ctg			1027
	Gly Ser Ala Gln Met Val Thr Ser Ala Asp Asp Val Arg Ser Leu Leu			
	295	300	305	
	ggt gca gtg ggt gca atg gat agc caa act cag tat gaa tta aac ttc			1075
	Gly Ala Val Gly Ala Met Asp Ser Gln Thr Gln Tyr Glu Leu Asn Phe			
	310	315	320	325
	gcg gcc act cca gta cag ggt tta acc aga aat gag ctg cga gtt ttt			1123
	Ala Ala Thr Pro Val Gln Gly Leu Thr Arg Asn Glu Leu Arg Val Phe			
	330	335	340	
	gat gcg tta gac gac cga gga gag ggg agg gaa gcg gcg agt atc gct			1171
	Asp Ala Leu Asp Asp Arg Gly Glu Gly Arg Glu Ala Ala Ser Ile Ala			
	345	350	355	

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acc gaa gcc ggg ttg acc ttg cag tta aca att ttc ctt ctc att gca 1219
Thr Glu Ala Gly Leu Thr Leu Gln Leu Thr Ile Phe Leu Leu Ile Ala
      360                      365                      370

ttg aac aag cgc gga atc gtg aaa cgc gac gga act gct tgg tcg aga 1267
Leu Asn Lys Arg Gly Ile Val Lys Arg Asp Gly Thr Ala Trp Ser Arg
      375                      380                      385

aat gcg gaa atg cca taaaacctgg gggttatata aaa 1305
Asn Ala Glu Met Pro
390

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<210> 2196

<211> 394

<212> PRT

<213> Corynebacterium glutamicum

<400> 2196

```

Met Ile Asp Ser Arg Leu Leu Ala Trp Ala Tyr Leu Ser Lys Val Val
  1              5              10              15

Glu Gly Pro Asn Ala His Leu Gln Lys Leu Leu Lys Glu Gly His Asp
      20              25              30

Val Glu Arg Ile Ala Phe Gly Ile Lys His Arg Glu Glu Trp Ile Gly
      35              40              45

Glu Gly Leu Leu Lys Asn Thr Asp Ser Arg Tyr Ser Ile Asp Thr Ala
      50              55              60

Gln Thr Asp Leu Glu Thr Ile Ala Lys Leu Gly Gly Arg Leu Ile Thr
      65              70              75              80

Pro Glu Asp Asp Glu Trp Pro Met Glu Glu Leu Asp His Ala Phe Gly
      85              90              95

Phe Ala Ala Ser Gly Met Ser Asp His Val Arg Thr Tyr Gln Asp Asp
      100             105             110

Ala Leu Pro Pro His Ala Leu Trp Ile Arg Gly Gly Asn Leu Arg Thr
      115             120             125

Leu Ser Ala Gln Ser Val Thr Leu Val Gly Thr Arg Ala Ile Ser Gln
      130             135             140

Tyr Gly Thr Glu Val Thr Arg Glu Phe Thr Gln Asn Leu Val Ser His
      145             150             155             160

Gln Trp Thr Ile Ile Ser Gly Gly Ala Leu Gly Val Asp Ser Val Ala
      165             170             175

His Ser Glu Ala Val Arg Ala Gln Gly Ser Thr Ile Ala Ile Ala Ala
      180             185             190

Cys Gly Leu Asp Arg Ser Tyr Pro Ser His Asn Arg Asp Leu Phe Asn
      195             200             205

Gln Ile Ala Lys Ser Gly Lys Gly Ala Leu Val Ser Glu Tyr Pro Pro
      210             215             220

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Gly Thr Pro Pro Gln Arg His Arg Phe Leu Thr Arg Asn Arg Leu Val
225 230 235 240

Ala Ala Leu Ser Gln Gly Thr Val Val Val Glu Ala Ala Trp Arg Ser
245 250 255

Gly Ala Leu Asn Thr Leu Ser Trp Cys Ala Gly Leu Gly Arg Ile Ala
260 265 270

Met Ala Val Pro Gly Pro Val Asn Thr Ala Gly Ser Leu Gly Cys His
275 280 285

Glu Arg Ile Arg Asn Gly Ser Ala Gln Met Val Thr Ser Ala Asp Asp
290 295 300

Val Arg Ser Leu Leu Gly Ala Val Gly Ala Met Asp Ser Gln Thr Gln
305 310 315 320

Tyr Glu Leu Asn Phe Ala Ala Thr Pro Val Gln Gly Leu Thr Arg Asn
325 330 335

Glu Leu Arg Val Phe Asp Ala Leu Asp Asp Arg Gly Glu Gly Arg Glu
340 345 350

Ala Ala Ser Ile Ala Thr Glu Ala Gly Leu Thr Leu Gln Leu Thr Ile
355 360 365

Phe Leu Leu Ile Ala Leu Asn Lys Arg Gly Ile Val Lys Arg Asp Gly
370 375 380

Thr Ala Trp Ser Arg Asn Ala Glu Met Pro
385 390

<210> 2197

<211> 513

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(490)

<223> RXA01366

<400> 2197

atgcatgaaa acaaattcta tgtgtgttga gctgccaaaa ggggttggcg cgccgatgat 60

gactgtccaa acctaaacca aaggtctaaa ctttggcttc gtg agt cag ttt cgt 115
Val Ser Gln Phe Arg
1 5

cgt tgt tcc cgc cct ggt tgt ggc aag cct gcc gtc gca acc ctc acc 163
Arg Cys Ser Arg Pro Gly Cys Gly Lys Pro Ala Val Ala Thr Leu Thr
10 15 20

tac gca tat tcg gat tcc act gcg gtg gtt ggt cct ttg gcg cct gca 211
Tyr Ala Tyr Ser Asp Ser Thr Ala Val Gly Pro Leu Ala Pro Ala
25 30 35

gca gag ccc cat agt tgg gat ctg tgt gag cat cat gcc gag cgt att 259

Ala Glu Pro His Ser Trp Asp Leu Cys Glu His His Ala Glu Arg Ile
 40 45 50

act gcg ccc ctt ggt tgg gag atg ctg cgg gtg aac gac atc aaa gtc 307
 Thr Ala Pro Leu Gly Trp Glu Met Leu Arg Val Asn Asp Ile Lys Val
 55 60 65

gat gac gat gag gat ctg acg gct ctt gct cag gct gtt cgt gag gct 355
 Asp Asp Asp Glu Asp Leu Thr Ala Leu Ala Gln Ala Val Arg Glu Ala
 70 75 80 85

gga cgc act gtg agt ggt ctg gtt cct gaa gac gaa gtg ggc ggc aac 403
 Gly Arg Thr Val Ser Gly Leu Val Pro Glu Asp Glu Val Gly Gly Asn
 90 95 100

cat ccg gtg aac cgg agt gcg cgg atc gcg gaa cag aag gtt cac cgc 451
 His Pro Val Asn Arg Ser Ala Arg Ile Ala Glu Gln Lys Val His Arg
 105 110 115

agg ggt cat ctc tat gtt gtg cct gat cag gac gaa tca taaggtttgc 500
 Arg Gly His Leu Tyr Val Val Pro Asp Gln Asp Glu Ser
 120 125 130

tattcggatt gga 513

<210> 2198
 <211> 130
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2198
 Val Ser Gln Phe Arg Arg Cys Ser Arg Pro Gly Cys Gly Lys Pro Ala
 1 5 10 15

Val Ala Thr Leu Thr Tyr Ala Tyr Ser Asp Ser Thr Ala Val Val Gly
 20 25 30

Pro Leu Ala Pro Ala Ala Glu Pro His Ser Trp Asp Leu Cys Glu His
 35 40 45

His Ala Glu Arg Ile Thr Ala Pro Leu Gly Trp Glu Met Leu Arg Val
 50 55 60

Asn Asp Ile Lys Val Asp Asp Asp Glu Asp Leu Thr Ala Leu Ala Gln
 65 70 75 80

Ala Val Arg Glu Ala Gly Arg Thr Val Ser Gly Leu Val Pro Glu Asp
 85 90 95

Glu Val Gly Gly Asn His Pro Val Asn Arg Ser Ala Arg Ile Ala Glu
 100 105 110

Gln Lys Val His Arg Arg Gly His Leu Tyr Val Val Pro Asp Gln Asp
 115 120 125

Glu Ser
 130

<210> 2199

<211> 525

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) .. (502)

<223> RXA01367

<400> 2199

cgcgccaacc ccttttggca gctcaacaca catagaattt gttttcatgc atacgagaac 60

tttccgcaat cggcacggac gcggtctcgc cggtccactc atg ccc gtc gaa gtt 115
Met Pro Val Glu Val
1 5

ccc cgc cac gcc tct aga cgc caa gcc ttc gac cgc gca gtc tta gag 163
Pro Arg His Ala Ser Arg Arg Gln Ala Phe Asp Arg Ala Val Leu Glu
10 15 20

gcc tac tcc cct ctt tac ggg att tac caa aaa gag ctc agc aat cta 211
Ala Tyr Ser Pro Leu Tyr Gly Ile Tyr Gln Lys Glu Leu Ser Asn Leu
25 30 35

gac atc gct gtc gat acc gtt cct cgc atg cga ctc agc gcc gac ctt 259
Asp Ile Ala Val Asp Thr Val Pro Arg Met Arg Leu Ser Ala Asp Leu
40 45 50

gcc att ctc ccc gat gaa atc acc gcc gac ggc ccc gtt cca ctt ggt 307
Ala Ile Leu Pro Asp Glu Ile Thr Ala Asp Gly Pro Val Pro Leu Gly
55 60 65

cgc gtc atc cca ccg gcg atc gat acc aag gga aac ccc acg aga gcg 355
Arg Val Ile Pro Pro Ala Ile Asp Thr Lys Gly Asn Pro Thr Arg Ala
70 75 80 85

cgc atc gtt att ttc aga atg ccg atc gag caa cga gtc acc aac gct 403
Arg Ile Val Ile Phe Arg Met Pro Ile Glu Gln Arg Val Thr Asn Ala
90 95 100

gtg gaa cgc cac gag cta ttg act cat gtt ctc acc tct ttg gtg gcg 451
Val Glu Arg His Glu Leu Leu Thr His Val Leu Thr Ser Leu Val Ala
105 110 115

aac tat ctg aat att gat cca cga gac atc gat ccg gga ttc cag gat 499
Asn Tyr Leu Asn Ile Asp Pro Arg Asp Ile Asp Pro Gly Phe Gln Asp
120 125 130

ctc tagcgtggcc ggtgcaccat ggg 525
Leu

<210> 2200

<211> 134

<212> PRT

<213> Corynebacterium glutamicum

<400> 2200

Met Pro Val Glu Val Pro Arg His Ala Ser Arg Arg Gln Ala Phe Asp
1 5 10 15

```

Arg Ala Val Leu Glu Ala Tyr Ser Pro Leu Tyr Gly Ile Tyr Gln Lys
      20                      25                      30
Glu Leu Ser Asn Leu Asp Ile Ala Val Asp Thr Val Pro Arg Met Arg
      35                      40                      45
Leu Ser Ala Asp Leu Ala Ile Leu Pro Asp Glu Ile Thr Ala Asp Gly
      50                      55                      60
Pro Val Pro Leu Gly Arg Val Ile Pro Pro Ala Ile Asp Thr Lys Gly
      65                      70                      75                      80
Asn Pro Thr Arg Ala Arg Ile Val Ile Phe Arg Met Pro Ile Glu Gln
      85                      90                      95
Arg Val Thr Asn Ala Val Glu Arg His Glu Leu Leu Thr His Val Leu
      100                     105                     110
Thr Ser Leu Val Ala Asn Tyr Leu Asn Ile Asp Pro Arg Asp Ile Asp
      115                     120                     125

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Pro Gly Phe Gln Asp Leu
      130

```

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<210> 2201
<211> 474
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(451)
<223> RXA01370

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<400> 2201
ctgtctgaat cgtgtgggcg ttagatgaat tgttataaac cggatgttta acggaattta 60

atacgtgtct tattacgcgg actagaaagg ttttagggac atg ggt gca tgg gac 115
Met Gly Ala Trp Asp
      1                      5

gat gca atc ttg act gag gaa gtc aac gtt gat ttt ctc gac gag atc 163
Asp Ala Ile Leu Thr Glu Glu Val Asn Val Asp Phe Leu Asp Glu Ile
      10                      15                      20

tca gaa tta gat act caa gac att ctt gag gcg ttg gaa gac gca tgt 211
Ser Glu Leu Asp Thr Gln Asp Ile Leu Glu Ala Leu Glu Asp Ala Cys
      25                      30                      35

ttg ctg gtg gtt aac cag gac aac gcc act gaa gac gaa cac ctc aac 259
Leu Leu Val Val Asn Gln Asp Asn Ala Thr Glu Asp Glu His Leu Asn
      40                      45                      50

ggg cag gcg gct gcg acg atc gcg gcc atc atg ttt ggc gct cca tat 307
Gly Gln Ala Ala Ala Thr Ile Ala Ala Ile Met Phe Gly Ala Pro Tyr
      55                      60                      65

tct gcg ggc cag gtg ctg gag aat tac cca ttt atc cgc gaa ctc gtc 355
Ser Ala Gly Gln Val Leu Glu Asn Tyr Pro Phe Ile Arg Glu Leu Val

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70              75              80              85
ggt gag ggc tct gaa gct ctt cgc ggt gct gca gcg cag gtt ttg gaa 403
Gly Glu Gly Ser Glu Ala Leu Arg Gly Ala Ala Ala Gln Val Leu Glu
          90              95              100

gag gca gat gtg gaa tat gac ctc gaa gct tat tta gag gcc ctc aac 451
Glu Ala Asp Val Glu Tyr Asp Leu Glu Ala Tyr Leu Glu Ala Leu Asn
          105              110              115

tagccctcca ctaaacagct tca 474

```

<210> 2202

<211> 117

<212> PRT

<213> Corynebacterium glutamicum

<400> 2202

```

Met Gly Ala Trp Asp Asp Ala Ile Leu Thr Glu Glu Val Asn Val Asp
 1              5              10              15

Phe Leu Asp Glu Ile Ser Glu Leu Asp Thr Gln Asp Ile Leu Glu Ala
          20              25              30

Leu Glu Asp Ala Cys Leu Leu Val Val Asn Gln Asp Asn Ala Thr Glu
          35              40              45

Asp Glu His Leu Asn Gly Gln Ala Ala Ala Thr Ile Ala Ala Ile Met
          50              55              60

Phe Gly Ala Pro Tyr Ser Ala Gly Gln Val Leu Glu Asn Tyr Pro Phe
          65              70              75              80

Ile Arg Glu Leu Val Gly Glu Gly Ser Glu Ala Leu Arg Gly Ala Ala
          85              90              95

Ala Gln Val Leu Glu Glu Ala Asp Val Glu Tyr Asp Leu Glu Ala Tyr
          100              105              110

Leu Glu Ala Leu Asn
          115

```

<210> 2203

<211> 614

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(591)

<223> RXA01372

<400> 2203

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cag gac acc ttc gtc ctt ccc acc ttg ccc acg gcc gca gcc ttg tcg 48
Gln Asp Thr Phe Val Leu Pro Thr Leu Pro Thr Ala Ala Gly Leu Ser
 1              5              10              15

cct gcc cgc atc gtg gcg tcg ata agc act ctt tta gat ctt tta gaa 96
Pro Ala Arg Ile Val Ala Ser Ile Ser Thr Leu Leu Asp Leu Leu Glu

```


	20	25	30	
	gca gac ccc agc att att tcc gac cgc ttg gaa cac ctc gcc gac tgc			144
	Ala Asp Pro Ser Ile Ile Ser Asp Arg Leu Glu His Leu Ala Asp Cys			
	35	40	45	
	att gat gag gaa gtg gaa tcg cta tcg ccg gaa cgt gac gaa cta gtc			192
	Ile Asp Glu Glu Val Glu Ser Leu Ser Pro Glu Arg Asp Glu Leu Val			
	50	55	60	
	aat ccc ggc cga aaa ctg cgc gca tac gta gat cac gca cgg atc gtg			240
	Asn Pro Gly Arg Lys Leu Arg Ala Tyr Val Asp His Ala Arg Ile Val			
	65	70	75	80
	cat acc ggc cga act gat gtg gga ctc gcg att gcc aac gtt atc gcc			288
	His Thr Gly Arg Thr Asp Val Gly Leu Ala Ile Ala Asn Val Ile Ala			
	85	90	95	
	cca atc tgg acc cga cga ggc ctg gta tca gcc gtg ctg gat ttt ccc			336
	Pro Ile Trp Thr Arg Arg Gly Leu Val Ser Ala Val Leu Asp Phe Pro			
	100	105	110	
	gag ctc atg gaa tca ttg ccg gaa ctc cgc gga ccc gag cca att acc			384
	Glu Leu Met Glu Ser Leu Pro Glu Leu Arg Gly Pro Glu Pro Ile Thr			
	115	120	125	
	gac gat ata ttc cat gac cca ttc ata gat gac gaa ccc ggg gtg gta			432
	Asp Asp Ile Phe His Asp Pro Phe Ile Asp Asp Glu Pro Gly Val Val			
	130	135	140	
	ccg ttt agg gct gtt gtc tgg gcc gaa gag gaa ccc gga atc ccc gat			480
	Pro Phe Arg Ala Val Val Trp Ala Glu Glu Glu Pro Gly Ile Pro Asp			
	145	150	155	160
	gcc atg gcg caa agc tgc gac gga cct agc aaa ggg gcg ctg aca caa			528
	Ala Met Ala Gln Ser Cys Asp Gly Pro Ser Lys Gly Ala Leu Thr Gln			
	165	170	175	
	gca ctg cgt ttg ctg gtg cgc gga cag tca gcc acg acc tat tcc att			576
	Ala Leu Arg Leu Leu Val Arg Gly Gln Ser Ala Thr Thr Tyr Ser Ile			
	180	185	190	
	gaa gaa aag gac ttg taaatggagc tattggaagg ctc			614
	Glu Glu Lys Asp Leu			
	195			

<210> 2204

<211> 197

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2204

Gln Asp Thr Phe Val Leu Pro Thr Leu Pro Thr Ala Ala Gly Leu Ser

1

5

10

15

Pro Ala Arg Ile Val Ala Ser Ile Ser Thr Leu Leu Asp Leu Leu Glu

20

25

30

Ala Asp Pro Ser Ile Ile Ser Asp Arg Leu Glu His Leu Ala Asp Cys

35

40

45

```

Ile Asp Glu Glu Val Glu Ser Leu Ser Pro Glu Arg Asp Glu Leu Val
  50                      55                      60

Asn Pro Gly Arg Lys Leu Arg Ala Tyr Val Asp His Ala Arg Ile Val
  65                      70                      75                      80

His Thr Gly Arg Thr Asp Val Gly Leu Ala Ile Ala Asn Val Ile Ala
      85                      90                      95

Pro Ile Trp Thr Arg Arg Gly Leu Val Ser Ala Val Leu Asp Phe Pro
 100                      105                      110

Glu Leu Met Glu Ser Leu Pro Glu Leu Arg Gly Pro Glu Pro Ile Thr
 115                      120                      125

Asp Asp Ile Phe His Asp Pro Phe Ile Asp Asp Glu Pro Gly Val Val
 130                      135                      140

Pro Phe Arg Ala Val Val Trp Ala Glu Glu Glu Pro Gly Ile Pro Asp
 145                      150                      155                      160

Ala Met Ala Gln Ser Cys Asp Gly Pro Ser Lys Gly Ala Leu Thr Gln
      165                      170                      175

Ala Leu Arg Leu Leu Val Arg Gly Gln Ser Ala Thr Thr Tyr Ser Ile
      180                      185                      190

Glu Glu Lys Asp Leu
      195

<210> 2205
<211> 1278
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1278)
<223> RXA01378

<400> 2205
cat gtg tgg att tca cca ggt gcg agc aat ccg atc aag gat cgc ctc   48
His Val Trp Ile Ser Pro Gly Ala Ser Asn Pro Ile Lys Asp Arg Leu
  1                      5                      10                      15

ttc cct tgg aca ttg gtg aag gct ttt ctc tcc tcc cct gca gcc ttg   96
Phe Pro Trp Thr Leu Val Lys Ala Phe Leu Ser Ser Pro Ala Ala Leu
      20                      25                      30

ggc gaa aca gtg tcc aat cgc ctc aaa aag gcc tct gca cca gaa gaa   144
Gly Glu Thr Val Ser Asn Arg Leu Lys Lys Ala Ser Ala Pro Glu Glu
      35                      40                      45

aaa cgc gcc cta gaa acc ctt tca caa ctt aat tct gcg atc acc ccg   192
Lys Arg Ala Leu Glu Thr Leu Ser Gln Leu Asn Ser Ala Ile Thr Pro
      50                      55                      60

cag acc tca cag aag tac caa tct cta ctg agc tac ctc ggt gac atc   240
Gln Thr Ser Gln Lys Tyr Gln Ser Leu Leu Ser Tyr Leu Gly Asp Ile

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65	70	75	80
gga gtg aag aag aac tcc gat acc cgc gtg gtg att ttc tct gag cgt Gly Val Lys Lys Asn Ser Asp Thr Arg Val Val Ile Phe Ser Glu Arg	288		
85	90	95	
gtc gct act ttg cac tgg ctg cag gaa aac ctc atc cgt gat ctc aag Val Ala Thr Leu His Trp Leu Gln Glu Asn Leu Ile Arg Asp Leu Lys	336		
100	105	110	
atg cca ccc aac tct att gct gtt atg cac ggc ggt ctc ccc gac cag Met Pro Pro Asn Ser Ile Ala Val Met His Gly Gly Leu Pro Asp Gln	384		
115	120	125	
gag caa atg cgc ctg gtg gat gag ttt aaa aag acg gat tct ccc atc Glu Gln Met Arg Leu Val Asp Glu Phe Lys Lys Thr Asp Ser Pro Ile	432		
130	135	140	
cgc atc atg atc acc ggc gat gtt gcc tca gaa ggt gtg aac ctg cat Arg Ile Met Ile Thr Gly Asp Val Ala Ser Glu Gly Val Asn Leu His	480		
145	150	155	160
act ctc tgc cac aac ttg gtg cac tat gac atc ccg tgg tca ctg atc Thr Leu Cys His Asn Leu Val His Tyr Asp Ile Pro Trp Ser Leu Ile	528		
165	170	175	
cgc att cag cag cgc aat ggc cgt att gat cgt tat ggt caa acc cac Arg Ile Gln Gln Arg Asn Gly Arg Ile Asp Arg Tyr Gly Gln Thr His	576		
180	185	190	
aac cot tcc atc gtt acc ttc ttg ctc gat ccc gcc gag gat tcc aaa Asn Pro Ser Ile Val Thr Phe Leu Leu Asp Pro Ala Glu Asp Ser Lys	624		
195	200	205	
gta ggt gaa gtc cat gtg ctg gag agg ctc atg gag cgc gaa cat gag Val Gly Glu Val His Val Leu Glu Arg Leu Met Glu Arg Glu His Glu	672		
210	215	220	
gcg cac tct ttg ctc ggt gat gcc gca tct ctc atg ggc aag cac tct Ala His Ser Leu Leu Gly Asp Ala Ala Ser Leu Met Gly Lys His Ser	720		
225	230	235	240
gag cgt ttg gaa gaa gaa acc atc cgc gaa gtc ctg cgc ggt gcc caa Glu Arg Leu Glu Glu Glu Thr Ile Arg Glu Val Leu Arg Gly Ala Gln	768		
245	250	255	
aac ttt aat gat gca gtg gct gat cca gcg gaa gtc cta gaa aac cca Asn Phe Asn Asp Ala Val Ala Asp Pro Ala Glu Val Leu Glu Asn Pro	816		
260	265	270	
gca ggc cta gat gat att gat tgg ttg cta gcc caa atc gcc caa gcc Ala Gly Leu Asp Asp Ile Asp Trp Leu Leu Ala Gln Ile Ala Gln Ala	864		
275	280	285	
gat gcc aag gca gaa aca gaa gca gaa gca gaa aca gaa aac caa aca Asp Ala Lys Ala Glu Thr Glu Ala Glu Ala Glu Thr Glu Asn Gln Thr	912		
290	295	300	
gca cca gat gca gct tcc aat agc acg cag cat gca caa cgc cgg ttg Ala Pro Asp Ala Ala Ser Asn Ser Thr Gln His Ala Gln Arg Arg Leu	960		
305	310	315	320

tat gca cag gaa agc tct ttc ctc tat gac tgc ctc ctc gaa ggt ttc 1008
 Tyr Ala Gln Glu Ser Ser Phe Leu Tyr Asp Cys Leu Leu Glu Gly Phe
 325 330 335

aat aac gta ccg gag gat tcc atc aac cgc ggt ggc gtg ggg ttc aaa 1056
 Asn Asn Val Pro Glu Asp Ser Ile Asn Arg Gly Gly Val Gly Phe Lys
 340 345 350

aaa cac gat aat gac atc gtg gag ctc acc ccc acc gat gat ctg cgc 1104
 Lys His Asp Asn Asp Ile Val Glu Leu Thr Pro Thr Asp Asp Leu Arg
 355 360 365

cgt cgt cta gat ttc ctc ccg cag gat tat gtg gct gct cgg aaa gtt 1152
 Arg Arg Leu Asp Phe Leu Pro Gln Asp Tyr Val Ala Ala Arg Lys Val
 370 375 380

aag gaa gat ctc cta cta gct tcc aca ctg atg cgt ggc caa gaa cgc 1200
 Lys Glu Asp Leu Leu Ala Ser Thr Leu Met Arg Gly Gln Glu Arg
 385 390 395 400

ctc aac gct gcg cgc act ggt gaa gat ggc agt acc tgg cca agt gcc 1248
 Leu Asn Ala Ala Arg Thr Gly Glu Asp Gly Ser Thr Trp Pro Ser Ala
 405 410 415

cac tat cta ggc ccc ctg cac cca gtc act 1278
 His Tyr Leu Gly Pro Leu His Pro Val Thr
 420 425

<210> 2206
 <211> 426
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2206
 His Val Trp Ile Ser Pro Gly Ala Ser Asn Pro Ile Lys Asp Arg Leu
 1 5 10 15
 Phe Pro Trp Thr Leu Val Lys Ala Phe Leu Ser Ser Pro Ala Ala Leu
 20 25 30
 Gly Glu Thr Val Ser Asn Arg Leu Lys Lys Ala Ser Ala Pro Glu Glu
 35 40 45
 Lys Arg Ala Leu Glu Thr Leu Ser Gln Leu Asn Ser Ala Ile Thr Pro
 50 55 60
 Gln Thr Ser Gln Lys Tyr Gln Ser Leu Leu Ser Tyr Leu Gly Asp Ile
 65 70 75 80
 Gly Val Lys Lys Asn Ser Asp Thr Arg Val Val Ile Phe Ser Glu Arg
 85 90 95
 Val Ala Thr Leu His Trp Leu Gln Glu Asn Leu Ile Arg Asp Leu Lys
 100 105 110
 Met Pro Pro Asn Ser Ile Ala Val Met His Gly Gly Leu Pro Asp Gln
 115 120 125
 Glu Gln Met Arg Leu Val Asp Glu Phe Lys Lys Thr Asp Ser Pro Ile

130	135	140
Arg Ile Met Ile Thr Gly Asp Val Ala Ser Glu Gly Val Asn Leu His 145 150 155 160		
Thr Leu Cys His Asn Leu Val His Tyr Asp Ile Pro Trp Ser Leu Ile 165 170 175		
Arg Ile Gln Gln Arg Asn Gly Arg Ile Asp Arg Tyr Gly Gln Thr His 180 185 190		
Asn Pro Ser Ile Val Thr Phe Leu Leu Asp Pro Ala Glu Asp Ser Lys 195 200 205		
Val Gly Glu Val His Val Leu Glu Arg Leu Met Glu Arg Glu His Glu 210 215 220		
Ala His Ser Leu Leu Gly Asp Ala Ala Ser Leu Met Gly Lys His Ser 225 230 235 240		
Glu Arg Leu Glu Glu Glu Thr Ile Arg Glu Val Leu Arg Gly Ala Gln 245 250 255		
Asn Phe Asn Asp Ala Val Ala Asp Pro Ala Glu Val Leu Glu Asn Pro 260 265 270		
Ala Gly Leu Asp Asp Ile Asp Trp Leu Leu Ala Gln Ile Ala Gln Ala 275 280 285		
Asp Ala Lys Ala Glu Thr Glu Ala Glu Ala Glu Thr Glu Asn Gln Thr 290 295 300		
Ala Pro Asp Ala Ala Ser Asn Ser Thr Gln His Ala Gln Arg Arg Leu 305 310 315 320		
Tyr Ala Gln Glu Ser Ser Phe Leu Tyr Asp Cys Leu Leu Glu Gly Phe 325 330 335		
Asn Asn Val Pro Glu Asp Ser Ile Asn Arg Gly Gly Val Gly Phe Lys 340 345 350		
Lys His Asp Asn Asp Ile Val Glu Leu Thr Pro Thr Asp Asp Leu Arg 355 360 365		
Arg Arg Leu Asp Phe Leu Pro Gln Asp Tyr Val Ala Ala Arg Lys Val 370 375 380		
Lys Glu Asp Leu Leu Leu Ala Ser Thr Leu Met Arg Gly Gln Glu Arg 385 390 395 400		
Leu Asn Ala Ala Arg Thr Gly Glu Asp Gly Ser Thr Trp Pro Ser Ala 405 410 415		
His Tyr Leu Gly Pro Leu His Pro Val Thr 420 425		

<210> 2207

<211> 2039

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(2016)

<223> RXA01380

<400> 2207

tcg ctg att ttg gga tgc gac acc aag gct cgc ctg gag gat ctg tac 48
 Ser Leu Ile Leu Gly Cys Asp Thr Lys Ala Arg Leu Glu Asp Leu Tyr

1

10

15

ctg ccg ttc aaa aaa cgg cgc aag acg aag gcc gat atc gct agg gag 96
 Leu Pro Phe Lys Lys Arg Arg Lys Thr Lys Ala Asp Ile Ala Arg Glu

20

25

30

gcg gcc ctg gag ggg ctc gtc gat aag ctt atc gac gcc ccg tcc ctc 144
 Ala Gly Leu Glu Gly Leu Val Asp Lys Leu Ile Asp Ala Pro Ser Leu

35

40

45

gac gcc gca cgc cag gca gct gca ttt acg act gag gcc ttt gag gat 192
 Asp Ala Ala Ala Gln Ala Ala Phe Thr Thr Glu Gly Phe Glu Asp

50

55

60

tcc aaa aaa gtt ttg gat ggc gct cgc gcc att ttg att gac cgc ttc 240
 Ser Lys Lys Val Leu Asp Gly Ala Arg Ala Ile Leu Ile Asp Arg Phe

65

70

75

80

gcg ctc gat gcc gat ttg gtg ggc gag gtg cgt gag caa atg tat cgc 288
 Ala Leu Asp Ala Asp Leu Val Gly Glu Val Arg Glu Gln Met Tyr Arg

85

90

95

gcg ggt tcc atg cgc gca tcg gtg gtg cgc gcc aag gag cag gaa gcc 336
 Ala Gly Ser Met Ala Ala Ser Val Val Ala Gly Lys Glu Gln Glu Gly

100

105

110

gca aag ttc aag gac tac ttt gag ttt tcc gaa cct ttt gac aag ctt 384
 Ala Lys Phe Lys Asp Tyr Phe Glu Phe Ser Glu Pro Phe Asp Lys Leu

115

120

125

cca tct cac cga att ttg cgc ctg ctg cgc ggt gaa aac gaa ggt gtg 432
 Pro Ser His Arg Ile Leu Ala Leu Leu Arg Gly Glu Asn Glu Gly Val

130

135

140

ctg agc ctc aac ctc gat cgc gcc gac gac ata atc tac gaa ggt ttg 480
 Leu Ser Leu Asn Leu Asp Ala Gly Asp Asp Ile Ile Tyr Glu Gly Leu

145

150

155

160

atc gcc gac cga ttc ctc ctg gac acc cac act tct agc tgg ctg gct 528
 Ile Ala Asp Arg Phe Ser Leu Asp Thr His Thr Ser Ser Trp Leu Ala

165

170

175

gag gct gtg cgc tgg ggt ttg cgc acc aaa ctg tat gtg tcc tcc gga 576
 Glu Ala Val Arg Trp Gly Trp Arg Thr Lys Leu Tyr Val Ser Ser Gly

180

185

190

ttg gat gtg cgc atg cgt ctg aaa gaa aaa gca gag gaa gcc gca ctc 624
 Leu Asp Val Arg Met Arg Leu Lys Glu Lys Ala Glu Glu Gly Ala Leu

195

200

205

gat gtg ttt gcc acc aac ctc cgc gac gtt ctc ctt gca gct ccc gct 672
 Asp Val Phe Ala Thr Asn Leu Arg Asp Val Leu Leu Ala Ala Pro Ala

210	215	220	
ggt cag cgc tcc aca att ggc ctt gac cgg gga ttc cgc aac ggt gtg 720 Gly Gln Arg Ser Thr Ile Gly Leu Asp Pro Gly Phe Arg Asn Gly Val 240 225 230 235			
aaa gta gct gtc gtg gat tcc acc ggt aag gat gtt gcc acc acg atc 768 Lys Val Ala Val Val Asp Ser Thr Gly Lys Asp Val Ala Thr Thr Ile 255 245 250			
gtc tac cca cac cag ccc caa aac cgc tgg aag gaa gcc gta tcc gaa 816 Val Tyr Pro His Gln Pro Gln Asn Arg Trp Lys Glu Ala Val Ser Glu 270 260 265			
ctg gct aac ctg tgc gcg acc cac ggt gtg gaa ctc atg gcg atc ggc 864 Leu Ala Asn Leu Cys Ala Thr His Gly Val Glu Leu Met Ala Ile Gly 285 275 280			
aac gga acc gcc tcg agg gaa acg gaa aaa ctc gcc gcc gaa gta gct 912 Asn Gly Thr Ala Ser Arg Glu Thr Glu Lys Leu Ala Gly Glu Val Ala 300 290 295			
gac atg atc aaa gcc gca ggt ggc acg cga cca acc ccc gtg gtg gtc 960 Asp Met Ile Lys Ala Ala Gly Gly Thr Arg Pro Thr Pro Val Val Val 320 305 310 315			
tcc gaa tcg gcc gca tcc gtg tac tcg gca tca ccg atc gca gcc gaa 1008 Ser Glu Ser Gly Ala Ser Val Tyr Ser Ala Ser Pro Ile Ala Ala Glu 335 325 330			
gaa ttc ccc gac atg gac gtc tcc ctc cgc ggt gca gtt tct atc gcg 1056 Glu Phe Pro Asp Met Asp Val Ser Leu Arg Gly Ala Val Ser Ile Ala 350 340 345			
agg cga ctc cag gat cca ctg gcg gag ctc gtc aag att gag ccc aaa 1104 Arg Arg Leu Gln Asp Pro Leu Ala Glu Leu Val Lys Ile Glu Pro Lys 365 355 360			
gcc atc gga gtc gcc cag tac caa cac gat gtc aac cag gtt gca ctt 1152 Ala Ile Gly Val Gly Gln Tyr Gln His Asp Val Asn Gln Val Ala Leu 380 370 375			
gcc aaa acc ctt gat ggt gtc gtc gaa gac gca gta aac gca gtc gga 1200 Ala Lys Thr Leu Asp Gly Val Val Glu Asp Ala Val Asn Ala Val Gly 400 385 390 395			
gtt aac ctc aac acc gca tcc gca cca ctt ctt acc cga gtt gcc gga 1248 Val Asn Leu Asn Thr Ala Ser Ala Pro Leu Leu Thr Arg Val Ala Gly 415 405 410			
gtg acc tcc acc ttg gca aac aat atc gtg gcc tac cgc aac gaa aac 1296 Val Thr Ser Thr Leu Ala Asn Asn Ile Val Ala Tyr Arg Asn Glu Asn 430 420 425			
ggt gga ttc tcc tcc cga aaa gaa ctg aac aaa gtt cct cgc ctg gga 1344 Gly Gly Phe Ser Ser Arg Lys Glu Leu Asn Lys Val Pro Arg Leu Gly 445 435 440			
ccc aaa gcc ttt gaa cag tgt gct gcc ttc ctc cgc att tct gga tcc 1392 Pro Lys Ala Phe Glu Gln Cys Ala Gly Phe Leu Arg Ile Ser Gly Ser 460 450 455			

acc gac cct ctc gac gcc tcc gct gtt cac ccc gag gcg tac cca gtt 1440
 Thr Asp Pro Leu Asp Ala Ser Ala Val His Pro Glu Ala Tyr Pro Val
 465 470 475 480

gtt cgc aac att gcg aaa gcc aca gga ttg gat gtc tcg gga ctg atc 1488
 Val Arg Asn Ile Ala Lys Ala Thr Gly Leu Asp Val Ser Gly Leu Ile
 485 490 495

gga aac tct gcg gtg ctc acc aaa ttg aag ccc gct gat ttc gct gat 1536
 Gly Asn Ser Ala Val Leu Thr Lys Leu Lys Pro Ala Asp Phe Ala Asp
 500 505 510

gaa cga ttc ggc atc ccc acc gtc acc gac atc atc gcc gag ctg gat 1584
 Glu Arg Phe Gly Ile Pro Thr Val Thr Asp Ile Ile Ala Glu Leu Asp
 515 520 525

aaa ccc gga cgt gac ccc cgc cca gaa ttc aaa acc gcc agc ttc aaa 1632
 Lys Pro Gly Arg Asp Pro Arg Pro Glu Phe Lys Thr Ala Ser Phe Lys
 530 535 540

gaa ggc gtg gag aaa atc tcc gac ctc aca ccc ggc atg atc ctg gaa 1680
 Glu Gly Val Glu Lys Ile Ser Asp Leu Thr Pro Gly Met Ile Leu Glu
 545 550 555 560

gga act gtc acc aac gtt gcg gcg ttc ggc gca ttc gtt gac gtg gga 1728
 Gly Thr Val Thr Asn Val Ala Ala Phe Gly Ala Phe Val Asp Val Gly
 565 570 575

gtg cac cga gat ggc ctc gtt cac gtt tcc gcg atg agc gac aaa ttc 1776
 Val His Arg Asp Gly Leu Val His Val Ser Ala Met Ser Asp Lys Phe
 580 585 590

atc tcc aac ccc cac gaa gtt gtt cgc tct ggt gag gtc gtg aag gta 1824
 Ile Ser Asn Pro His Glu Val Val Arg Ser Gly Glu Val Val Lys Val
 595 600 605

aag gtc atg gaa gtt gac gtc gac cgc aaa cgc atc ggc ctt tcc ctc 1872
 Lys Val Met Glu Val Asp Val Asp Arg Lys Arg Ile Gly Leu Ser Leu
 610 615 620

cgc ttg acc gat gaa ccc ggt gcc cca gct ccg caa aag cgc gga aac 1920
 Arg Leu Thr Asp Glu Pro Gly Ala Pro Ala Pro Gln Lys Arg Gly Asn
 625 630 635 640

cga cca gcc aaa cag cag cga gct ccg caa aaa cag tcc gct aag ccc 1968
 Arg Pro Ala Lys Gln Gln Arg Ala Pro Gln Lys Gln Ser Ala Lys Pro
 645 650 655

gcc aca ggt tcc atg gca gat gct tta cga cgc gcc ggc ctc ggt gcc 2016
 Ala Thr Gly Ser Met Ala Asp Ala Leu Arg Arg Ala Gly Leu Gly Gly
 660 665 670

taaggcaact ttcaaaccaa gcg 2039

<210> 2208

<211> 672

<212> PRT

<213> Corynebacterium glutamicum

<400> 2208

Ser Leu Ile Leu Gly Cys Asp Thr Lys Ala Arg Leu Glu Asp Leu Tyr
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Leu Pro Phe Lys Lys Arg Arg Lys Thr Lys Ala Asp Ile Ala Arg Glu
 20 25 30

Ala Gly Leu Glu Gly Leu Val Asp Lys Leu Ile Asp Ala Pro Ser Leu
 35 40 45

Asp Ala Ala Ala Gln Ala Ala Ala Phe Thr Thr Glu Gly Phe Glu Asp
 50 55 60

Ser Lys Lys Val Leu Asp Gly Ala Arg Ala Ile Leu Ile Asp Arg Phe
 65 70 75 80

Ala Leu Asp Ala Asp Leu Val Gly Glu Val Arg Glu Gln Met Tyr Arg
 85 90 95

Ala Gly Ser Met Ala Ala Ser Val Val Ala Gly Lys Glu Gln Glu Gly
 100 105 110

Ala Lys Phe Lys Asp Tyr Phe Glu Phe Ser Glu Pro Phe Asp Lys Leu
 115 120 125

Pro Ser His Arg Ile Leu Ala Leu Leu Arg Gly Glu Asn Glu Gly Val
 130 135 140

Leu Ser Leu Asn Leu Asp Ala Gly Asp Asp Ile Ile Tyr Glu Gly Leu
 145 150 155 160

Ile Ala Asp Arg Phe Ser Leu Asp Thr His Thr Ser Ser Trp Leu Ala
 165 170 175

Glu Ala Val Arg Trp Gly Trp Arg Thr Lys Leu Tyr Val Ser Ser Gly
 180 185 190

Leu Asp Val Arg Met Arg Leu Lys Glu Lys Ala Glu Glu Gly Ala Leu
 195 200 205

Asp Val Phe Ala Thr Asn Leu Arg Asp Val Leu Leu Ala Ala Pro Ala
 210 215 220

Gly Gln Arg Ser Thr Ile Gly Leu Asp Pro Gly Phe Arg Asn Gly Val
 225 230 235 240

Lys Val Ala Val Val Asp Ser Thr Gly Lys Asp Val Ala Thr Thr Ile
 245 250 255

Val Tyr Pro His Gln Pro Gln Asn Arg Trp Lys Glu Ala Val Ser Glu
 260 265 270

Leu Ala Asn Leu Cys Ala Thr His Gly Val Glu Leu Met Ala Ile Gly
 275 280 285

Asn Gly Thr Ala Ser Arg Glu Thr Glu Lys Leu Ala Gly Glu Val Ala
 290 295 300

Asp Met Ile Lys Ala Ala Gly Gly Thr Arg Pro Thr Pro Val Val Val
 305 310 315 320

Ser Glu Ser Gly Ala Ser Val Tyr Ser Ala Ser Pro Ile Ala Ala Glu
 325 330 335
 Glu Phe Pro Asp Met Asp Val Ser Leu Arg Gly Ala Val Ser Ile Ala
 340 345 350
 Arg Arg Leu Gln Asp Pro Leu Ala Glu Leu Val Lys Ile Glu Pro Lys
 355 360 365
 Ala Ile Gly Val Gly Gln Tyr Gln His Asp Val Asn Gln Val Ala Leu
 370 375 380
 Ala Lys Thr Leu Asp Gly Val Val Glu Asp Ala Val Asn Ala Val Gly
 385 390 395 400
 Val Asn Leu Asn Thr Ala Ser Ala Pro Leu Leu Thr Arg Val Ala Gly
 405 410 415
 Val Thr Ser Thr Leu Ala Asn Asn Ile Val Ala Tyr Arg Asn Glu Asn
 420 425 430
 Gly Gly Phe Ser Ser Arg Lys Glu Leu Asn Lys Val Pro Arg Leu Gly
 435 440 445
 Pro Lys Ala Phe Glu Gln Cys Ala Gly Phe Leu Arg Ile Ser Gly Ser
 450 455 460
 Thr Asp Pro Leu Asp Ala Ser Ala Val His Pro Glu Ala Tyr Pro Val
 465 470 475 480
 Val Arg Asn Ile Ala Lys Ala Thr Gly Leu Asp Val Ser Gly Leu Ile
 485 490 495
 Gly Asn Ser Ala Val Leu Thr Lys Leu Lys Pro Ala Asp Phe Ala Asp
 500 505 510
 Glu Arg Phe Gly Ile Pro Thr Val Thr Asp Ile Ile Ala Glu Leu Asp
 515 520 525
 Lys Pro Gly Arg Asp Pro Arg Pro Glu Phe Lys Thr Ala Ser Phe Lys
 530 535 540
 Glu Gly Val Glu Lys Ile Ser Asp Leu Thr Pro Gly Met Ile Leu Glu
 545 550 555 560
 Gly Thr Val Thr Asn Val Ala Ala Phe Gly Ala Phe Val Asp Val Gly
 565 570 575
 Val His Arg Asp Gly Leu Val His Val Ser Ala Met Ser Asp Lys Phe
 580 585 590
 Ile Ser Asn Pro His Glu Val Val Arg Ser Gly Glu Val Val Lys Val
 595 600 605
 Lys Val Met Glu Val Asp Val Asp Arg Lys Arg Ile Gly Leu Ser Leu
 610 615 620
 Arg Leu Thr Asp Glu Pro Gly Ala Pro Ala Pro Gln Lys Arg Gly Asn
 625 630 635 640
 Arg Pro Ala Lys Gln Gln Arg Ala Pro Gln Lys Gln Ser Ala Lys Pro

645

650

655

Ala Thr Gly Ser Met Ala Asp Ala Leu Arg Arg Ala Gly Leu Gly Gly
 660 665 670

<210> 2209

<211> 1839

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1816)

<223> RXA01384

<400> 2209

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gtgggaagcg tcgacaagca tctttaagta gcgttgatgt atg cgc tca ctt caa 115
 Met Arg Ser Leu Gln
 1 5

tcg gtc ctt gac ctg ctg act tct aag tcc aaa gtg gct acc aaa att 163
 Ser Val Leu Asp Leu Leu Thr Ser Lys Ser Lys Val Ala Thr Lys Ile
 10 15 20

gtg gtg gaa cga att gaa aag cat cct gtt cat gga ttg gga tgg atg 211
 Val Val Glu Arg Ile Glu Lys His Pro Val His Gly Leu Gly Trp Met
 25 30 35

atg tat ccg cca ttt cat cca tgg act gat gct tcg acc ttg acg att 259
 Met Tyr Pro Pro Phe His Pro Trp Thr Asp Ala Ser Thr Leu Thr Ile
 40 45 50

gag cga aac gga acc agt cgg cgc gcg agt cag aat ggc gtt gcg gtt 307
 Glu Arg Asn Gly Thr Ser Arg Arg Ala Ser Gln Asn Gly Val Ala Val
 55 60 65

ctt cat cag cat gag caa gtt caa act atc ggt cta gcc agc tat ttt 355
 Leu His Gln His Glu Gln Val Gln Thr Ile Gly Leu Ala Ser Tyr Phe
 70 75 80 85

atc gac tcc aag att tgg gta aac gag ctg gct ggc ctt gat cgt atc 403
 Ile Asp Ser Lys Ile Trp Val Asn Glu Leu Ala Gly Leu Asp Arg Ile
 90 95 100

aac att tct gag agt gaa gtt gct ggt cgt gac gta tta gtt ctg ccg 451
 Asn Ile Ser Glu Ser Glu Val Ala Gly Arg Asp Val Leu Val Leu Pro
 105 110 115

tta tct gat ctg act tta agc atc gat gcg aaa tac ggc gtg gtt ttg 499
 Leu Ser Asp Leu Thr Leu Ser Ile Asp Ala Lys Tyr Gly Val Val Leu
 120 125 130

gct gcg gaa gac agc gat gaa tca gtg cgc gcg gta tcc gtg gag ttc 547
 Ala Ala Glu Asp Ser Asp Glu Ser Val Arg Ala Val Ser Val Glu Phe
 135 140 145

ctg gac cag tgg gta gat gaa gaa gaa ccc cca gcg gaa gaa gtg cct Leu Asp Gln Trp Val Asp Glu Glu Glu Pro Pro Ala Glu Glu Val Pro 150 155 160 165	595
aaa tat acg gaa acc agg gag gaa ctt cct cca ctt gag att cct ccg Lys Tyr Thr Glu Thr Arg Glu Glu Leu Pro Pro Leu Glu Ile Pro Pro 170 175 180	643
gct cct tcc gga aat cgt aat ctc cga gtt ctg tgc acg tgg gga gcg Ala Pro Ser Gly Asn Arg Asn Leu Arg Val Leu Cys Thr Trp Gly Ala 185 190 195	691
atg gaa gga att att cct gag tgg aaa ccc gcc gat caa gtt tca ctg Met Glu Gly Ile Ile Pro Glu Trp Lys Pro Gly Asp Gln Val Ser Leu 200 205 210	739
ttt ttg tct ttc gac ctc gac gat ccg ccg ttc gaa cag ctc aaa acc Phe Leu Ser Phe Asp Leu Asp Pro Pro Phe Glu Gln Leu Lys Thr 215 220 225	787
act cgt cgc ggg tac acc gaa cct gcc gag att tat gga aac cag cgc Thr Arg Arg Gly Tyr Thr Glu Pro Gly Glu Ile Tyr Gly Asn Gln Arg 230 235 240 245	835
agc tat aaa ttt cac gct gat ggt tgg aac gct gtt att tcc gcc aaa Ser Tyr Lys Phe His Ala Asp Gly Trp Asn Ala Val Ile Ser Ala Lys 250 255 260	883
gtg cca ctg cgc acc gaa gaa aac ctc acc gcc tac ttc acc cac agc Val Pro Leu Arg Thr Glu Glu Asn Leu Thr Thr Gly Tyr Phe Thr His Ser 265 270 275	931
tcc tac gcg gac acg agc cgc cgc acg tca gcg gtc atc acc gca gtc Ser Tyr Ala Asp Thr Ser Arg Arg Thr Ser Ala Val Ile Thr Ala Val 280 285 290	979
tac cgc cac ggt aag gac gca att atc gac gtg acc ctc gac ggt gcg Tyr Arg His Gly Lys Asp Ala Ile Ile Asp Val Thr Leu Asp Gly Ala 295 300 305	1027
aaa cct cct aga tat caa gaa tcc ttg gat tgg agc agc acc agt acc Lys Pro Pro Arg Tyr Gln Glu Ser Leu Asp Trp Ser Ser Thr Ser Thr 310 315 320 325	1075
tgt gac ggt gaa aca atc tgg ctg tcc gat aag agc ttg ccc ttc gtc Cys Asp Gly Glu Thr Ile Trp Leu Ser Asp Lys Ser Leu Pro Phe Val 330 335 340	1123
cgc ggt ttc aat gtc tcc aca gcc aag cta gta cac gag atc tcc ata Arg Gly Phe Asn Val Ser Thr Gly Lys Leu Val His Glu Ile Ser Ile 345 350 355	1171
ccc acc ttc aat gag atc gcc ctc gaa tcc gcc aat aga gcc cgc gca Pro Thr Phe Asn Glu Ile Ala Leu Glu Ser Gly Asn Arg Ala Arg Ala 360 365 370	1219
gcg aaa aaa ctt tgg gaa ctt cca gat ctt aaa gag gca acc gac cct Ala Lys Lys Leu Trp Glu Leu Pro Asp Leu Lys Glu Ala Thr Asp Pro 375 380 385	1267

gtc cca gcg atc ccc gcg ggc tgg aaa cta cac aaa aga ttc ggg aaa 1315
 Val Pro Ala Ile Pro Ala Gly Trp Lys Leu His Lys Arg Phe Gly Lys
 390 395 400 405

aac ttc cat atc gta agc gct gac aac gga acc tgg aaa caa acc atc 1363
 Asn Phe His Ile Val Ser Ala Asp Asn Gly Thr Trp Lys Gln Thr Ile
 410 415 420

ctt agg atc aaa ccc ttc aaa gca att gag ctt gat ctt gga tac gcc 1411
 Leu Arg Ile Lys Pro Phe Lys Ala Ile Glu Leu Asp Leu Gly Tyr Ala
 425 430 435

aag att tcg acg att tac caa tac ggt gaa cga att tat ctg cgt tcc 1459
 Lys Ile Ser Thr Ile Tyr Gln Tyr Gly Glu Arg Ile Tyr Leu Arg Ser
 440 445 450

gat ctt cac cag atc acg ttt aat cag gat ctt gaa atc ctc agt gta 1507
 Asp Leu His Gln Ile Thr Phe Asn Gln Asp Leu Glu Ile Leu Ser Val
 455 460 465

gag gtc cac gga aat ccc gat gca ggt tat tgg cca ctt tcc gat ctt 1555
 Glu Val His Gly Asn Pro Asp Ala Gly Tyr Trp Pro Leu Ser Asp Leu
 470 475 480 485

cca cca ggg gat tct cca acg ctg gga ttt cct atc gga tca ctc atg 1603
 Pro Pro Gly Asp Ser Pro Thr Leu Gly Phe Pro Ile Gly Ser Leu Met
 490 495 500

atg ttc cac gaa caa caa gat atc tac gct ttc cac gat cct aaa aca 1651
 Met Phe His Glu Gln Gln Asp Ile Tyr Ala Phe His Asp Pro Lys Thr
 505 510 515

aca aag caa cta aca act gtg aac ttg ccc aaa agg cag ttt gaa gtg 1699
 Thr Lys Gln Leu Thr Thr Val Asn Leu Pro Lys Arg Gln Phe Glu Val
 520 525 530

gaa tat gct tct cag aac aga att gtt att tcg ctg aaa aat cca gaa 1747
 Glu Tyr Ala Ser Gln Asn Arg Ile Val Ile Ser Leu Lys Asn Pro Glu
 535 540 545

agc cgc ctc att gac aaa ctg ttg gtg tgg gaa cca caa acc agg tgg 1795
 Ser Arg Leu Ile Asp Lys Leu Leu Val Trp Glu Pro Gln Thr Arg Trp
 550 555 560 565

cgg gaa caa aac ctg gag agc tgagcacggt ttgattaacg tcg 1839
 Arg Glu Gln Asn Leu Glu Ser
 570

<210> 2210

<211> 572

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2210

Met Arg Ser Leu Gln Ser Val Leu Asp Leu Leu Thr Ser Lys Ser Lys
 1 5 10 15

Val Ala Thr Lys Ile Val Val Glu Arg Ile Glu Lys His Pro Val His
 20 25 30

Gly Leu Gly Trp Met Met Tyr Pro Pro Phe His Pro Trp Thr Asp Ala
 35 40 45
 Ser Thr Leu Thr Ile Glu Arg Asn Gly Thr Ser Arg Arg Ala Ser Gln
 50 55 60
 Asn Gly Val Ala Val Leu His Gln His Glu Gln Val Gln Thr Ile Gly
 65 70 75 80
 Leu Ala Ser Tyr Phe Ile Asp Ser Lys Ile Trp Val Asn Glu Leu Ala
 85 90 95
 Gly Leu Asp Arg Ile Asn Ile Ser Glu Ser Glu Val Ala Gly Arg Asp
 100 105 110
 Val Leu Val Leu Pro Leu Ser Asp Leu Thr Leu Ser Ile Asp Ala Lys
 115 120 125
 Tyr Gly Val Val Leu Ala Ala Glu Asp Ser Asp Glu Ser Val Arg Ala
 130 135 140
 Val Ser Val Glu Phe Leu Asp Gln Trp Val Asp Glu Glu Glu Pro Pro
 145 150 155 160
 Ala Glu Glu Val Pro Lys Tyr Thr Glu Thr Arg Glu Glu Leu Pro Pro
 165 170 175
 Leu Glu Ile Pro Pro Ala Pro Ser Gly Asn Arg Asn Leu Arg Val Leu
 180 185 190
 Cys Thr Trp Gly Ala Met Glu Gly Ile Ile Pro Glu Trp Lys Pro Gly
 195 200 205
 Asp Gln Val Ser Leu Phe Leu Ser Phe Asp Leu Asp Asp Pro Pro Phe
 210 215 220
 Glu Gln Leu Lys Thr Thr Arg Arg Gly Tyr Thr Glu Pro Gly Glu Ile
 225 230 235 240
 Tyr Gly Asn Gln Arg Ser Tyr Lys Phe His Ala Asp Gly Trp Asn Ala
 245 250 255
 Val Ile Ser Ala Lys Val Pro Leu Arg Thr Glu Glu Asn Leu Thr Gly
 260 265 270
 Tyr Phe Thr His Ser Ser Tyr Ala Asp Thr Ser Arg Arg Thr Ser Ala
 275 280 285
 Val Ile Thr Ala Val Tyr Arg His Gly Lys Asp Ala Ile Ile Asp Val
 290 295 300
 Thr Leu Asp Gly Ala Lys Pro Pro Arg Tyr Gln Glu Ser Leu Asp Trp
 305 310 315 320
 Ser Ser Thr Ser Thr Cys Asp Gly Glu Thr Ile Trp Leu Ser Asp Lys
 325 330 335
 Ser Leu Pro Phe Val Arg Gly Phe Asn Val Ser Thr Gly Lys Leu Val
 340 345 350
 His Glu Ile Ser Ile Pro Thr Phe Asn Glu Ile Ala Leu Glu Ser Gly

355	360	365
Asn Arg Ala Arg Ala Ala Lys Lys Leu Trp Glu Leu Pro Asp Leu Lys		
370	375	380
Glu Ala Thr Asp Pro Val Pro Ala Ile Pro Ala Gly Trp Lys Leu His		
385	390	395
Lys Arg Phe Gly Lys Asn Phe His Ile Val Ser Ala Asp Asn Gly Thr		
405	410	415
Trp Lys Gln Thr Ile Leu Arg Ile Lys Pro Phe Lys Ala Ile Glu Leu		
420	425	430
Asp Leu Gly Tyr Ala Lys Ile Ser Thr Ile Tyr Gln Tyr Gly Glu Arg		
435	440	445
Ile Tyr Leu Arg Ser Asp Leu His Gln Ile Thr Phe Asn Gln Asp Leu		
450	455	460
Glu Ile Leu Ser Val Glu Val His Gly Asn Pro Asp Ala Gly Tyr Trp		
465	470	475
Pro Leu Ser Asp Leu Pro Pro Gly Asp Ser Pro Thr Leu Gly Phe Pro		
485	490	495
Ile Gly Ser Leu Met Met Phe His Glu Gln Gln Asp Ile Tyr Ala Phe		
500	505	510
His Asp Pro Lys Thr Thr Lys Gln Leu Thr Thr Val Asn Leu Pro Lys		
515	520	525
Arg Gln Phe Glu Val Glu Tyr Ala Ser Gln Asn Arg Ile Val Ile Ser		
530	535	540
Leu Lys Asn Pro Glu Ser Arg Leu Ile Asp Lys Leu Leu Val Trp Glu		
545	550	555
Pro Gln Thr Arg Trp Arg Glu Gln Asn Leu Glu Ser		
565	570	

<210> 2211

<211> 381

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(358)

<223> RXA01396

<400> 2211

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caacgcgtga gatocaggct cagcttcaac ctccgcggtt ttg aag gct ttc aac	115
Leu Lys Ala Phe Asn	
1	5

acc aac ttc gca gcc act ttg gct acc gga aag gtt ggc gat atc acc	163
Thr Asn Phe Ala Ala Thr Leu Ala Thr Gly Lys Val Gly Asp Ile Thr	

	10	15	20	
acc acc gtt tta gtt gca ggc gat gat gaa gac gca aag aac gct ctt				211
Thr Thr Val Leu Val Ala Gly Asp Asp Glu Asp Ala Lys Asn Ala Leu				
	25	30	35	
atc acc gac gtc aac gct ggc ggc ctc gac gcc ctt gac gct ggt tcc				259
Ile Thr Asp Val Asn Ala Gly Gly Leu Asp Ala Leu Asp Ala Gly Ser				
	40	45	50	
ctc aag cgt gca cac gag ctt gaa gca gtt ggt ttc ctg cag ctc acc				307
Leu Lys Arg Ala His Glu Leu Glu Ala Val Gly Phe Leu Gln Leu Thr				
	55	60	65	
ctt gca ggt tcc gag aag att gga tgg acc ggc gga ttc ggc ctg gtc				355
Leu Ala Gly Ser Glu Lys Ile Gly Trp Thr Gly Gly Phe Gly Leu Val				
	70	75	80	85
aag taacacccag cctcaaaagc act				381
Lys				

<210> 2212
 <211> 86
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2212
 Leu Lys Ala Phe Asn Thr Asn Phe Ala Ala Thr Leu Ala Thr Gly Lys
 1 5 10 15
 Val Gly Asp Ile Thr Thr Thr Val Leu Val Ala Gly Asp Asp Glu Asp
 20 25 30
 Ala Lys Asn Ala Leu Ile Thr Asp Val Asn Ala Gly Gly Leu Asp Ala
 35 40 45
 Leu Asp Ala Gly Ser Leu Lys Arg Ala His Glu Leu Glu Ala Val Gly
 50 55 60
 Phe Leu Gln Leu Thr Leu Ala Gly Ser Glu Lys Ile Gly Trp Thr Gly
 65 70 75 80
 Gly Phe Gly Leu Val Lys
 85

<210> 2213
 <211> 543
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(520)
 <223> RXA01397

<400> 2213
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actaataact tgacacgtca agtaattagg gtctagtgtt gtg ttc atg atc aaa 115
Val Phe Met Ile Lys
1 5

gaa ctg ctc aac aag ctc ttc gga aac aag aag gct tcc ccg gca atg 163
Glu Leu Leu Asn Lys Leu Phe Gly Asn Lys Lys Ala Ser Pro Ala Met
10 15 20

aca caa tct gaa acc att tca cac aag gag aac aac aca atg acc act 211
Thr Gln Ser Glu Thr Ile Ser His Lys Glu Asn Asn Thr Met Thr Thr
25 30 35

tac acc atc ttc ggc cgc ggc aac atg ggc acc gca atc gca ggc gtc 259
Tyr Thr Ile Phe Gly Arg Gly Asn Met Gly Thr Ala Ile Ala Gly Val
40 45 50

ctc acc aag ggt ggt gca act gta gaa cac atc ggt tct gca gat tct 307
Leu Thr Lys Gly Gly Ala Thr Val Glu His Ile Gly Ser Ala Asp Ser
55 60 65

gac atc gca acc atc aac ggt gac gtt gtt atc ctt gct gtt cct tac 355
Asp Ile Ala Thr Ile Asn Gly Asp Val Val Ile Leu Ala Val Pro Tyr
70 75 80 85

cca gca gta gag tcc atc att gca agc cac aag gat gct ctc gca ggc 403
Pro Ala Val Glu Ser Ile Ile Ala Ser His Lys Asp Ala Leu Ala Gly
90 95 100

aag acc gtt atc gat atc acc aac cca ctt aac ttc gag acc ttc gat 451
Lys Thr Val Ile Asp Ile Thr Asn Pro Leu Asn Phe Glu Thr Phe Asp
105 110 115

tcc ctc gtc gtt cca gtt ggt tct tct gca acc gct gag atc cag gct 499
Ser Leu Val Val Pro Val Gly Ser Ser Ala Thr Ala Glu Ile Gln Ala
120 125 130

cag ctt caa cct ccc gcg ttt tgaaggttt caacaccaac ttc 543
Gln Leu Gln Pro Pro Ala Phe
135 140

<210> 2214

<211> 140

<212> PRT

<213> Corynebacterium glutamicum

<400> 2214

Val Phe Met Ile Lys Glu Leu Leu Asn Lys Leu Phe Gly Asn Lys Lys
1 5 10 15

Ala Ser Pro Ala Met Thr Gln Ser Glu Thr Ile Ser His Lys Glu Asn
20 25 30

Asn Thr Met Thr Thr Tyr Thr Ile Phe Gly Arg Gly Asn Met Gly Thr
35 40 45

Ala Ile Ala Gly Val Leu Thr Lys Gly Gly Ala Thr Val Glu His Ile
50 55 60

Gly Ser Ala Asp Ser Asp Ile Ala Thr Ile Asn Gly Asp Val Val Ile
65 70 75 80

Leu	Ala	Val	Pro	Tyr	Pro	Ala	Val	Glu	Ser	Ile	Ile	Ala	Ser	His	Lys
				85					90					95	
Asp	Ala	Leu	Ala	Gly	Lys	Thr	Val	Ile	Asp	Ile	Thr	Asn	Pro	Leu	Asn
			100					105					110		
Phe	Glu	Thr	Phe	Asp	Ser	Leu	Val	Val	Pro	Val	Gly	Ser	Ser	Ala	Thr
		115					120					125			
Ala	Glu	Ile	Gln	Ala	Gln	Leu	Gln	Pro	Pro	Ala	Phe				
	130					135					140				

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<210> 2215
<211> 384
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(361)  
<223> RXA01401
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agtatctata gattgataga aaataattta ggaagtttcc atg aac tct ccc cta	115
	Met Asn Ser Pro Leu 1 5
caa cac agc gcc ttc ccc gtc ccc ggc gcg caa ctg tcc acc tca tac	163
Gln His Ser Ala Phe Pro Val Pro Gly Ala Gln Leu Ser Thr Ser Tyr	10 15 20
agc gac gaa cac ggc caa gcc gtc atc caa ctt cac ggc ctg acc tcc	211
Ser Asp Glu His Gly Gln Ala Val Ile Gln Leu His Gly Leu Thr Ser	25 30 35
tcc cgc caa cgc gac cgc ctg ctg gac ctg gac ctg ggc cgt ggc ctt	259
Ser Arg Gln Arg Asp Arg Leu Leu Asp Leu Asp Leu Gly Arg Gly Leu	40 45 50
tcc ggc acg cgc ctt ttg cgt tac gac gcc cgc gcc cac gcc acc tcc	307
Ser Gly Thr Arg Leu Leu Arg Tyr Asp Ala Arg Gly His Gly Thr Ser	55 60 65
acc ggc cgc gct gcc tcc acc gat tat cag tgg gac acc cta gcg ggt	355
Thr Gly Arg Ala Ala Ser Thr Asp Tyr Gln Trp Asp Thr Leu Ala Gly	70 75 80 85
gac ctt taatgcttct cgacgccccc ttc	384
Asp Leu	

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<210> 2216
<211> 87
<212> PRT
<213> Corynebacterium glutamicum
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<400> 2216

Met Asn Ser Pro Leu Gln His Ser Ala Phe Pro Val Pro Gly Ala Gln
 1 5 10 15

Leu Ser Thr Ser Tyr Ser Asp Glu His Gly Gln Ala Val Ile Gln Leu
 20 25 30

His Gly Leu Thr Ser Ser Arg Gln Arg Asp Arg Leu Leu Asp Leu Asp
 35 40 45

Leu Gly Arg Gly Leu Ser Gly Thr Arg Leu Leu Arg Tyr Asp Ala Arg
 50 55 60

Gly His Gly Thr Ser Thr Gly Arg Ala Ala Ser Thr Asp Tyr Gln Trp
 65 70 75 80

Asp Thr Leu Ala Gly Asp Leu
 85

<210> 2217

<211> 597

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(574)

<223> RXA01402

<400> 2217

cgctgcctcc accgattatc agtggggacac cctagcgggt gaccttaaat gcttctcgac 60

gcccacttcc ccacgaacaa gtccacggcg tcggcccctc atg ggt tgc gcc acc 115
 Met Gly Cys Ala Thr
 1 5

ctc ctc aaa gcc gcg gtg tta aac ccc gac cgc ttc agt gga ttc aca 163
 Leu Leu Lys Ala Ala Val Leu Asn Pro Asp Arg Phe Ser Gly Phe Thr
 10 15 20

ctc atg ctc cca ccc acc gcc tgg gaa tcc cga aaa gcc caa gcc tcc 211
 Leu Met Leu Pro Pro Thr Ala Trp Glu Ser Arg Lys Ala Gln Ala Ser
 25 30 35

gaa tac cta tcc cga gca gaa ttc cta gaa acc cac gcc atg gac gcc 259
 Glu Tyr Leu Ser Arg Ala Glu Phe Leu Glu Thr His Gly Met Asp Ala
 40 45 50

ttc ctc aac gcc gaa aaa ctc cac gcc caa cca cca gca acc gta gga 307
 Phe Leu Asn Ala Glu Lys Leu His Ala Gln Pro Pro Ala Thr Val Gly
 55 60 65

acc ccc gac aca gtc ccc gac att tcc gcc gaa ctc ctc ccc tgg gct 355
 Thr Pro Asp Thr Val Pro Asp Ile Ser Ala Glu Leu Leu Pro Trp Ala
 70 75 80 85

tac cga ggc gcc gcc caa agc gac ctc ccc tca aag aaa gaa atc gcc 403
 Tyr Arg Gly Ala Ala Gln Ser Asp Leu Pro Ser Lys Lys Glu Ile Ala
 90 95 100

aaa ata aca gcc ccc acc act att ctg agc tgg acc gac gat ccc gga 451
 Lys Ile Thr Ala Pro Thr Thr Ile Leu Ser Trp Thr Asp Asp Pro Gly
 105 110 115

cac ccc gta tcc acg gca atc gag cta acc cgc ctc atg cca aac gcc 499
 His Pro Val Ser Thr Ala Ile Glu Leu Thr Arg Leu Met Pro Asn Ala
 120 125 130

caa ctg cgc att gcc act acc cca gcg gaa gtc gcg cgg tgg cca caa 547
 Gln Leu Arg Ile Ala Thr Thr Pro Ala Glu Val Ala Arg Trp Pro Gln
 135 140 145

cac ctt cgc gat gac ctg cag ttg gac taaaaacctt cattatctgg 594
 His Leu Arg Asp Asp Leu Gln Leu Asp
 150 155

ttt 597

<210> 2218

<211> 158

<212> PRT

<213> Corynebacterium glutamicum

<400> 2218

Met Gly Cys Ala Thr Leu Leu Lys Ala Ala Val Leu Asn Pro Asp Arg
 1 5 10 15

Phe Ser Gly Phe Thr Leu Met Leu Pro Pro Thr Ala Trp Glu Ser Arg
 20 25 30

Lys Ala Gln Ala Ser Glu Tyr Leu Ser Arg Ala Glu Phe Leu Glu Thr
 35 40 45

His Gly Met Asp Ala Phe Leu Asn Ala Glu Lys Leu His Ala Gln Pro
 50 55 60

Pro Ala Thr Val Gly Thr Pro Asp Thr Val Pro Asp Ile Ser Ala Glu
 65 70 75 80

Leu Leu Pro Trp Ala Tyr Arg Gly Ala Ala Gln Ser Asp Leu Pro Ser
 85 90 95

Lys Lys Glu Ile Ala Lys Ile Thr Ala Pro Thr Thr Ile Leu Ser Trp
 100 105 110

Thr Asp Asp Pro Gly His Pro Val Ser Thr Ala Ile Glu Leu Thr Arg
 115 120 125

Leu Met Pro Asn Ala Gln Leu Arg Ile Ala Thr Thr Pro Ala Glu Val
 130 135 140

Ala Arg Trp Pro Gln His Leu Arg Asp Asp Leu Gln Leu Asp
 145 150 155

<210> 2219

<211> 579

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> {101}..(556)

<223> RXA01405

<400> 2219

aattagacgt ctgtctctag ggaatgccga tcccgccggc gctcctagag tccgtttgta 60

aaacctagaa ttccgaatac gtccgaata ggggtggggg atg agt aag ata gtt 115
 Met Ser Lys Ile Val 5

gat ctg cgc tat ggg acc cgg cgt tcc tgg gag ttg agc aaa cgc tct 163
 Asp Leu Arg Tyr Gly Thr Arg Arg Ser Ser Glu Leu Ser Lys Arg Ser 20

gct gaa gtc ttt gcc gaa get gaa gaa cat ccc att act gtg aca cgt 211
 Ala Glu Val Phe Ala Glu Ala Glu His Pro Ile Thr Val Thr Arg 35

cgt gat ggt gaa gcg ttg gta ttg atg tgg cag cgc gaa gct gac ggg 259
 Arg Asp Gly Glu Ala Leu Val Leu Met Ser Gln Arg Glu Ala Asp Gly 50

cga gcc cgc ctg ctg gag ttg gct gca cag tta att act gtg gcc act 307
 Arg Ala Arg Leu Leu Glu Leu Ala Ala Gln Leu Ile Thr Val Ala Thr 65

gat cat cag gcc acg tta gcc gaa cgt atg gcg aaa gta ttc ccg tgg 355
 Asp His Gln Gly Thr Leu Ala Glu Arg Met Ala Lys Val Phe Pro Trp 85

atg ctg gcc ctg tca gtg gcg gat cgt gag gcg tgt gcc cgt gag att 403
 Met Leu Ala Leu Ser Val Ala Asp Arg Glu Ala Cys Ala Arg Glu Ile 95

ctt gac get gca cga gca tgg ttt gca acc gaa caa cct cac ctc gct 451
 Leu Asp Ala Ala Arg Ala Ser Phe Ala Thr Glu Gln Pro His Leu Ala 115

ctt act gaa ctg acc tca tgg aaa gaa aca gca gca gct gtt gct gct 499
 Leu Thr Glu Leu Thr Ser Trp Lys Glu Thr Ala Ala Val Ala Ala 130

gga ttg agt aac act gat ctg cag tgg tac gac gat ccg cat ctg gtg 547
 Gly Leu Ser Asn Thr Asp Leu Gln Trp Tyr Asp Asp Pro His Leu Val 145

gag cgt ccc taagcgtggc tggaaagaaa agc 579
 Glu Arg Pro 150

<210> 2220

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 2220

Met Ser Lys Ile Val Asp Leu Arg Tyr Gly Thr Arg Arg Ser Ser Glu
 1 5 10 15

Leu Ser Lys Arg Ser Ala Glu Val Phe Ala Glu Ala Glu Glu His Pro
20 25 30

Ile Thr Val Thr Arg Arg Asp Gly Glu Ala Leu Val Leu Met Ser Gln
35 40 45

Arg Glu Ala Asp Gly Arg Ala Arg Leu Leu Glu Leu Ala Ala Gln Leu
50 55 60

Ile Thr Val Ala Thr Asp His Gln Gly Thr Leu Ala Glu Arg Met Ala
65 70 75 80

Lys Val Phe Pro Trp Met Leu Ala Leu Ser Val Ala Asp Arg Glu Ala
85 90 95

Cys Ala Arg Glu Ile Leu Asp Ala Ala Arg Ala Ser Phe Ala Thr Glu
100 105 110

Gln Pro His Leu Ala Leu Thr Glu Leu Thr Ser Trp Lys Glu Thr Ala
115 120 125

Ala Ala Val Ala Ala Gly Leu Ser Asn Thr Asp Leu Gln Trp Tyr Asp
130 135 140

Asp Pro His Leu Val Glu Arg Pro
145 150

<210> 2221

<211> 723

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(700)

<223> RXA01413

<400> 2221

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cgggtttctc cagcgtttaa ccatctgaaa ccatotgaga ttg acc cat ctg ttc 115
Leu Thr His Leu Phe
1 5

tta gaa ctc gat gag cgt tta gta ctg ggt gtt cag caa gat ggt tac 163
Leu Glu Leu Asp Glu Arg Leu Val Leu Gly Val Gln Gln Asp Gly Tyr
10 15 20

caa tgg act gag cat ttg ttc cgg ctg cca ctg caa cat ctc cgt aac 211
Gln Trp Thr Glu His Leu Phe Arg Leu Pro Leu Gln His Leu Arg Asn
25 30 35

tgc ccc aat gac ctg cag gga ttg aag ata cga tgg tgt gaa ctt tat 259
Ser Pro Asn Asp Leu Gln Gly Leu Lys Ile Arg Trp Cys Glu Leu Tyr
40 45 50

tcc aca acg ggg aaa gat caa ggg gta gaa ctt ctg cct caa gca acc 307
Ser Thr Thr Gly Lys Asp Gln Gly Val Glu Leu Leu Pro Gln Ala Thr
55 60 65

gtc gtt acc cca aat aac ttc gag gct tcc acc ctc tcc ggc ctt gag 355
 Val Val Thr Pro Asn Asn Phe Glu Ala Ser Thr Leu Ser Gly Leu Glu 85
 70 75 80

aag ctt gag acc gtc gag gac ctc aag gag gct gcc cgc ctc att tat 403
 Lys Leu Glu Thr Val Glu Asp Leu Lys Glu Ala Ala Arg Leu Ile Tyr 100
 90 95

gag caa ggc ccc cag tac gta gtc gtc aag ggt ggc atg gac ttc ccc 451
 Glu Gln Gly Pro Gln Tyr Val Val Val Lys Gly Gly Met Asp Phe Pro 115
 105 110

ggc gag aac gcc gtg gat gtg ctt ttc gac gga tcc tcc tac cac gtc 499
 Gly Glu Asn Ala Val Asp Val Leu Phe Asp Gly Ser Ser Tyr His Val 130
 120 125

ttc tct gag cca aag att ggt gaa gag cgc gtt tcc ggc gca gtc tgc 547
 Phe Ser Glu Pro Lys Ile Gly Glu Glu Arg Val Ser Gly Ala Val Cys 145
 135 140

acc ttc gca gct gtt atc acc gca gag cta gca aag ggt gct gag gtt 595
 Thr Phe Ala Ala Val Ile Thr Ala Glu Leu Ala Lys Gly Ala Glu Val 165
 150 155 160

gta gac cca gtg gca acc gca aag cgt gtg gtc acc cgt gcg gtt caa 643
 Val Asp Pro Val Ala Thr Ala Lys Arg Val Val Thr Arg Ala Val Gln 180
 170 175

gat gct gtt gca tcc aac gca cct ttt acc tcc gta tgg ctt gct gag 691
 Asp Ala Val Ala Ser Asn Ala Pro Phe Thr Ser Val Trp Leu Ala Glu 195
 185 190

gac aac aag tagagtttta aaataccgat caa 723
 Asp Asn Lys 200

<210> 2222
 <211> 200
 <212> PRT
 <213> *Corynebacterium glutamicum*
 <400> 2222
 Leu Thr His Leu Phe Leu Glu Leu Asp Glu Arg Leu Val Leu Gly Val 15
 1 5 10
 Gln Gln Asp Gly Tyr Gln Trp Thr Glu His Leu Phe Arg Leu Pro Leu 30
 20 25 30
 Gln His Leu Arg Asn Ser Pro Asn Asp Leu Gln Gly Leu Lys Ile Arg 45
 35 40 45
 Trp Cys Glu Leu Tyr Ser Thr Thr Gly Lys Asp Gln Gly Val Glu Leu 60
 50 55 60
 Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn Phe Glu Ala Ser Thr 80
 65 70 75 80
 Leu Ser Gly Leu Glu Lys Leu Glu Thr Val Glu Asp Leu Lys Glu Ala 95
 85 90 95

Ala Arg Leu Ile Tyr Glu Gln Gly Pro Gln Tyr Val Val Val Lys Gly
 100 105 110

Gly Met Asp Phe Pro Gly Glu Asn Ala Val Asp Val Leu Phe Asp Gly
 115 120 125

Ser Ser Tyr His Val Phe Ser Glu Pro Lys Ile Gly Glu Glu Arg Val
 130 135 140

Ser Gly Ala Val Cys Thr Phe Ala Ala Val Ile Thr Ala Glu Leu Ala
 145 150 155 160

Lys Gly Ala Glu Val Val Asp Pro Val Ala Thr Ala Lys Arg Val Val
 165 170 175

Thr Arg Ala Val Gln Asp Ala Val Ala Ser Asn Ala Pro Phe Thr Ser
 180 185 190

Val Trp Leu Ala Glu Asp Asn Lys
 195 200

<210> 2223
 <211> 630
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(607)
 <223> RXA01414

<400> 2223
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 gttttaagaa tttattacct ctctacagga gaaccacgcg atg gcc gtt ttt gat 115
 Met Ala Val Phe Asp
 1 5

ttc cct aac ccc gtt aac gaa tat gca gct cgc tgc act gcg ggt ttg 163
 Phe Pro Asn Pro Val Asn Glu Tyr Ala Ala Arg Cys Thr Ala Gly Leu
 10 15 20

gtt gtt ttg ctg agc gcc gcc acg ctt ttt gcc tct ggt gac ctt cgt 211
 Val Val Leu Leu Ser Ala Ala Thr Leu Phe Ala Ser Gly Asp Leu Arg
 25 30 35

att att ttg gca agc atc ttg acc ttc ggc ttc gca ttg cgc gtg gcc 259
 Ile Ile Leu Ala Ser Ile Leu Thr Phe Gly Phe Ala Leu Arg Val Ala
 40 45 50

ggc gga ccc cgt tac tcc ccc ttt gga cgt ctt tca gta cac gta ctt 307
 Gly Gly Pro Arg Tyr Ser Pro Phe Gly Arg Leu Ser Val His Val Leu
 55 60 65

gta cca ctg ctg aag aaa gca ccg atc ctg acc cct ggc cca cca aag 355
 Val Pro Leu Leu Lys Lys Ala Pro Ile Leu Thr Pro Gly Pro Pro Lys
 70 75 80 85

cgc ttc gcg cag acc atc ggc ctg ggc ttt agc ggt act tcc ctt atc 403


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Arg Phe Ala Gln Thr Ile Gly Leu Gly Phe Ser Gly Thr Ser Leu Ile
      90                      95                      100

ctt atg gcc ttt gga ttt aac gtt gca gct tcc gta gtc cta gtc atg 451
Leu Met Ala Phe Gly Phe Asn Val Ala Ala Ser Val Val Leu Val Met
      105                      110                      115

ctc atc gca gca gcc acc tta gaa tcc gtc ttt ggt atc tgc ctc ggt 499
Leu Ile Ala Ala Thr Leu Glu Ser Val Phe Gly Ile Cys Leu Gly
      120                      125                      130

tgc tgg gga ttc ggc aag ctc atg cgc tac ggc gtc atc cca gaa gac 547
Cys Trp Gly Phe Gly Lys Leu Met Arg Tyr Gly Val Ile Pro Glu Asp
      135                      140                      145

gtt tgc gag cag tgc ttc cag aag gaa tcc tcc cgc acc ggc tgg ctc 595
Val Cys Glu Gln Cys Phe Gln Lys Glu Ser Ser Arg Thr Gly Trp Leu
      150                      155                      160

gtt agc ctg aag tagcacttcg aatctaagac cac 630
Val Ser Leu Lys

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<210> 2224

<211> 169

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2224

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Met Ala Val Phe Asp Phe Pro Asn Pro Val Asn Glu Tyr Ala Ala Arg
  1              5              10              15

Cys Thr Ala Gly Leu Val Val Leu Leu Ser Ala Ala Thr Leu Phe Ala
  20              25              30

Ser Gly Asp Leu Arg Ile Ile Leu Ala Ser Ile Leu Thr Phe Gly Phe
  35              40              45

Ala Leu Arg Val Ala Gly Gly Pro Arg Tyr Ser Pro Phe Gly Arg Leu
  50              55              60

Ser Val His Val Leu Val Pro Leu Leu Lys Lys Ala Pro Ile Leu Thr
  65              70              75              80

Pro Gly Pro Pro Lys Arg Phe Ala Gln Thr Ile Gly Leu Gly Phe Ser
  85              90              95

Gly Thr Ser Leu Ile Leu Met Ala Phe Gly Phe Asn Val Ala Ala Ser
  100             105             110

Val Val Leu Val Met Leu Ile Ala Ala Thr Leu Glu Ser Val Phe
  115             120             125

Gly Ile Cys Leu Gly Cys Trp Gly Phe Gly Lys Leu Met Arg Tyr Gly
  130             135             140

Val Ile Pro Glu Asp Val Cys Glu Gln Cys Phe Gln Lys Glu Ser Ser
  145             150             155             160

Arg Thr Gly Trp Leu Val Ser Leu Lys

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165

<210> 2225
 <211> 720
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(697)
 <223> RXA01417

<400> 2225
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 Met Thr Asp Lys Phe
 1 5
 gac aga gtc ctt gct gta gag gtg tgc att cag gag tgg atc gac gag 163
 Asp Arg Val Leu Ala Val Glu Val Cys Ile Gln Glu Trp Ile Asp Glu
 10 15 20
 caa aac ctc acg cta gag gtg cca tta atg att gca cgt ttg cag ctt 211
 Gln Asn Leu Thr Leu Glu Val Pro Leu Met Ile Ala Arg Leu Gln Leu
 25 30 35
 aga gac gtc gcg aag gat atc act gct gtt cac gaa gaa aaa ttc tac 259
 Arg Asp Val Ala Lys Asp Ile Thr Ala Val His Glu Glu Lys Phe Tyr
 40 45 50
 gac ctc act gat atc gat act gat gcc ttt gtg aaa aac atc aaa ctg 307
 Asp Leu Thr Asp Ile Asp Thr Asp Ala Phe Val Lys Asn Ile Lys Leu
 55 60 65
 gga tgg aat gaa cgc ttg atc aag aaa agc ctc ttt cca caa ccg gac 355
 Gly Trp Asn Glu Arg Leu Ile Lys Lys Ser Leu Phe Pro Gln Pro Asp
 70 75 80 85
 gtg cat aaa caa cat ttc aca gaa act gaa cat ggc att gac gcg act 403
 Val His Lys Gln His Phe Thr Glu Thr Glu His Gly Ile Asp Ala Thr
 90 95 100
 gtg acg gtc tgg tcg aag gcc ttc gat ccg gaa agt ggc ccc gac ttc 451
 Val Thr Val Trp Ser Lys Gly Phe Asp Pro Glu Ser Gly Pro Asp Phe
 105 110 115
 ttg gtt tcc tat gtg gat ggt ctt tgg tca gcc gat att aga aac cgc 499
 Leu Val Ser Tyr Val Asp Gly Leu Trp Ser Ala Asp Ile Arg Asn Arg
 120 125 130
 atc acg aaa ttt cag aat aga gaa atc gtt agc aaa ttc tat ttt act 547
 Ile Thr Lys Phe Gln Asn Arg Glu Ile Val Ser Lys Phe Tyr Phe Thr
 135 140 145
 cca gaa cat att aag gag gat ttc tcc gca gag att ttt att 595
 Pro Glu His Ile Lys Glu Asp Gly Asp Phe Ser Ala Glu Ile Phe Ile
 150 155 160 165
 aac cga cca gaa aat gac gac gac tca caa gat ttg gtc gag gtg tgg 643

Asn Arg Pro Glu Asn Asp Asp Asp Ser Gln Asp Leu Val Glu Val Trp
 170 175 180

act gat caa gac acc aga tac tgc ggt gaa atg atc atc tat ttc aaa 691
 Thr Asp Gln Asp Thr Arg Tyr Cys Gly Glu Met Ile Ile Tyr Phe Lys
 185 190 195

tgg ctc taaattccac ttttctgcat cag 720
 Trp Leu

<210> 2226
 <211> 199
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2226
 Met Thr Asp Lys Phe Asp Arg Val Leu Ala Val Glu Val Cys Ile Gln
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Glu Trp Ile Asp Glu Gln Asn Leu Thr Leu Glu Val Pro Leu Met Ile
 20 25 30

Ala Arg Leu Gln Leu Arg Asp Val Ala Lys Asp Ile Thr Ala Val His
 35 40 45

Glu Glu Lys Phe Tyr Asp Leu Thr Asp Ile Asp Thr Asp Ala Phe Val
 50 55 60

Lys Asn Ile Lys Leu Gly Trp Asn Glu Arg Leu Ile Lys Lys Ser Leu
 65 70 75 80

Phe Pro Gln Pro Asp Val His Lys Gln His Phe Thr Glu Thr Glu His
 85 90 95

Gly Ile Asp Ala Thr Val Thr Val Trp Ser Lys Gly Phe Asp Pro Glu
 100 105 110

Ser Gly Pro Asp Phe Leu Val Ser Tyr Val Asp Gly Leu Trp Ser Ala
 115 120 125

Asp Ile Arg Asn Arg Ile Thr Lys Phe Gln Asn Arg Glu Ile Val Ser
 130 135 140

Lys Phe Tyr Phe Thr Pro Glu His Ile Lys Glu Asp Gly Asp Phe Ser
 145 150 155 160

Ala Glu Ile Phe Ile Asn Arg Pro Glu Asn Asp Asp Asp Ser Gln Asp
 165 170 175

Leu Val Glu Val Trp Thr Asp Gln Asp Thr Arg Tyr Cys Gly Glu Met
 180 185 190

Ile Ile Tyr Phe Lys Trp Leu
 195

<210> 2227
 <211> 510
 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(487)

<223> RXA01421

<400> 2227

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	Met	Thr	Ser	Lys	Ser	
	1				5	

att agc ggc aag cgc cgg aat ctg cgg tcg ctc act gga gcg cgg tgg	163
Ile Ser Gly Lys Arg Pro Asn Leu Pro Ser Leu Thr Gly Ala Arg Trp	
	10 15 20

ctc gcg gcg ctc gct gtt tat ttt ttg cat gcg ttg gtg ttt ttg tcg	211
Leu Ala Ala Val Tyr Phe Leu His Ala Leu Val Phe Leu Ser	
	25 30 35

gtg tat cgg ttc cag cag tcg gaa ctg ttt gcc aca atc cat aaa ttt	259
Val Tyr Pro Phe Gln Gln Ser Glu Leu Phe Ala Thr Ile His Lys Phe	
	40 45 50

gtc ccc atg cag ctg ggt tca gct ggt gta acc ttc ttc ttt atc ttg	307
Val Pro Met Gln Leu Gly Ser Ala Gly Val Thr Phe Phe Phe Ile Leu	
	55 60 65

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Ser Gly Phe Leu Ile Tyr Trp Ser Asn Ser Gln Leu Lys Gly Met Lys	
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aat gtg ctg tat tac tgc aag cgc cgc atc acc aag att tat ccc atg	403
Asn Val Leu Tyr Tyr Cys Lys Arg Arg Ile Thr Lys Ile Tyr Pro Met	
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cac ttg att gcg ttg cgg atg ttt att gag gcg tcg gcg aag ttc acg	451
His Leu Ile Ala Leu Pro Met Phe Ile Glu Ala Ser Ala Lys Phe Thr	
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act aca ggc att acc tgg gtg ctg att ttg cgc gag taaagctgtg	497
Thr Thr Gly Ile Thr Trp Val Leu Ile Leu Arg Glu	
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<212> FRT

<213> Corynebacterium glutamicum

<400> 2228

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 35 40 45
 Thr Ile His Lys Phe Val Pro Met Gln Leu Gly Ser Ala Gly Val Thr
 50 55 60
 Phe Phe Phe Ile Leu Ser Gly Phe Leu Ile Tyr Trp Ser Asn Ser Gln
 65 70 75 80
 Leu Lys Gly Met Lys Asn Val Leu Tyr Tyr Cys Lys Arg Arg Ile Thr
 85 90 95
 Lys Ile Tyr Pro Met His Leu Ile Ala Leu Pro Met Phe Ile Glu Ala
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 Ser Ala Lys Phe Thr Thr Thr Gly Ile Thr Trp Val Leu Ile Leu Arg
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 Glu

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 <212> DNA
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 <222> (101)..(985)
 <223> RXA01425

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 Val Leu Ser Pro Asp
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 tcc gga att acc tgg gcc ttg tcg atc atg ttc ttg acc ttc acc gtg 163
 Ser Gly Ile Thr Trp Ala Leu Ser Ile Met Phe Leu Thr Phe Thr Val
 10 15 20
 cgt atg gtt ctg gtc aag ccg atg gtc aac acc atg cgt tca cag cgc 211
 Arg Met Val Leu Val Lys Pro Met Val Asn Thr Met Arg Ser Gln Arg
 25 30 35
 aag atg caa gac atg gct cca aag atg cag gcc atc cgc gag aag tac 259
 Lys Met Gln Asp Met Ala Pro Lys Met Gln Ala Ile Arg Glu Lys Tyr
 40 45 50
 aaa aat gac cag cag aag atg atg gag gag acc cgc aaa ctt caa aaa 307
 Lys Asn Asp Gln Gln Lys Met Met Glu Glu Thr Arg Lys Leu Gln Lys
 55 60 65
 gaa gtg ggc gtt aac ccc atc gca gcc tgt ttg cca atg ttg gtg cag 355
 Glu Val Gly Val Asn Pro Ile Ala Gly Cys Leu Pro Met Leu Val Gln
 70 75 80 85
 atc cca gtg ttc ctg ggt ctg ttc cac gtg ctg cgc tcc ttc aac cgc 403
 Ile Pro Val Phe Leu Gly Leu Phe His Val Leu Arg Ser Phe Asn Arg

	90	95	100	
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	Thr Gly Ser Gly Val Gly Gln Leu Glu Met Thr Val Glu Gln Asn Ala			
	105	110	115	
	aac acc ccg aac tac atc ttc ggt gtc gac gag gtt cag tcc ttc ctg	499		
	Asn Thr Pro Asn Tyr Ile Phe Gly Val Asp Glu Val Gln Ser Phe Leu			
	120	125	130	
	cgt gca gac ctg ttc ggt gcg cca ctg tcg tcc tac atc acc atg cct	547		
	Arg Ala Asp Leu Phe Gly Ala Pro Leu Ser Ser Tyr Ile Thr Met Pro			
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	gct gac gcg ttc gac gcg ttc ctt ggc ctg gat gtc tcc cgc ctc aac	595		
	Ala Asp Ala Phe Asp Ala Phe Leu Gly Leu Asp Val Ser Arg Leu Asn			
	150	155	160	165
	atc gcg ctg gtt gca gct cca atg att ttg atc att gtc gtg gca act	643		
	Ile Ala Leu Val Ala Ala Pro Met Ile Leu Ile Ile Val Val Ala Thr			
	170	175	180	
	cac atg aac gcg cgt ctg tcc gtc aac cgc cag gaa gct cgc aag gca	691		
	His Met Asn Ala Arg Leu Ser Val Asn Arg Gln Glu Ala Arg Lys Ala			
	185	190	195	
	gcc gcc aag cag cag gcc gct tcc agc gat cag atg gcc atg cag atg	739		
	Ala Gly Lys Gln Gln Ala Ala Ser Ser Asp Gln Met Ala Met Gln Met			
	200	205	210	
	caa atg atg aac aag atg atg ctc tgg ttc atg cca gcc acc att ttg	787		
	Gln Met Met Asn Lys Met Met Leu Trp Phe Met Pro Ala Thr Ile Leu			
	215	220	225	
	ttc acc gcc ttc atc tgg acc atc ggt ctt ctt gtc tac atg atg tcc	835		
	Phe Thr Gly Phe Ile Trp Thr Ile Gly Leu Leu Val Tyr Met Met Ser			
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	aac aac gtg tgg acc ttc ttc cag cag cgc tac atc ttc gcc aag atg	883		
	Asn Asn Val Trp Thr Phe Phe Gln Gln Arg Tyr Ile Phe Ala Lys Met			
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	gac gct gag gaa gca gct gag gag gag gaa aag cgc gca gca aag cgc	931		
	Asp Ala Glu Glu Ala Ala Glu Glu Glu Lys Arg Ala Ala Lys Arg			
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	act acc gct cca aag cct gcc gtg aag cca gaa aac ccc aag aag cgt	979		
	Thr Thr Ala Pro Lys Pro Gly Val Lys Pro Glu Asn Pro Lys Lys Arg			
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	Lys Lys			
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	<213> Corynebacterium glutamicum			
	<400> 2230			

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 35 40 45
 Ile Arg Glu Lys Tyr Lys Asn Asp Gln Gln Lys Met Met Glu Glu Thr
 50 55 60
 Arg Lys Leu Gln Lys Glu Val Gly Val Asn Pro Ile Ala Gly Cys Leu
 65 70 75 80
 Pro Met Leu Val Gln Ile Pro Val Phe Leu Gly Leu Phe His Val Leu
 85 90 95
 Arg Ser Phe Asn Arg Thr Gly Ser Gly Val Gly Gln Leu Glu Met Thr
 100 105 110
 Val Glu Gln Asn Ala Asn Thr Pro Asn Tyr Ile Phe Gly Val Asp Glu
 115 120 125
 Val Gln Ser Phe Leu Arg Ala Asp Leu Phe Gly Ala Pro Leu Ser Ser
 130 135 140
 Tyr Ile Thr Met Pro Ala Asp Ala Phe Asp Ala Phe Leu Gly Leu Asp
 145 150 155 160
 Val Ser Arg Leu Asn Ile Ala Leu Val Ala Ala Pro Met Ile Leu Ile
 165 170 175
 Ile Val Val Ala Thr His Met Asn Ala Arg Leu Ser Val Asn Arg Gln
 180 185 190
 Glu Ala Arg Lys Ala Ala Gly Lys Gln Gln Ala Ala Ser Ser Asp Gln
 195 200 205
 Met Ala Met Gln Met Gln Met Met Asn Lys Met Met Leu Trp Phe Met
 210 215 220
 Pro Ala Thr Ile Leu Phe Thr Gly Phe Ile Trp Thr Ile Gly Leu Leu
 225 230 235 240
 Val Tyr Met Met Ser Asn Asn Val Trp Thr Phe Phe Gln Gln Arg Tyr
 245 250 255
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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(718)

<223> RXA01429

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Leu	Phe	Pro	Ile	Val	Gln	Glu	His	Ile	Asp	Phe	Leu	His	Pro	Gln	Ala	
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cgc	aag	tgc	gtg	ttt	tgg	gag	ctc	gca	cct	gag	ggt	gca	gct	aaa	gct	211
Arg	Lys	Ser	Val	Phe	Trp	Glu	Leu	Ala	Pro	Glu	Val	Ala	Ala	Lys	Ala	
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gat	cgc	gtg	ttt	gag	aag	gaa	gcc	tgg	ctg	tcc	acc	acg	ctg	ctg	gaa	259
Asp	Pro	Val	Phe	Glu	Lys	Glu	Ala	Trp	Leu	Ser	Thr	Thr	Leu	Leu	Glu	
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Tyr	Glu	Ser	Cys	Gly	Phe	Asn	Ile	Gly	Tyr	Arg	Asn	Gly	Thr	Pro	Ala	
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Leu	Ala	Ser	Val	Ile	Phe	Cys	Glu	Arg	Asp	Ala	Ala	Pro	Gly	Ala	Lys	
	70				75					80				85		

gcg	ctg	cct	acg	gca	ccg	gtg	tct	agc	gac	gct	gcg	atc	atc	agc	agc	403
Ala	Leu	Pro	Thr	Ala	Pro	Val	Ser	Ser	Asp	Ala	Ala	Ile	Ile	Ser	Ser	
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ctg	ttc	atc	gac	gag	gtt	ttc	cgc	ggc	acg	ggc	atg	gaa	tgc	gcg	ctt	451
Leu	Phe	Ile	Asp	Glu	Val	Phe	Arg	Gly	Thr	Gly	Met	Glu	Ser	Ala	Leu	
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ctc	gac	gct	tcc	ctc	atg	gaa	ctc	att	cgc	cgc	gac	tac	cca	gcc	gtt	499
Leu	Asp	Ala	Ser	Leu	Met	Glu	Ile	Arg	Arg	Asp	Tyr	Pro	Ala	Val		
			120				125				130					

gag	gcg	ttt	gga	tac	cgc	tgc	gaa	aac	aca	gaa	gcg	gat	gcg	atc	gca	547
Glu	Ala	Phe	Gly	Tyr	Arg	Ser	Glu	Asn	Thr	Glu	Ala	Asp	Ala	Ile	Ala	
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gct	agg	cgt	tta	gaa	atc	ggc	ctg	att	gat	gtg	gag	gcg	tta	gaa	tca	595
Ala	Arg	Arg	Leu	Glu	Ile	Gly	Leu	Ile	Asp	Val	Glu	Ala	Leu	Glu	Ser	
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Ala	Gly	Phe	Glu	Val	Val	Ala	Asp	His	Pro	Val	Leu	Pro	Arg	Leu	Arg	
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atg	gaa	tta	cca	ccc	gca	acg	gtg	ctg	ctc	aca	gct	aag	gat	gcc	cag	691
Met	Glu	Leu	Pro	Pro	Ala	Thr	Val	Leu	Leu	Thr	Ala	Lys	Asp	Ala	Gln	
			185				190						195			

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caa 741

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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2232
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 Val Ala Ala Lys Ala Asp Pro Val Phe Glu Lys Glu Ala Trp Leu Ser
 35 40 45
 Thr Thr Leu Leu Glu Tyr Glu Ser Cys Gly Phe Asn Ile Gly Tyr Arg
 50 55 60
 Asn Gly Thr Pro Ala Leu Ala Ser Val Ile Phe Cys Glu Arg Asp Ala
 65 70 75 80
 Ala Pro Gly Ala Lys Ala Leu Pro Thr Ala Pro Val Ser Ser Asp Ala
 85 90 95
 Ala Ile Ile Ser Ser Leu Phe Ile Asp Glu Val Phe Arg Gly Thr Gly
 100 105 110
 Met Glu Ser Ala Leu Leu Asp Ala Ser Leu Met Glu Leu Ile Arg Arg
 115 120 125
 Asp Tyr Pro Ala Val Glu Ala Phe Gly Tyr Arg Ser Glu Asn Thr Glu
 130 135 140
 Ala Asp Ala Ile Ala Ala Arg Arg Leu Glu Ile Gly Leu Ile Asp Val
 145 150 155 160
 Glu Ala Leu Glu Ser Ala Gly Phe Glu Val Val Ala Asp His Pro Val
 165 170 175
 Leu Pro Arg Leu Arg Met Glu Leu Pro Pro Ala Thr Val Leu Leu Thr
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 Ala Lys Asp Ala Gln Arg Leu Leu Gln Glu Met Gly Ala Ile
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS

<222> (101)..(646)

<223> RXA01439

<400> 2233

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Met Thr Arg Tyr Phe
1 5

gca gtt tcc aat ctt cag gag ctt ggc tcc ctc gaa gta cac aaa ttg 163
Ala Val Ser Asn Leu Gln Glu Leu Gly Ser Leu Glu Val His Lys Leu
10 15 20

tac aaa ctt cgt gta gat att ttc gtc cac gag cag cag act cgg tac 211
Tyr Lys Leu Arg Val Asp Ile Phe Val His Glu Gln Gln Thr Pro Tyr
25 30 35

gcg gag atc gat gac acc gat gct gcc cca acc acc aat cac atc ctg 259
Ala Glu Ile Asp Asp Thr Asp Ala Ala Pro Thr Thr Asn His Ile Leu
40 45 50

gtt tgg gag cgc gcc gac gcc acc cca acc aac ctc atc ggc tgc gca 307
Val Trp Glu Arg Ala Asp Ala Thr Pro Thr Asn Leu Ile Gly Cys Ala
55 60 65

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Arg Leu Ala Pro Ile Thr Ala Ala Glu Leu Lys Ala Tyr Thr Gly Lys
70 75 80 85

ggc att tcg ctt gac gac gcc acc ccg ctc tca caa ctc ggc cgc gta 403
Gly Ile Ser Leu Asp Asp Ala Thr Pro Leu Ser Gln Leu Gly Arg Val
90 95 100

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Ala Val Ala Gln Glu Gly Arg Gly Ser Gly Leu Ser Gly Glu Leu Met
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cgc aac gcg ctg cgt ctt gca tat gag cag tac ccc gac cgc gat gtt 499
Arg Asn Ala Leu Arg Leu Ala Tyr Glu Gln Tyr Pro Asp Arg Asp Val
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gtc ctg acc gcg cag aag cct ttg gta gat ttc tac gca gaa tac ggc 547
Val Leu Thr Ala Gln Lys Pro Leu Val Asp Phe Tyr Ala Glu Tyr Gly
135 140 145

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Phe Glu Val Leu Gly Glu Glu Tyr Leu Asp Ser Gly Val Pro His Leu
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ccg atg ttg ctc aag gct gat gag ctt gaa agg ttc tca gac cta gac 643
Pro Met Leu Leu Lys Ala Asp Glu Leu Glu Arg Phe Ser Asp Leu Asp
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<211> 182

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2234

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 35 40 45

Thr Asn His Ile Leu Val Trp Glu Arg Ala Asp Ala Thr Pro Thr Asn
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Leu Ile Gly Cys Ala Arg Leu Ala Pro Ile Thr Ala Ala Glu Leu Lys
 65 70 75 80

Ala Tyr Thr Gly Lys Gly Ile Ser Leu Asp Asp Ala Thr Pro Leu Ser
 85 90 95

Gln Leu Gly Arg Val Ala Val Ala Gln Glu Gly Arg Gly Ser Gly Leu
 100 105 110

Ser Gly Glu Leu Met Arg Asn Ala Leu Arg Leu Ala Tyr Glu Gln Tyr
 115 120 125

Pro Asp Arg Asp Val Val Leu Thr Ala Gln Lys Pro Leu Val Asp Phe
 130 135 140

Tyr Ala Glu Tyr Gly Phe Glu Val Leu Gly Glu Glu Tyr Leu Asp Ser
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Phe Ser Asp Leu Asp Ala
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<210> 2235

<211> 1131

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1108)

<223> RXA01440

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acgattttgg agccggcaca cactaatttt aggagcactg atg aaa acc aag tgg 115
 Met Lys Thr Lys Trp
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tta gcg atc att oca ttc gtg gcg ctt gcg gtg gtt gca tgc tct gat 163
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Thr Ser Glu Thr Ala Ala Gln Pro Pro Gln Pro Thr Thr Pro Ala Glu	
40 45 50	
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Thr Thr Thr Gln Gln Ala Glu Gly Ile Asn Leu Thr Thr Pro Arg Tyr Thr	
55 60 65	
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Arg Gln Asn Val Gly His Phe Ser Ser Gly Tyr Gln Pro Gly Gln Val	
70 75 80 85	
agt ttt tcc tca gct gat gga acc att aaa tgt gag ttt cgc ccc atg	403
Ser Phe Ser Ser Asp Gly Thr Ile Lys Cys Glu Phe Arg Pro Met	
90 95 100	
gaa cag gac gca cct atc aac cgg gag ccc tcc acc gat tgg cgg ttg	451
Glu Gln Asp Ala Pro Ile Asn Arg Glu Pro Ser Thr Asp Trp Arg Leu	
105 110 115	
agt ttc gtg cag ggt gcg tgc caa ttc gac gat ggt tac gta gtg gcg	499
Ser Phe Val Gln Gly Ala Cys Gln Phe Asp Asp Gly Tyr Val Val Ala	
120 125 130	
gat aca aat gtg gaa aac aga cca ggt ttt gct gag tac acc acg gcg	547
Asp Thr Asn Val Glu Asn Arg Pro Gly Phe Ala Glu Tyr Thr Thr Ala	
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Ile Ser His Val Met Pro Glu Asn Tyr Thr Thr Leu Pro Pro Gly Thr	
150 155 160 165	
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Tyr Ile Asp Leu His Thr Met Ala Cys Phe Thr Glu Ser Ala Asp Glu	
170 175 180	
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Ile Ser Cys Ile Lys Tyr Ala Thr Asn Glu Thr Phe Arg Ile Ser Ala	
185 190 195	
cag ggt ttt gag atg ctc tca aat gcc cag cgc gac gcg gaa cta acc	739
Gln Gly Phe Glu Met Leu Ser Asn Ala Gln Arg Asp Ala Glu Leu Thr	
200 205 210	
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Thr Gln Gly Gly Leu Tyr Gln Ala Phe Ser Asn Ile Ala Glu Leu Arg	
215 220 225	
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Phe Ser Asp Gly Asn Ala Met Ser Cys Phe Phe Asp Ala Pro Gly Ser	
230 235 240 245	
caa gat ttc tgg tgc caa aca ctc agc acc ccc gcc tgg gac gac gcc	883
Gln Asp Phe Trp Cys Gln Thr Leu Ser Thr Pro Gly Trp Asp Asp Gly	
250 255 260	

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Ser Asn Leu Ile His Leu Thr Val Thr Gly Gly Lys Leu Ser Leu Met
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ggc acc caa gtg ggc aac ccc ggc ctc gac tat ttc cgc ggc cgc cag 979
Gly Thr Gln Val Gly Asn Pro Gly Leu Asp Tyr Phe Arg Gly Arg Gln
      280                      285                      290

ctc att gag gcg cca aat tgg ctt ctc gac gcc tcc ctc tcc gta aca 1027
Leu Ile Glu Ala Pro Asn Ser Leu Leu Asp Ala Ser Leu Ser Val Thr
      295                      300                      305

ctc gac ggc gat cgg gtg cgt ttc cgc acc gcg acc ggc gag gag atg 1075
Leu Asp Gly Asp Arg Val Arg Phe Arg Thr Ala Thr Gly Glu Glu Met
      310                      315                      320                      325

tgg gtg agt tcc agt gac tac gga tta ggc gtc taggtctgag aacctttcaa 1128
Trp Val Ser Ser Ser Asp Tyr Gly Leu Gly Val
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gct 1131

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<213> Corynebacterium glutamicum

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Thr Ala Pro Gln Pro Thr Ser Glu Thr Ala Ala Gln Pro Pro Gln Pro
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Thr Thr Pro Ala Glu Thr Thr Thr Gln Gln Ala Glu Gly Ile Asn Leu
 50          55          60

Thr Pro Arg Tyr Thr Arg Gln Asn Val Gly His Phe Ser Ser Gly Tyr
 65          70          75          80

Gln Pro Gly Gln Val Ser Phe Ser Ser Ala Asp Gly Thr Ile Lys Cys
          85          90          95

Glu Phe Arg Pro Met Glu Gln Asp Ala Pro Ile Asn Arg Glu Pro Ser
 100          105          110

Thr Asp Trp Arg Leu Ser Phe Val Gln Gly Ala Cys Gln Phe Asp Asp
 115          120          125

Gly Tyr Val Val Ala Asp Thr Asn Val Glu Asn Arg Pro Gly Phe Ala
 130          135          140

Glu Tyr Thr Thr Ala Ile Ser His Val Met Pro Glu Asn Tyr Thr Thr
 145          150          155          160

Leu Pro Pro Gly Thr Tyr Ile Asp Leu His Thr Met Ala Cys Phe Thr
 165          170          175

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Glu Ser Ala Asp Glu Ile Ser Cys Ile Lys Tyr Ala Thr Asn Glu Thr
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Phe Arg Ile Ser Ala Gln Gly Phe Glu Met Leu Ser Asn Ala Gln Arg
195 200 205

Asp Ala Glu Leu Thr Thr Gln Gly Gly Leu Tyr Gln Ala Phe Ser Asn
210 215 220

Ile Ala Glu Leu Arg Phe Ser Asp Gly Asn Ala Met Ser Cys Phe Phe
225 230 235 240

Asp Ala Pro Gly Ser Gln Asp Phe Trp Cys Gln Thr Leu Ser Thr Pro
245 250 255

Gly Trp Asp Asp Gly Ser Asn Leu Ile His Leu Thr Val Thr Gly Gly
260 265 270

Lys Leu Ser Leu Met Gly Thr Gln Val Gly Asn Pro Gly Leu Asp Tyr
275 280 285

Phe Arg Gly Arg Gln Leu Ile Glu Ala Pro Asn Ser Leu Leu Asp Ala
290 295 300

Ser Leu Ser Val Thr Leu Asp Gly Asp Arg Val Arg Phe Arg Thr Ala
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Thr Gly Glu Glu Met Trp Val Ser Ser Ser Asp Tyr Gly Leu Gly Val
325 330 335

<210> 2237

<211> 1152

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1129)

<223> RXA01441

<400> 2237

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Met Ala Arg Thr Thr
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aca gcg cac gca gtt ctc atg gcg ctt agt tca gtc ggg ctt ttg atg 163
Thr Ala His Ala Val Leu Met Ala Leu Ser Ser Val Gly Leu Leu Met
10 15 20

ctc cag gcc tgc tcc gaa cag gaa caa acc cca gaa caa acg cca gcg 211
Leu Gln Ala Cys Ser Glu Gln Glu Gln Thr Pro Glu Gln Thr Pro Ala
25 30 35

ccc acc ctg act tcg cag gct ccc gag act cct caa gcc tca aca acc 259

Pro	Thr	Leu	Thr	Ser	Gln	Ala	Pro	Glu	Thr	Pro	Gln	Ala	Ser	Thr	Thr	
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Ser	Ser	Ala	Ser	Ser	Thr	Ala	Thr	Pro	Ile	Ala	Thr	Pro	Ile	Ala	Ala	
	55				60					65						
acc	gag	ttg	gat	tat	ctc	cac	atc	gat	cca	gca	acg	tat	gac	atc	ggc	355
Thr	Glu	Leu	Asp	Tyr	Leu	His	Ile	Asp	Pro	Ala	Thr	Tyr	Asp	Ile	Gly	
	70				75					80				85		
gtc	caa	gac	caa	gaa	act	gcc	gta	ttt	acc	act	ggc	gat	ggg	atc	aca	403
Val	Gln	Asp	Gln	Glu	Thr	Ala	Val	Phe	Thr	Thr	Gly	Asp	Gly	Ile	Thr	
				90				95					100			
gcg	cag	tgt	ttc	ttc	gag	gca	aca	ccg	ggg	gag	acc	agc	tat	cag	atc	451
Ala	Gln	Cys	Phe	Phe	Glu	Ala	Thr	Pro	Gly	Glu	Thr	Ser	Tyr	Gln	Ile	
			105					110					115			
aag	gag	ttt	gat	ttc	gac	gaa	act	gcg	gga	acg	tgc	gct	ttt	ggc	gat	499
Lys	Glu	Phe	Asp	Phe	Asp	Glu	Thr	Ala	Gly	Thr	Cys	Ala	Phe	Gly	Asp	
	120						125					130				
caa	cac	atc	agc	gtc	acc	acg	gat	gaa	aat	gtc	cgg	gaa	cgc	ttt	gcc	547
Gln	His	Ile	Ser	Val	Thr	Thr	Asp	Glu	Asn	Val	Arg	Glu	Arg	Phe	Ala	
	135				140						145					
gaa	ttg	agt	gaa	acc	gaa	gaa	gaa	tta	cca	gaa	gcg	caa	gcg	act	ctc	595
Glu	Leu	Ser	Glu	Thr	Glu	Glu	Glu	Leu	Pro	Glu	Ala	Gln	Ala	Thr	Leu	
	150				155					160				165		
gat	gtt	ggc	gag	atg	gtg	cat	ctt	ggc	cac	atg	ggc	tgt	tgg	gcg	ccg	643
Asp	Val	Gly	Glu	Met	Val	His	Leu	Gly	His	Met	Gly	Cys	Trp	Ala	Pro	
			170					175					180			
agt	gta	tcg	gag	ttt	agt	tgt	ctc	gat	ttc	gcc	tcc	aac	cag	gcg	ttc	691
Ser	Val	Ser	Glu	Phe	Ser	Cys	Leu	Asp	Phe	Ala	Ser	Asn	Gln	Ala	Phe	
			185					190					195			
acc	atg	aat	gaa	cag	ggc	ttc	cat	gag	ctt	gat	cct	gca	aaa	gcc	act	739
Thr	Met	Asn	Glu	Gln	Gly	Phe	His	Glu	Leu	Asp	Pro	Ala	Lys	Ala	Thr	
	200						205					210				
gag	cag	cta	att	aat	tcg	agt	ggc	cag	gtt	caa	acg	tta	tcg	aaa	atg	787
Glu	Gln	Leu	Ile	Asn	Ser	Ser	Gly	Gln	Val	Gln	Thr	Leu	Ser	Lys	Met	
	215				220					225						
acg	aat	ttc	cag	ttc	acc	gat	ggc	acc	agc	atc	acc	tgt	gtc	agt	gag	835
Thr	Asn	Phe	Gln	Phe	Thr	Asp	Gly	Thr	Ser	Ile	Thr	Cys	Val	Ser	Glu	
	230				235					240				245		
ttg	cag	gcg	gaa	gag	ttc	ttg	tgc	cac	aac	agt	ggc	cct	gga	ggc	tgg	883
Leu	Gln	Ala	Glu	Glu	Phe	Leu	Cys	His	Asn	Ser	Gly	Pro	Gly	Gly	Trp	
			250					255					260			
tca	act	tca	gct	ggc	cct	gcc	aac	acc	ctg	tgg	tgg	aat	ctg	aac	cag	931
Ser	Thr	Ser	Ala	Gly	Pro	Ala	Asn	Thr	Leu	Trp	Trp	Asn	Leu	Asn	Gln	
			265				270						275			
gcc	gac	tcc	gag	ttt	gag	ggc	gct	cgc	ccc	acg	aat	cca	acg	caa	agc	979
Ala	Asp	Ser	Glu	Phe	Glu	Gly	Ala	Arg	Pro	Thr	Asn	Pro	Thr	Gln	Ser	

280	285	290	
gtt tat aaa tct caa caa ata ttc ggt ccg gga tgg tat ctc ctc gcg			1027
Val Tyr Lys Ser Gln Gln Ile Phe Gly Pro Gly Ser Tyr Leu Leu Ala			
295	300	305	
aac ggt gtg agt gca gaa ttt gat gga acc acc ctc acg ctg acc acg			1075
Asn Gly Val Ser Ala Glu Phe Asp Gly Thr Thr Leu Thr Leu Thr Thr			
310	315	320	325
cct cag ggg aat cag tat tgg gca aac aca cac gat ttt gga gcc gcc			1123
Pro Gln Gly Asn Gln Tyr Trp Ala Asn Thr His Asp Phe Gly Ala Gly			
330	335	340	
aca cac taattttagg agcactgatg aaa			1152
Thr His			
<210> 2238			
<211> 343			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 2238			
Met Ala Arg Thr Thr Thr Ala His Ala Val Leu Met Ala Leu Ser Ser			
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Val Gly Leu Leu Met Leu Gln Ala Cys Ser Glu Gln Glu Gln Thr Pro			
20	25	30	
Glu Gln Thr Pro Ala Pro Thr Leu Thr Ser Gln Ala Pro Glu Thr Pro			
35	40	45	
Gln Ala Ser Thr Thr Ser Ser Ala Ser Ser Thr Ala Thr Pro Ile Ala			
50	55	60	
Thr Pro Ile Ala Ala Thr Glu Leu Asp Tyr Leu His Ile Asp Pro Ala			
65	70	75	80
Thr Tyr Asp Ile Gly Val Gln Asp Gln Glu Thr Ala Val Phe Thr Thr			
85	90	95	
Gly Asp Gly Ile Thr Ala Gln Cys Phe Phe Glu Ala Thr Pro Gly Glu			
100	105	110	
Thr Ser Tyr Gln Ile Lys Glu Phe Asp Phe Asp Glu Thr Ala Gly Thr			
115	120	125	
Cys Ala Phe Gly Asp Gln His Ile Ser Val Thr Thr Asp Glu Asn Val			
130	135	140	
Arg Glu Arg Phe Ala Glu Leu Ser Glu Thr Glu Glu Glu Leu Pro Glu			
145	150	155	160
Ala Gln Ala Thr Leu Asp Val Gly Glu Met Val His Leu Gly His Met			
165	170	175	
Gly Cys Trp Ala Pro Ser Val Ser Glu Phe Ser Cys Leu Asp Phe Ala			
180	185	190	

Ser Asn Gln Ala Phe Thr Met Asn Glu Gln Gly Phe His Glu Leu Asp
195 200 205

Pro Ala Lys Ala Thr Glu Gln Leu Ile Asn Ser Ser Gly Gln Val Gln
210 215 220

Thr Leu Ser Lys Met Thr Asn Phe Gln Phe Thr Asp Gly Thr Ser Ile
225 230 235 240

Thr Cys Val Ser Glu Leu Gln Ala Glu Glu Phe Leu Cys His Asn Ser
245 250 255

Gly Pro Gly Gly Trp Ser Thr Ser Ala Gly Pro Ala Asn Thr Leu Trp
260 265 270

Trp Asn Leu Asn Gln Ala Asp Ser Glu Phe Glu Gly Ala Arg Pro Thr
275 280 285

Asn Pro Thr Gln Ser Val Tyr Lys Ser Gln Gln Ile Phe Gly Pro Gly
290 295 300

Ser Tyr Leu Leu Ala Asn Gly Val Ser Ala Glu Phe Asp Gly Thr Thr
305 310 315 320

Leu Thr Leu Thr Thr Pro Gln Gly Asn Gln Tyr Trp Ala Asn Thr His
325 330 335

Asp Phe Gly Ala Gly Thr His
340

<210> 2239

<211> 1116

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1093)

<223> RXA01445

<400> 2239

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aggccttggga aattttggca tccaggaat cgcgctgtca atg atc cca ctt att 115

Met Ile Pro Leu Ile
1 5

aat gta cgt ttt ccc gtt gcc gcc tta cct ctc gca tta gtg gcg act 163

Asn Val Arg Phe Pro Val Ala Ala Leu Pro Leu Ala Leu Val Ala Thr
10 15 20

gta tgg ctt aat gct tgg gca gac cat ctt ctc cta act ggt ttt att 211

Val Trp Leu Asn Ala Trp Ala Asp His Leu Leu Leu Thr Gly Phe Ile
25 30 35

gtt tat ctt gct gtg gaa tac gca aca agc cgt ggg cgc ttc gct ctc 259

Val Tyr Leu Ala Val Glu Tyr Ala Thr Ser Arg Gly Arg Phe Ala Leu
40 45 50

gca ttg att ttg gga gtt gaa tgg atc tta att gct tat ggg gta gct 307

Ala Leu Ile Leu Gly Val Glu Trp Ile Leu Ile Ala Tyr Gly Val Ala	
55 60 65	
ttg gaa agg cct ctt gag gct aaa gac tct cca tct ctc att acc gaa	355
Leu Glu Arg Pro Leu Glu Ala Lys Asp Ser Pro Ser Leu Ile Thr Glu	
70 75 80 85	
att ttg ctc ata ctt gta gca gct ggc aca ggg gca ggt cgg tgg aaa	403
Ile Leu Leu Ile Leu Val Ala Ala Gly Thr 95 Gly Ala Gly Arg Trp Lys	
90 95 100	
att ttg agt gaa cgc aag caa cgt gca att act cag cag gaa atc atc	451
Ile Leu Ser Glu Arg Lys Gln Arg Ala Ile Thr Gln Gln Glu Ile Ile	
105 110 115	
aaa aaa atc cgt act gat ata gcg cac tat ttg cat gac agt atg gca	499
Lys Lys Ile Arg Thr Asp Ile Ala His Tyr Leu His Asp Ser Met Ala	
120 125 130	
aga tcg ttg gca ata atg ata gtt caa tca aag ctg act gaa cta gag	547
Arg Ser Leu Ala Ile Met Ile Val Gln Ser Lys Leu Thr Glu Leu Glu	
135 140 145	
cct gat cca aaa aag att caa gaa aaa cta aac agt att gcc aaa att	595
Pro Asp Pro Lys Lys Ile Gln Glu Lys Leu Asn Ser Ile Ala Lys Ile	
150 155 160 165	
gga caa gag gca gtg gct gat ttg cat caa tta gtt aga cac ctc gtg	643
Gly Gln Glu Ala Val Ala Asp Leu His Gln Leu Val Arg His Leu Val	
170 175 180	
gtc gag gag tct gct gaa aaa gcc aca gcg ttt gga gca tgg gct gca	691
Val Glu Glu Ser Ala Glu Lys Ala Thr Ala Phe Gly Ala Trp Ala Ala	
185 190 195	
gtt tct att cat gac acg gtt aat tct gcc att cag tta tta gta gat	739
Val Ser Ile His Asp Thr Val Asn Ser Ala Ile Gln Leu Leu Val Asp	
200 205 210	
gca gga cat gtc gtt tcc ttt gac agt aga aaa aag aac tat aag ctg	787
Ala Gly His Val Val Ser Phe Asp Ser Arg Lys Lys Asn Tyr Lys Leu	
215 220 225	
gac cat att gct gaa acg gcg ttt gct tta gcc ttc aat gag gca gtc	835
Asp His Ile Ala Glu Thr Ala Phe Ala Leu Ala Phe Asn Glu Ala Val	
230 235 240 245	
tgt aat gca att aaa cat tct ccg ccc aag gca aac gtt act att cgc	883
Cys Asn Ala Ile Lys His Ser Pro Pro Lys Ala Asn Val Thr Ile Arg	
250 255 260	
ata aca gaa aaa gca cag tct ctt cag att cta gta atg aat cct att	931
Ile Thr Glu Lys Ala Gln Ser Leu Gln Ile Leu Val Met Asn Pro Ile	
265 270 275	
gga gat tgg cat gca aat ggg gag tcc gca att cca ggt gtg ggc att	979
Gly Asp Trp His Ala Asn Gly Glu Ser Ala Ile Pro Gly Val Gly Ile	
280 285 290	
ggc gta gaa agc tta acc aga agg ata cgt aat att aaa gga cag gtc	1027
Gly Val Glu Ser Leu Thr Arg Arg Ile Arg Asn Ile Lys Gly Gln Val	

295	300	305	
tgt gtg act tca ctg	caa gga tac tgg aaa gta gtt att tca cta cct		1075
Cys Val Thr Ser Leu	Gln Gly Tyr Trp Lys Val Val Ile Ser Leu Pro		
310	315 320 325		
ttg aaa tgt gag gat tct taaattgtct ctatttggtg aac			1116
Leu Lys Cys Glu Asp Ser			
330			
 <210> 2240			
<211> 331			
<212> PRT			
<213> <i>Corynebacterium glutamicum</i>			
 <400> 2240			
Met Ile Pro Leu Ile Asn Val Arg Phe Pro Val Ala Ala Leu Pro Leu			
1 5 10 15			
Ala Leu Val Ala Thr Val Trp Leu Asn Ala Trp Ala Asp His Leu Leu			
20 25 30			
Leu Thr Gly Phe Ile Val Tyr Leu Ala Val Glu Tyr Ala Thr Ser Arg			
35 40 45			
Gly Arg Phe Ala Leu Ala Leu Ile Leu Gly Val Glu Trp Ile Leu Ile			
50 55 60			
Ala Tyr Gly Val Ala Leu Glu Arg Pro Leu Glu Ala Lys Asp Ser Pro			
65 70 75 80			
Ser Leu Ile Thr Glu Ile Leu Leu Ile Leu Val Ala Ala Gly Thr Gly			
85 90 95			
Ala Gly Arg Trp Lys Ile Leu Ser Glu Arg Lys Gln Arg Ala Ile Thr			
100 105 110			
Gln Gln Glu Ile Ile Lys Lys Ile Arg Thr Asp Ile Ala His Tyr Leu			
115 120 125			
His Asp Ser Met Ala Arg Ser Leu Ala Ile Met Ile Val Gln Ser Lys			
130 135 140			
Leu Thr Glu Leu Glu Pro Asp Pro Lys Lys Ile Gln Glu Lys Leu Asn			
145 150 155 160			
Ser Ile Ala Lys Ile Gly Gln Glu Ala Val Ala Asp Leu His Gln Leu			
165 170 175			
Val Arg His Leu Val Val Glu Glu Ser Ala Glu Lys Ala Thr Ala Phe			
180 185 190			
Gly Ala Trp Ala Ala Val Ser Ile His Asp Thr Val Asn Ser Ala Ile			
195 200 205			
Gln Leu Leu Val Asp Ala Gly His Val Val Ser Phe Asp Ser Arg Lys			
210 215 220			
Lys Asn Tyr Lys Leu Asp His Ile Ala Glu Thr Ala Phe Ala Leu Ala			
225 230 235 240			

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Phe Asn Glu Ala Val Cys Asn Ala Ile Lys His Ser Pro Pro Lys Ala
      245                      250                      255

Asn Val Thr Ile Arg Ile Thr Glu Lys Ala Gln Ser Leu Gln Ile Leu
      260                      265                      270

Val Met Asn Pro Ile Gly Asp Trp His Ala Asn Gly Glu Ser Ala Ile
      275                      280                      285

Pro Gly Val Gly Ile Gly Val Glu Ser Leu Thr Arg Arg Ile Arg Asn
      290                      295                      300

Ile Lys Gly Gln Val Cys Val Thr Ser Leu Gln Gly Tyr Trp Lys Val
      305                      310                      315                      320

Val Ile Ser Leu Pro Leu Lys Cys Glu Asp Ser
      325                      330

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<210> 2241

<211> 972

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(949)

<223> RXA01447

<400> 2241

tccatgaagt tggagtatgc acgcgtgtgc gcacacagac gttatttcat cttactatcc 60

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catgtgaggt ttttaatcat cgcgatacta agcttgcggt atg cgt ctt ctg gtt 115
      Met Arg Leu Leu Val
      1                      5

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ttg cgg tgc gat gcc cca cac atc aac gaa ttc cct gcc ctt tcc acc 163
Leu Arg Cys Asp Ala Pro His Ile Asn Glu Phe Pro Ala Leu Ser Thr
      10                      15                      20

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tct gtg gag atc cac gat ttg cct gcg gtg ccc acc cga aaa gac ctc 211
Ser Val Glu Ile His Asp Leu Pro Ala Val Pro Thr Arg Lys Asp Leu
      25                      30                      35

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aaa att ctt gat gat gtg gcc ttt gat gtg ctc cct cag gat ccc acg 259
Lys Ile Leu Asp Asp Val Ala Phe Asp Val Leu Pro Gln Asp Pro Thr
      40                      45                      50

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cct tct ctc gat gag atc gcc aag cag cct gat gtc gag cat ttg agc 307
Pro Ser Leu Asp Glu Ile Ala Lys Gln Pro Asp Val Glu His Leu Ser
      55                      60                      65

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agc cct aag ttt gcg cca caa cag cct gaa acc cgt ttg cgc atc gtg 355
Ser Pro Lys Phe Ala Pro Gln Gln Pro Glu Thr Arg Leu Arg Ile Val
      70                      75                      80                      85

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gtg atc ggt tcg gat gca gcg ctg tct gcg gtc ctg act cgt ctc atg 403
Val Ile Gly Ser Asp Ala Ala Leu Ser Ala Val Leu Thr Arg Leu Met
      90                      95                      100

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cgc gcc gat aat ttg tgg gcg gag att gga ttc gtg ccc gtt ggt cct 451
 Arg Ala Asp Asn Leu Trp Ala Glu Ile Gly Phe Val Pro Val Gly Pro
 105 110 115

tca acg gct gcg aag aac tgg ggt ctg ccc gcc gat gag gct gcc gcg 493
 Ser Thr Ala Ala Lys Asn Trp Gly Leu Pro Ala Asp Glu Ala Ala Ala
 120 125 130

ctt gag ctg gca ctg acc gga ttg gtc aat cct gcc cgg ctg atc cgc 547
 Leu Glu Leu Ala Leu Thr Gly Leu Val Asn Pro Ala Pro Leu Ile Arg
 135 140 145

gat gac gtt gcg gtc gcc gtc gcc ggt tca gcc acc atc acc aac tgg 595
 Asp Asp Val Ala Val Ala Val Ala Gly Ser Ala Thr Ile Thr Asn Trp
 150 155 160 165

gag cgg ggt gag atc acc ggc gaa gtc atc gtc gat gat cat gtt ctg 643
 Glu Pro Gly Glu Ile Thr Gly Glu Val Ile Val Asp Asp His Val Leu
 170 175 180

atc cgc cac gag gct gcc tcg aag gcc cca cgc cgt gcc gtc tac ggt 691
 Ile Arg His Glu Ala Ala Ser Lys Ala Pro Arg Arg Gly Val Tyr Gly
 185 190 195

gcc cgc ttg gtg ccg atg ctt gac gcc cca gcc atc gct gcg gtc atc 739
 Ala Arg Leu Val Pro Met Leu Asp Ala Pro Gly Ile Ala Ala Val Ile
 200 205 210

atg gac act ccc ctg ccc ggc gag gtg ccc tcc cgc agc ctg ttc cct 787
 Met Asp Thr Pro Leu Pro Gly Glu Val Pro Ser Arg Ser Leu Phe Pro
 215 220 225

cgc ccc tcg gcc tcg gtt att cca gag agc ttt tcg acg gcc cgt gcc 835
 Arg Pro Ser Gly Ser Val Ile Pro Glu Ser Phe Ser Thr Gly Arg Ala
 230 235 240 245

atg caa gcc gcc gcc ccc tcg cta caa atc cgg gtt gac gga att tcc 883
 Met Gln Ala Gly Gly Pro Ser Leu Gln Ile Arg Val Asp Gly Ile Ser
 250 255 260

cgc aaa cgt aaa gtg gag cgc gtt acc ttc tat cga cat ttg cgc gat 931
 Arg Lys Arg Lys Val Glu Arg Val Thr Phe Tyr Arg His Leu Arg Asp
 265 270 275

ctg caa atc gtg cgg ccg taaaacaagg agccagcatg gca 972
 Leu Gln Ile Val Arg Pro
 280

<210> 2242
 <211> 283
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 2242
 Met Arg Leu Leu Val Leu Arg Cys Asp Ala Pro His Ile Asn Glu Phe
 1 5 10 15
 Pro Ala Leu Ser Thr Ser Val Glu Ile His Asp Leu Pro Ala Val Pro
 20 25 30

Thr Arg Lys Asp Leu Lys Ile Leu Asp Asp Val Ala Phe Asp Val Leu
 35 40 45
 Pro Gln Asp Pro Thr Pro Ser Leu Asp Glu Ile Ala Lys Gln Pro Asp
 50 55 60
 Val Glu His Leu Ser Ser Pro Lys Phe Ala Pro Gln Gln Pro Glu Thr
 65 70 75 80
 Arg Leu Arg Ile Val Ile Gly Ser Asp Ala Ala Leu Ser Ala Val
 85 90 95
 Leu Thr Arg Leu Met Arg Ala Asp Asn Leu Trp Ala Glu Ile Gly Phe
 100 105 110
 Val Pro Val Gly Pro Ser Thr Ala Ala Lys Asn Trp Gly Leu Pro Ala
 115 120 125
 Asp Glu Ala Ala Ala Leu Glu Leu Ala Leu Thr Gly Leu Val Asn Pro
 130 135 140
 Ala Pro Leu Ile Arg Asp Asp Val Ala Val Ala Val Ala Gly Ser Ala
 145 150 155 160
 Thr Ile Thr Asn Trp Glu Pro Gly Glu Ile Thr Gly Glu Val Ile Val
 165 170 175
 Asp Asp His Val Leu Ile Arg His Glu Ala Ala Ser Lys Ala Pro Arg
 180 185 190
 Arg Gly Val Tyr Gly Ala Arg Leu Val Pro Met Leu Asp Ala Pro Gly
 195 200 205
 Ile Ala Ala Val Ile Met Asp Thr Pro Leu Pro Gly Glu Val Pro Ser
 210 215 220
 Arg Ser Leu Phe Pro Arg Pro Ser Gly Ser Val Ile Pro Glu Ser Phe
 225 230 235 240
 Ser Thr Gly Arg Ala Met Gln Ala Gly Gly Pro Ser Leu Gln Ile Arg
 245 250 255
 Val Asp Gly Ile Ser Arg Lys Arg Lys Val Glu Arg Val Thr Phe Tyr
 260 265 270
 Arg His Leu Arg Asp Leu Gln Ile Val Arg Pro
 275 280

<210> 2243

<211> 402

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(379)

<223> RXA01452

<400> 2243

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cgctctagcgt tattgacgct cctcgttata cgctgggtctc gtg atc aga tcg ttc 115
Val Ile Arg Ser Phe
1 5

gcc gac cgc gac acc gag ttg gtc tgg ttg cgt gaa ggt gcg aaa cgc 163
Ala Asp Arg Asp Thr Glu Leu Val Trp Leu Arg Glu Gly Ala Lys Arg
10 15 20

gtc gat ccg cga ata cac aaa gtg gcg aat cgg aag ctg cat ctg ctg 211
Val Asp Pro Arg Ile His Lys Val Ala Asn Arg Lys Leu His Leu Leu
25 30 35

gac gcg gcg acg acc ctc gat gct ctg cgt gtg act ccg ggg aat cgc 259
Asp Ala Ala Thr Thr Leu Asp Ala Leu Arg Val Thr Pro Gly Asn Arg
40 45 50

ctg gaa acg ctc gag ggt gat cga gtc ggt cag tac agc att cga gtc 307
Leu Glu Thr Leu Glu Gly Asp Arg Val Gly Gln Tyr Ser Ile Arg Val
55 60 65

aac gac cag tgg cgg atc tgc ttc cgt tgg aac gac tcg ggc ccc gaa 355
Asn Asp Gln Trp Arg Ile Cys Phe Arg Trp Asn Asp Ser Gly Pro Glu
70 75 80 85

aac gtc gag atc gtg gat tat cac tgaggaggag acgatggctc aga 402
Asn Val Glu Ile Val Asp Tyr His
90

<210> 2244

<211> 93

<212> PRT

<213> Corynebacterium glutamicum

<400> 2244

Val Ile Arg Ser Phe Ala Asp Arg Asp Thr Glu Leu Val Trp Leu Arg
1 5 10 15

Glu Gly Ala Lys Arg Val Asp Pro Arg Ile His Lys Val Ala Asn Arg
20 25 30

Lys Leu His Leu Leu Asp Ala Ala Thr Thr Leu Asp Ala Leu Arg Val
35 40 45

Thr Pro Gly Asn Arg Leu Glu Thr Leu Glu Gly Asp Arg Val Gly Gln
50 55 60

Tyr Ser Ile Arg Val Asn Asp Gln Trp Arg Ile Cys Phe Arg Trp Asn
65 70 75 80

Asp Ser Gly Pro Glu Asn Val Glu Ile Val Asp Tyr His
85 90

<210> 2245

<211> 645

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(622)

<223> RXA01456

<400> 2245

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cctataaagg ccaacaagta gttcacaaaa ggaaaaaatt atg aac gat tcc att 115
                                         Met Asn Asp Ser Ile
                                         1 5

ttt agt ccc caa gca ctg aat aaa gcg atg ctc gaa gcc gtc gag ttt 163
Phe Ser Pro Gln Ala Leu Asn Lys Ala Met Leu Glu Ala Val Glu Glu Phe
                                         10 15 20

atc cac gcc gaa ggt tgg gac gcc gcc cct acc ctg ttc gca ttg gtc 211
Ile His Ala Glu Gly Trp Asp Ala Gly Pro Thr Leu Phe Ala Leu Val
                                         25 30 35

ccc act gaa atg ctg gtg gat act ctt gat gag gca gct gac gac tcc 259
Pro Thr Glu Met Leu Val Asp Thr Leu Asp Glu Ala Ala Asp Asp Ser
                                         40 45 50

cca cta acc ctt gtt gta cag gac aac ctc cct gac aac ttg ctg cca 307
Pro Leu Thr Leu Val Val Gln Asp Asn Leu Pro Asp Asn Leu Leu Pro
                                         55 60 65

ggg tcc gaa gcg tta ggt gac tat gtg tcc cgt ttg gcg tgg cca gca 355
Gly Ser Glu Ala Leu Gly Asp Tyr Val Ser Arg Leu Ala Trp Pro Ala
                                         70 75 80 85

gag att gcc gcc gcg gtg ttg gct cag gaa att atg ttc acc gat gct 403
Glu Ile Ala Gly Ala Val Leu Ala Gln Glu Ile Met Phe Thr Asp Ala
                                         90 95 100

gcc gtt gca gcc tca gaa cca cga ccc gct cgt ctt ttt tcc gcc gtt 451
Ala Val Ala Gly Ser Glu Pro Arg Pro Ala Arg Leu Phe Ser Gly Val
                                         105 110 115

ttg cgc gcc gaa gca gaa ctc acc ctt ctg cag ctt cgc ccc acc gaa 499
Leu Arg Gly Glu Ala Glu Leu Thr Leu Leu Gln Leu Arg Pro Thr Glu
                                         120 125 130

gag gaa ttg gca gaa cgc gga ccg ttt gct gaa gat gaa atc gaa ctg 547
Glu Glu Leu Ala Glu Arg Gly Pro Phe Ala Glu Asp Glu Ile Glu Leu
                                         135 140 145

cgc gcc gcc cca ggg gtt gca ccg ggt gta atc gca gca ctg cgc tac 595
Arg Gly Gly Pro Gly Val Ala Pro Gly Val Ile Ala Ala Leu Arg Tyr
                                         150 155 160 165

acc ctc gaa gcg gac cca gac gaa atc taaaaactga cttttcgtcc 642
Thr Leu Glu Ala Asp Pro Asp Glu Ile
                                         170

agg 645

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<210> 2246

<211> 174

<212> PRT

<213> Corynebacterium glutamicum

<400> 2246

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Glu	Ala	Val	Glu	Phe	Ile	His	Ala	Glu	Gly	Trp	Asp	Ala	Gly	Pro	Thr
			20					25					30		

Leu	Phe	Ala	Leu	Val	Pro	Thr	Glu	Met	Leu	Val	Asp	Thr	Leu	Asp	Glu
		35					40				45				

Ala	Ala	Asp	Asp	Ser	Pro	Leu	Thr	Leu	Val	Val	Gln	Asp	Asn	Leu	Pro
	50					55					60				

Asp	Asn	Leu	Leu	Pro	Gly	Ser	Glu	Ala	Leu	Gly	Asp	Tyr	Val	Ser	Arg
65					70					75					80

Leu	Ala	Trp	Pro	Ala	Glu	Ile	Ala	Gly	Ala	Val	Leu	Ala	Gln	Glu	Ile
			85					90					95		

Met	Phe	Thr	Asp	Ala	Ala	Val	Ala	Gly	Ser	Glu	Pro	Arg	Pro	Ala	Arg
			100					105					110		

Leu	Phe	Ser	Gly	Val	Leu	Arg	Gly	Glu	Ala	Glu	Leu	Thr	Leu	Leu	Gln
		115					120					125			

Leu	Arg	Pro	Thr	Glu	Glu	Glu	Leu	Ala	Glu	Arg	Gly	Pro	Phe	Ala	Glu
	130					135					140				

Asp	Glu	Ile	Glu	Leu	Arg	Gly	Gly	Pro	Gly	Val	Ala	Pro	Gly	Val	Ile
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Ala	Ala	Leu	Arg	Tyr	Thr	Leu	Glu	Ala	Asp	Pro	Asp	Glu	Ile
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<210> 2247

<211> 798

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(775)

<223> RXA01457

<400> 2247

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				Val	Ala	Ser	Thr	Pro	
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cac	aag	cat	gtc	cgc	gtt	gca	ctg	gga	tta	gtg	gcg	ctc	att	oct	ctt	163
His	Lys	His	Val	Arg	Val	Ala	Leu	Gly	Leu	Val	Ala	Leu	Ile	Pro	Leu	
			10					15					20			

tta	gct	gca	tgt	acg	ggc	ggc	gga	tcc	acc	gaa	act	tcc	act	gaa	tcc	211
Leu	Ala	Ala	Cys	Thr	Gly	Gly	Gly	Ser	Thr	Glu	Thr	Ser	Thr	Glu	Ser	
			25					30					35			

acg gca gaa aca act cct gcg aca aca acg gaa gca acg aca act cct 259
 Thr Ala Glu Thr Thr Pro Ala Thr Thr Thr Glu Ala Thr Thr Thr Pro
 40 45 50

gct acc act gct tcg tct tca gta att gaa acg aca gag tca agc act 307
 Ala Thr Thr Ala Ser Ser Ser Val Ile Glu Thr Thr Glu Ser Ser Thr
 55 60 65

gcc gaa acg tcg acg aaa gag agt ggg gag acg tcg aca agc aaa cct 355
 Ala Glu Thr Ser Thr Lys Glu Ser Gly Glu Thr Ser Thr Ser Lys Pro
 70 75 80 85

cgt atg acc aag gac gtt gaa gtc gcc tat aaa gct ttc tcc tcg ctc 403
 Arg Met Thr Lys Asp Val Glu Val Ala Tyr Lys Ala Phe Ser Ser Leu
 90 95 100

gcg ccc gtc gag ctt ttt gag caa ttc gaa acc tgc gac ccg tca ggg 451
 Ala Pro Val Glu Leu Phe Glu Gln Phe Glu Thr Cys Asp Pro Ser Gly
 105 110 115

gtc gag gat tcc ttc gcg tgc aac ggg ccg gaa gtt ggc caa ttc caa 499
 Val Glu Asp Ser Phe Ala Cys Asn Gly Pro Glu Val Gly Gln Phe Gln
 120 125 130

ttc ttt gac aat gcg tcg aag gcc acg agc acg acg cag ctg ctc acg 547
 Phe Phe Asp Asn Ala Ser Lys Ala Thr Ser Thr Thr Gln Leu Leu Thr
 135 140 145

gaa ctg cgc agc tca cgc gtg gtt gag gat tcc gga tcc aag gtt gtg 595
 Glu Leu Arg Ser Ser Arg Val Val Glu Asp Ser Gly Ser Lys Val Val
 150 155 160 165

ggc tgg acc acg att ggc acg atg tcg att atc acg gtc gtt gat aat 643
 Gly Trp Thr Thr Ile Gly Thr Met Ser Ile Ile Thr Val Val Asp Asn
 170 175 180

gac caa ggc cta gtg ctg cag caa atg gtg tcc tcc gac aaa atc gat 691
 Asp Gln Gly Leu Val Leu Gln Gln Met Val Ser Ser Asp Lys Ile Asp
 185 190 195

ccg gag gaa cgc atc tac gaa ctt ggg ctg tcg aca ccg aag gac act 739
 Pro Glu Glu Arg Ile Tyr Glu Leu Gly Leu Ser Thr Pro Lys Asp Thr
 200 205 210

gaa gag tcc tcg gaa gaa acc gcg tct aaa aac tagccacacg 785
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<211> 225

<212> PRT

<213> Corynebacterium glutamicum

<400> 2248

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2	2002	2	2002	2	2002	2	2002
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11	2011	11	2011	11	2011	11	2011
12	2012	12	2012	12	2012	12	2012
13	2013	13	2013	13	2013	13	2013
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17	2017	17	2017	17	2017	17	2017
18	2018	18	2018	18	2018	18	2018
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Met	Ala	Gln	Met	Glu	Ile	Gln	Arg	Trp	Thr	Leu	Leu	Ile	Ser	Asn	Pro	
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gag	gcg	gac	gct	agc	act	ctt	gtc	atg	gag	ttg	aaa	acc	gtc	acg	ggg	259
Glu	Ala	Asp	Ala	Ser	Thr	Leu	Val	Met	Glu	Leu	Lys	Thr	Val	Thr	Gly	
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gaa	tcc	aag	cat	ttt	atc	aac	cag	gct	att	aac	gcc	atg	tgg	gct	tta	307
Glu	Ser	Lys	His	Phe	Ile	Asn	Gln	Ala	Ile	Asn	Ala	Met	Trp	Ala	Leu	
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Met	Lys	Leu	Pro	Ile	Leu	Arg	Val	Val	Val	Glu	Thr	His	Phe	His	Val	
			70			75				80					85	
cgg	att	ccg	tac	ctg	gcc	cgc	att	atg	cag	gca	gtc	aag	cag	gct	aaa	403
Arg	Ile	Pro	Tyr	Leu	Ala	Arg	Ile	Met	Gln	Ala	Val	Lys	Gln	Ala	Lys	
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cgc	gag	ttg	tgg	gat	gag	ttg	gac	cat	cgc	att	gcc	gaa	aag	ctg	aca	451
Pro	Glu	Leu	Trp	Asp	Glu	Leu	Asp	His	Arg	Ile	Ala	Glu	Lys	Leu	Thr	
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cgc	cgc	att	gct	ggc	cag	gca	ctg	atg	gaa	gcc	tcc	gca	ctt	gca	ggg	499
Pro	Arg	Ile	Ala	Gly	Gln	Ala	Leu	Met	Glu	Ala	Ser	Ala	Leu	Ala	Gly	
			120				125					130				
ctg	att	act	cgc	tgg	atc	aag	gaa	ctg	gat	cca	acc	ttc	aca	gga	aag	547
Leu	Ile	Thr	Arg	Trp	Ile	Lys	Glu	Leu	Asp	Pro	Thr	Phe	Thr	Gly	Lys	
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Lys	Arg	Gly	Pro	Lys	Gly	Ser	Asp	Gly	Thr	Leu	Thr	Phe	Arg	His	Val	
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Asp	Gly	Arg	Thr	Tyr	Ile	Ser	Gly	Asn	Ile	Asp	Gly	Val	Thr	Gly	Lys	
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ctg	ttc	caa	aaa	gct	ctg	gaa	aaa	gtg	aaa	cag	aag	ggc	gag	gac	ctc	691
Leu	Phe	Gln	Lys	Ala	Leu	Glu	Lys	Val	Lys	Gln	Lys	Gly	Glu	Asp	Leu	
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gcg	egg	gcc	ctg	gtc	acc	ttc	ctg	ggg	ggg	cgg	acc	aaa	gtg	aaa	atc	739
Ala	Arg	Ala	Leu	Val	Thr	Phe	Leu	Ala	Gly	Arg	Thr	Lys	Val	Lys	Ile	
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gtc	agc	gcg	gta	tac	acg	ccc	ctg	gtg	ggg	gtg	tcc	tgg	att	ccg		787
Val	Ser	Ala	Val	Tyr	Thr	Pro	Leu	Val	Gly	Gly	Val	Ser	Trp	Ile	Pro	
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Gly	Val	Gly	Phe	Leu	Ser	Gln	Glu	Glu	Ser	Arg	Lys	Leu	Gly	Lys	Thr	
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gcc	tcg	aag	gtc	att	gac	ctg	gat	acg	atc	gcc	act	cgt	gtg	gaa	aat	883
Ala	Ser	Lys	Val	Ile	Asp	Leu	Asp	Thr	Ile	Ala	Thr	Arg	Val	Glu	Asn	

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	ggc tac acc cca agt ccc gag cta cgc ctt tat gtg atg ggg cgg gac			931
	Gly Tyr Thr Pro Ser Pro Glu Leu Arg Leu Tyr Val Met Gly Arg Asp			
	265	270	275	
	ggc acc tgt agg cat ccg ggc tgc acg gtg tct gcc gac aac tgc cag			979
	Gly Thr Cys Arg His Pro Gly Cys Thr Val Ser Ala Asp Asn Cys Gln			
	280	285	290	
	atc gat cac gtg atc ccg ttc ggt gag ggt ggg ttg act gtg gcc tgg			1027
	Ile Asp His Val Ile Pro Phe Gly Glu Gly Gly Leu Thr Val Ala Trp			
	295	300	305	
	aac ttg cag tgc ctc tgc gcg cat cat cac aat atg aag act gat ggg			1075
	Asn Leu Gln Cys Leu Cys Ala His His His Asn Met Lys Thr Asp Gly			
	310	315	320	325
	cgc atc cag gcg gcg att gat tcc atg ggt cgg gtc gcc tgg att ggg			1123
	Arg Ile Gln Ala Ala Ile Asp Ser Met Gly Arg Val Ala Trp Ile Gly			
	330	335	340	
	ccg tgc aat cgc aca gtg gta acc gaa cct gtc gga ccg ttg gcg caa			1171
	Pro Cys Asn Arg Thr Val Val Thr Glu Pro Val Gly Pro Leu Ala Gln			
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	gag atg ccc acg ggg cag tgg ggg cag act ctg gaa gca cgg atg gag			1219
	Glu Met Pro Thr Gly Gln Trp Gly Gln Thr Leu Glu Ala Arg Met Glu			
	360	365	370	
	aag act ttt gaa aag ctc cgc agt tca ctc gag gta ttg gat gac			1264
	Lys Thr Phe Glu Lys Leu Arg Ser Ser Leu Glu Val Leu Asp Asp			
	375	380	385	
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	<400> 2250			
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	Leu Ile Ser Asn Pro Glu Ala Asp Ala Ser Thr Leu Val Met Glu Leu			
	35 40 45			
	Lys Thr Val Thr Gly Glu Ser Lys His Phe Ile Asn Gln Ala Ile Asn			
	50 55 60			
	Ala Met Trp Ala Leu Met Lys Leu Pro Ile Leu Arg Val Val Val Glu			
	65 70 75 80			
	Thr His Phe His Val Arg Ile Pro Tyr Leu Ala Arg Ile Met Gln Ala			
	85 90 95			

Val Lys Gln Ala Lys Pro Glu Leu Trp Asp Glu Leu Asp His Arg Ile
 100 105 110
 Ala Glu Lys Leu Thr Pro Arg Ile Ala Gly Gln Ala Leu Met Glu Ala
 115 120 125
 Ser Ala Leu Ala Gly Leu Ile Thr Arg Trp Ile Lys Glu Leu Asp Pro
 130 135 140
 Thr Phe Thr Gly Lys Lys Arg Gly Pro Lys Gly Ser Asp Gly Thr Leu
 145 150 155
 Thr Phe Arg His Val Asp Gly Arg Thr Tyr Ile Ser Gly Asn Ile Asp
 165 170 175
 Gly Val Thr Gly Lys Leu Phe Gln Lys Ala Leu Glu Lys Val Lys Gln
 180 185 190
 Lys Gly Glu Asp Leu Ala Arg Ala Leu Val Thr Phe Leu Ala Gly Arg
 195 200 205
 Thr Lys Val Lys Ile Val Ser Ala Val Tyr Thr Pro Leu Val Gly Gly
 210 215 220
 Val Ser Trp Ile Pro Gly Val Gly Phe Leu Ser Gln Glu Glu Ser Arg
 225 230 235 240
 Lys Leu Gly Lys Thr Ala Ser Lys Val Ile Asp Leu Asp Thr Ile Ala
 245 250 255
 Thr Arg Val Glu Asn Gly Tyr Thr Pro Ser Pro Glu Leu Arg Leu Tyr
 260 265 270
 Val Met Gly Arg Asp Gly Thr Cys Arg His Pro Gly Cys Thr Val Ser
 275 280 285
 Ala Asp Asn Cys Gln Ile Asp His Val Ile Pro Phe Gly Glu Gly Gly
 290 295 300
 Leu Thr Val Ala Trp Asn Leu Gln Cys Leu Cys Ala His His His Asn
 305 310 315 320
 Met Lys Thr Asp Gly Arg Ile Gln Ala Ala Ile Asp Ser Met Gly Arg
 325 330 335
 Val Ala Trp Ile Gly Pro Cys Asn Arg Thr Val Val Thr Glu Pro Val
 340 345 350
 Gly Pro Leu Ala Gln Glu Met Pro Thr Gly Gln Trp Gly Gln Thr Leu
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 Glu Ala Arg Met Glu Lys Thr Phe Glu Lys Leu Arg Ser Ser Leu Glu
 370 375 380
 Val Leu Asp Asp
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<210> 2251

<211> 1155

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1132)

<223> RXA01469

<400> 2251

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ccagatgagc agcagttcac tgactagtat tctgtaggtc atg gca ttt gca gac 115
 Met Ala Phe Ala Asp
 1 5

att gtg cgc agc gtc gaa aac cgc acc aac gca gcg acc ctc aac tgg 163
 Ile Val Arg Ser Val Glu Asn Arg Thr Asn Ala Ala Thr Leu Asn Trp
 10 15 20

tcc atc aaa aat ggc tgg aag ccc gaa gtc acc gga ttt tcc ggg tac 211
 Ser Ile Lys Asn Gly Trp Lys Pro Glu Val Thr Gly Phe Ser Gly Tyr
 25 30 35

ggc tcc ggg cgt cga gtg cgc gtc ctt gcg cgc gtg ctc atg tcc aac 259
 Gly Ser Gly Arg Arg Val Arg Val Leu Ala Arg Val Leu Met Ser Asn
 40 45 50

ccc gaa aat ttg ctt gtc gac gcc ccc tcc caa tca att acc caa caa 307
 Pro Glu Asn Leu Leu Val Asp Ala Pro Ser Gln Ser Ile Thr Gln Gln
 55 60 65

gca cag cgc ggt tgg cgc cag ttc ttc acc atc caa gtg ccc aac ctg 355
 Ala Gln Arg Gly Trp Arg Gln Phe Phe Thr Ile Gln Val Pro Asn Leu
 70 75 80 85

cca gta act gtc acc gtt ggt ggg aaa aca gtt acc tca tcc acc aac 403
 Pro Val Thr Val Thr Val Gly Gly Lys Thr Val Thr Ser Ser Thr Asn
 90 95 100

gac aac ggc tac gtt gac ctc ctg gtg gaa gac cac aac ctt gac ccc 451
 Asp Asn Gly Tyr Val Asp Leu Leu Val Glu Asp His Asn Leu Asp Pro
 105 110 115

ggc tgg cac acc atc cag atc caa gcc gaa ggt tcc acc ccc gcc gaa 499
 Gly Trp His Thr Ile Gln Ile Gln Ala Glu Gly Ser Thr Pro Ala Glu
 120 125 130

gcc cgc gtc ctc atc gtg gaa aac acc gcc cga atc gga ctc atc tcc 547
 Ala Arg Val Leu Ile Val Glu Asn Thr Ala Arg Ile Gly Leu Ile Ser
 135 140 145

gac atc gac gac acc atc atg gtc acc tgg ctt ccc cga gca ctc ctc 595
 Asp Ile Asp Asp Thr Ile Met Val Thr Trp Leu Pro Arg Ala Leu Leu
 150 155 160 165

gcc gca tgg aac tcg tgg gtt ttg cac acc aac acc cgc aaa cca gtc 643
 Ala Ala Trp Asn Ser Trp Val Leu His Thr Asn Thr Arg Lys Pro Val
 170 175 180

ccc gga atg aac cgc ttc tac gaa gaa ctc ctc aaa gac cac ccc gac 691
 Pro Gly Met Asn Arg Phe Tyr Glu Glu Leu Leu Lys Asp His Pro Asp
 185 190 195

gca ccc gtg ttc tac ctc tcc acc ggc gca tgg aac acc ttt gaa acc 739
Ala Pro Val Phe Tyr Leu Ser Thr Gly Ala Trp Asn Thr Phe Glu Thr
200 205 210

ctc caa gag ttc atc aac aaa cac gca ctc ccc gac ggc ccc atg ctg 787
Leu Gln Glu Phe Ile Asn Lys His Ala Leu Pro Asp Gly Pro Met Leu
215 220 225

ctc acc gac tgg gga cca acc ccc aca gga cta ttc cgc tca ggt caa 835
Leu Thr Asp Trp Gly Pro Thr Pro Thr Gly Leu Phe Arg Ser Gly Gln
230 235 240 245

gag cac aag aaa gtc caa ctg cgc aac ctg ttt atc gaa tac ccc gac 883
Glu His Lys Lys Val Gln Leu Arg Asn Asp Phe Ile Glu Tyr Pro Asp
250 255 260

atg aaa tgg atc ctc gtc ggc gac gat ggc caa cac gat ccc ctc atc 931
Met Lys Trp Ile Leu Val Gly Asp Gly Gln His Asp Pro Leu Ile
265 270 275

tac ggc gaa gca gtc gaa gaa cac ccc aac cgc atc gca ggc gtt gca 979
Tyr Gly Glu Ala Val Glu Glu His Pro Asn Arg Ile Ala Gly Val Ala
280 285 290

atc cgt gag ctc tcc ccc ggc gaa cat gtg ctc tcc cac gga aca act 1027
Ile Arg Glu Leu Ser Pro Gly Glu His Val Leu Ser His Gly Thr Thr
295 300 305

gcg tca ctg tcc acc atc acg acc aac ggg ggc caa gga gtc cca gta 1075
Ala Ser Leu Ser Thr Ile Thr Thr Asn Gly Gly Gln Gly Val Pro Val
310 315 320 325

gtt cac ggc cgc gat gga tat gag ttg ctg cag cgc tac gag acg aag 1123
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330 335 340

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<210> 2252

<211> 344

<212> PRT

<213> Corynebacterium glutamicum

<400> 2252

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20 25 30

Gly Phe Ser Gly Tyr Gly Ser Gly Arg Arg Val Arg Val Leu Ala Arg
35 40 45

Val Leu Met Ser Asn Pro Glu Asn Leu Leu Val Asp Ala Pro Ser Gln
50 55 60

Ser Ile Thr Gln Gln Ala Gln Arg Gly Trp Arg Gln Phe Phe Thr Ile

65	70	75	80
Gln Val Pro Asn Leu Pro Val Thr Val Thr Val Gly Gly Lys Thr Val	85	90	95
Thr Ser Ser Thr Asn Asp Asn Gly Tyr Val Asp Leu Leu Val Glu Asp	100	105	110
His Asn Leu Asp Pro Gly Trp His Thr Ile Gln Ile Gln Ala Glu Gly	115	120	125
Ser Thr Pro Ala Glu Ala Arg Val Leu Ile Val Glu Asn Thr Ala Arg	130	135	140
Ile Gly Leu Ile Ser Asp Ile Asp Asp Thr Ile Met Val Thr Trp Leu	145	150	155
Pro Arg Ala Leu Leu Ala Ala Trp Asn Ser Trp Val Leu His Thr Asn	165	170	175
Thr Arg Lys Pro Val Pro Gly Met Asn Arg Phe Tyr Glu Glu Leu Leu	180	185	190
Lys Asp His Pro Asp Ala Pro Val Phe Tyr Leu Ser Thr Gly Ala Trp	195	200	205
Asn Thr Phe Glu Thr Leu Gln Glu Phe Ile Asn Lys His Ala Leu Pro	210	215	220
Asp Gly Pro Met Leu Leu Thr Asp Trp Gly Pro Thr Pro Thr Gly Leu	225	230	235
Phe Arg Ser Gly Gln Glu His Lys Lys Val Gln Leu Arg Asn Leu Phe	245	250	255
Ile Glu Tyr Pro Asp Met Lys Trp Ile Leu Val Gly Asp Asp Gly Gln	260	265	270
His Asp Pro Leu Ile Tyr Gly Glu Ala Val Glu Glu His Pro Asn Arg	275	280	285
Ile Ala Gly Val Ala Ile Arg Glu Leu Ser Pro Gly Glu His Val Leu	290	295	300
Ser His Gly Thr Thr Ala Ser Leu Ser Thr Ile Thr Thr Asn Gly Gly	305	310	315
Gln Gly Val Pro Val Val His Gly Arg Asp Gly Tyr Glu Leu Leu Gln	325	330	335
Arg Tyr Glu Thr Lys Pro Phe Ala	340		

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<211> 549

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

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<222> (101)..(526)

<223> RXA01470

<400> 2253

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 Met Thr Asn Asn Ala 5
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tta acc gtg cca acc cgg acc cgt cat cag gcg gat ttg ctc acg gca 163
 Leu Thr Val Pro Thr Arg Thr Arg His Gln Ala Asp Leu Leu Thr Ala 20
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gac ttc tgg gaa gac atg ggg ttg ccc caa ctg aaa act acc atc gaa 211
 Asp Phe Trp Glu Asp Met Gly Leu Pro Gln Leu Lys Thr Thr Ile Glu 35
 25 30

gaa tcc atc gac gat gta gcc ctc cca atg cat acc gct gtt cta gaa 259
 Glu Ser Ile Asp Asp Val Ala Leu Pro Met His Thr Ala Val Leu Glu 50
 40 45

atc agc gga atg cca aag gaa ctg cgt cag acc gtg gaa tcc gca atg 307
 Ile Ser Gly Met Pro Lys Glu Leu Arg Gln Thr Val Glu Ser Ala Met 65
 55 60

gtt gtg tgt att ccg agt cct tcg gag ctg tcc ggc tcc aac agg gac 355
 Val Val Cys Ile Pro Ser Pro Ser Glu Leu Ser Gly Ser Asn Arg Asp 85
 70 75 80

ccg ctc acc gca cga tgg ttc act gca tgg cgc cgt gac cca ttc gaa 403
 Pro Leu Thr Ala Arg Trp Phe Thr Ala Trp Arg Arg Asp Pro Phe Glu 100
 90 95

ctt ggc ctc act gag tgt cga gag gtg atc acc gga act cca cgc gaa 451
 Leu Gly Leu Thr Glu Cys Arg Glu Val Ile Thr Gly Thr Pro Arg Glu 115
 105 110

ctc gac aaa ctt cga gga gtg ctg gaa tct ctg gct gat gaa tac cgt 499
 Leu Asp Lys Leu Arg Gly Val Leu Glu Ser Leu Ala Asp Glu Tyr Arg 130
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<211> 142

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2254

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Lys	Thr	Thr	Ile	Glu	Glu	Ser	Ile	Asp	Asp	Val	Ala	Leu	Pro	Met	His
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Thr	Ala	Val	Leu	Glu	Ile	Ser	Gly	Met	Pro	Lys	Glu	Leu	Arg	Gln	Thr
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Val	Glu	Ser	Ala	Met	Val	Val	Cys	Ile	Pro	Ser	Pro	Ser	Glu	Leu	Ser
	65				70					75					80
Gly	Ser	Asn	Arg	Asp	Pro	Leu	Thr	Ala	Arg	Trp	Phe	Thr	Ala	Trp	Arg
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Arg	Asp	Pro	Phe	Glu	Leu	Gly	Leu	Thr	Glu	Cys	Arg	Glu	Val	Ile	Thr
		100					105					110			
Gly	Thr	Pro	Arg	Glu	Leu	Asp	Lys	Leu	Arg	Gly	Val	Leu	Glu	Ser	Leu
	115						120					125			
Ala	Asp	Glu	Tyr	Arg	Phe	Glu	Val	Glu	Leu	Arg	Ile	Val	Asp		
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<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS
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	ctcggtggaa accgtcgcgg aaaaatggag gatctcgcgc atg aac caa gca aac	115
		Met Asn Gln Ala Asn 1 5
	ctg cct gcc gaa atc gcg gac ctc tcc gat gaa acc gca ctg tgg gaa	163
Leu Pro Ala Glu Ile Ala Asp Leu Ser Asp Glu Thr Ala Leu Trp Glu		10 15 20
	atc atc aac gaa tac aac tgg gac gac gcc ttc gcg gtt ccc ctt gca	211
Ile Ile Asn Glu Tyr Asn Trp Asp Asp Gly Phe Ala Val Pro Leu Ala		25 30 35
	gta gtc cga cac ccc aaa tgc gac cga gcg cta gcc ctt cgc ctg ttt	259
Val Val Arg His Pro Lys Cys Asp Arg Ala Leu Ala Leu Arg Leu Phe		40 45 50
	tgg gac atc gat gaa acc gcc caa atc cac cac tcc gac gaa gaa tca	307
Trp Asp Ile Asp Glu Thr Ala Gln Ile His His Ser Asp Glu Glu Ser		55 60 65
	gcg atc gcc gag ttg tac gcc ser acc gcc gaa aac gac cca gca gaa	355
Ala Ile Ala Glu Leu Tyr Ala Ser Thr Ala Glu Asn Asp Pro Ala Glu		70 75 80 85
	ttc gac aga atc atg gac tac tgc acc aca cta gcg gaa ggg ctc cgc	403
Phe Asp Arg Ile Met Asp Tyr Cys Thr Thr Leu Val Glu Gly Leu Arg		

	90	95	100	
aag cag acc tat cct cgg ggc gcc aac cgt ttc gac acg gga ttt ttc				451
Lys Gln Thr Tyr Pro Arg Gly Ala Asn Arg Phe Asp Thr Gly Phe Phe	105	110	115	
aac ctc gag gac cct tct ttg acc gac cgt cag cgc aaa atc cgc gcc				499
Asn Leu Glu Asp Pro Ser Leu Thr Asp Arg Gln Arg Lys Ile Arg Ala	120	125	130	
ggg aaa acc aaa ttt gcg ctc aag aat ttc gag gaa gct ttc ctc caa				547
Gly Lys Thr Lys Phe Ala Leu Lys Asn Phe Glu Glu Ala Phe Leu Gln	135	140	145	
cca gag cta taaaaaaggt tgtagaagaa att				579
Pro Glu Leu				
150				

<210> 2256

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 2256

Met	Asn	Gln	Ala	Asn	Leu	Pro	Ala	Glu	Ile	Ala	Asp	Leu	Ser	Asp	Glu
1				5					10					15	

Thr	Ala	Leu	Trp	Glu	Ile	Ile	Asn	Glu	Tyr	Asn	Trp	Asp	Asp	Gly	Phe
		20						25					30		

Ala	Val	Pro	Leu	Ala	Val	Val	Arg	His	Pro	Lys	Cys	Asp	Arg	Ala	Leu
		35					40					45			

Ala	Leu	Arg	Leu	Phe	Trp	Asp	Ile	Asp	Glu	Thr	Ala	Gln	Ile	His	His
	50					55					60				

Ser	Asp	Glu	Glu	Ser	Ala	Ile	Ala	Glu	Leu	Tyr	Ala	Ser	Thr	Ala	Glu
	65				70					75				80	

Asn	Asp	Pro	Ala	Glu	Phe	Asp	Arg	Ile	Met	Asp	Tyr	Cys	Thr	Thr	Leu
			85						90				95		

Val	Glu	Gly	Leu	Arg	Lys	Gln	Thr	Tyr	Pro	Arg	Gly	Ala	Asn	Arg	Phe
			100				105						110		

Asp	Thr	Gly	Phe	Phe	Asn	Leu	Glu	Asp	Pro	Ser	Leu	Thr	Asp	Arg	Gln
		115					120					125			

Arg	Lys	Ile	Arg	Ala	Gly	Lys	Thr	Lys	Phe	Ala	Leu	Lys	Asn	Phe	Glu
	130					135					140				

Glu	Ala	Phe	Leu	Gln	Pro	Glu	Leu
145					150		

<210> 2257

<211> 888

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(865)

<223> RXA01473

<400> 2257

cgtaagcaat tcccaccaat gcagtttctt cgggtgcgtta tagtgtcgag tagggccaaa 60

aaccaacaat atcctggtag ccaagaataa gatcgtgctt atg act gac atc ggt 115
Met Thr Asp Ile Gly 5
1

gat gtc gat caa ata gtc tgg gaa ttc atc cat ttc cac gat gac tcg 163
Asp Val Asp Gln Ile Val Trp Glu Phe Ile His Phe His Asp Asp Ser 20
10 15

ata aat cca ttc ttt gag ttc atc aag gat tgc atc aac gat gag 211
Ile Asn Pro Phe Phe Glu Phe Ile Lys Ser Asp Cys Ile Asn Asp Glu 35
25 30

gca atc gaa cgc aaa acc cag atc ctc gga atc atc ttg ggt aac gag 259
Ala Ile Glu Arg Lys Thr Gln Ile Leu Gly Ile Ile Leu Gly Asn Glu 50
40 45

cca tgc ggg agt gtt att cac gcc cgc cag aat aca ata aag ccc atg 307
Pro Cys Gly Ser Val Ile His Ala Arg Gln Asn Thr Ile Lys Pro Met 65
55 60

agc cat acg gtc tct ttt ggc gac ggc tgg atc caa gtc ctt gag gat 355
Ser His Thr Val Ser Phe Gly Asp Gly Trp Ile Gln Val Leu Glu Asp 85
70 75 80

gct gca gaa acc gtg tcg atc acc gac acg ttg gat gcc ctc cga ttt 403
Ala Ala Glu Thr Val Ser Ile Thr Asp Thr Leu Asp Ala Leu Arg Phe 95
90 95 100

tct ccc gag caa cgc gaa tgg gct gca gaa ttc gga cca cta ctg tgc 451
Ser Pro Glu Gln Ala Glu Trp Ala Ala Glu Phe Gly Pro Leu Leu Cys 110
105 110 115

ggc cca cgc aac caa ccg ccg gcg tat ctc acg gct tta gac ggg cac 499
Gly Pro Ala Asn Gln Pro Pro Ala Tyr Leu Thr Ala Leu Asp Gly His 120
125 130

aca aag cta ccg ctt agc ccg cag ctg acg gag ttc tat agc tac gcc 547
Thr Lys Leu Pro Leu Ser Pro Gln Leu Thr Glu Phe Tyr Ser Tyr Ala 140
135 140 145

cga tcc tgg aca aac agt gag gcc ttg gga aac gtc att gat ccc gat 595
Arg Ser Trp Thr Asn Ser Glu Ala Leu Gly Asn Val Ile Asp Pro Asp 155
150 160 165

gac tac ctc gat cat ctc acc gac cct cgc ctt cat ttg cag gat ctt 643
Asp Tyr Leu Asp His Leu Thr Asp Pro Arg Leu His Leu Gln Asp Leu 170
175 180

ctg gat aat gag ttt gaa cgg gtg ggg gtg ctc gtc gat aag caa aat 691
Leu Asp Asn Glu Phe Glu Arg Val Gly Val Leu Val Asp Lys Gln Asn 185
190 195

cgc ccg ctc gac cct gcc ccg tgc gcg ctg ttc tcg ctc gac gca ctt 739

Arg Pro Leu Asp Pro Ala Arg Cys Ala Leu Phe Ser Leu Asp Ala Leu
 200 205 210

gca cgc gcg ccc tac aac cgc gcc tac ttc gtc ttc gcc gcg ccc gag 787
 Ala Arg Ala Pro Tyr Asn Arg Ala Tyr Phe Val Phe Ala Ala Pro Glu
 215 220 225

cct gag atc tgg gcg ttt gag aac gag cac gtc cac gcg ccg gac ttg 835
 Pro Glu Ile Trp Ala Phe Glu Asn Glu His Val His Ala Pro Asp Leu
 230 235 240 245

cgc gcc tat tta caa gca cgc tta tcg acg taattacact cggtgaaac 885
 Arg Ala Tyr Leu Gln Ala Arg Leu Ser Thr
 250 255

cgt 888

<210> 2258

<211> 255

<212> PRT

<213> Corynebacterium glutamicum

<400> 2258

Met Thr Asp Ile Gly Asp Val Asp Gln Ile Val Trp Glu Phe Ile His
 1 5 10 15

Phe His Asp Asp Ser Ile Asn Pro Phe Glu Phe Ile Lys Ser Asp
 20 25 30

Cys Ile Asn Asp Glu Ala Ile Glu Arg Lys Thr Gln Ile Leu Gly Ile
 35 40 45

Ile Leu Gly Asn Glu Pro Cys Gly Ser Val Ile His Ala Arg Gln Asn
 50 55 60

Thr Ile Lys Pro Met Ser His Thr Val Ser Phe Gly Asp Gly Trp Ile
 65 70 75 80

Gln Val Leu Glu Asp Ala Ala Glu Thr Val Ser Ile Thr Asp Thr Leu
 85 90 95

Asp Ala Leu Arg Phe Ser Pro Glu Gln Ala Glu Trp Ala Ala Glu Phe
 100 105 110

Gly Pro Leu Leu Cys Gly Pro Ala Asn Gln Pro Pro Ala Tyr Leu Thr
 115 120 125

Ala Leu Asp Gly His Thr Lys Leu Pro Leu Ser Pro Gln Leu Thr Glu
 130 135 140

Phe Tyr Ser Tyr Ala Arg Ser Trp Thr Asn Ser Glu Ala Leu Gly Asn
 145 150 155 160

Val Ile Asp Pro Asp Asp Tyr Leu Asp His Leu Thr Asp Pro Arg Leu
 165 170 175

His Leu Gln Asp Leu Leu Asp Asn Glu Phe Glu Arg Val Gly Val Leu
 180 185 190

Val Asp Lys Gln Asn Arg Pro Leu Asp Pro Ala Arg Cys Ala Leu Phe

```

195                200                205
Ser Leu Asp Ala Leu Ala Arg Ala Pro Tyr Asn Arg Ala Tyr Phe Val
210                215                220
Phe Ala Ala Pro Glu Pro Glu Ile Trp Ala Phe Glu Asn Glu His Val
225                230                235                240
His Ala Pro Asp Leu Arg Ala Tyr Leu Gln Ala Arg Leu Ser Thr
245                250                255

```

<210> 2259

<211> 669

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(646)

<223> RXA01474

<400> 2259

catcaccgat gtcagtcata agcacgatct tattcttggc taccaggata ttgttggttt 60

```

ttggccctac tcgacactat aacgcaccga ggaaactgca ttg gtg gga att gct 115
                1          5
Leu Val Gly Ile Ala

```

```

tac gcc cgt ttc cct gat acc cgc gac gat tcc atc agc cgc ggc aaa 163
Tyr Ala Arg Phe Pro Asp Thr Arg Asp Asp Ser Ile Ser Arg Gly Lys
                10          15          20

```

```

gca cga tca gcg ttg gag aaa tcc acg ggc ctt aaa gag cgt ttc gcg 211
Ala Arg Ser Ala Leu Glu Lys Ser Thr Gly Leu Lys Glu Arg Phe Ala
                25          30          35

```

```

cgt cat ttt cct gca att tcc ata cct gtc gat acg ggt gat gct gca 259
Arg His Phe Pro Ala Ile Ser Ile Pro Val Asp Thr Gly Asp Ala Ala
                40          45          50

```

```

gat att ctc gta tcg ggt tgg tgg ctt tca ggt tct aaa aag aag atc 307
Asp Ile Leu Val Ser Gly Trp Trp Leu Ser Gly Ser Lys Lys Lys Ile
                55          60          65

```

```

ctg act gca gcg gaa atc cag acc tta ttt atc aac cga ttg gcc aca 355
Leu Thr Ala Ala Glu Ile Gln Thr Leu Phe Ile Asn Arg Leu Ala Thr
                70          75          80          85

```

```

ggt cca ttg agc act caa ttg gaa act gct acc ggg ttg aaa ctg cag 403
Gly Pro Leu Ser Thr Gln Leu Glu Thr Ala Thr Gly Leu Lys Leu Gln
                90          95          100

```

```

gtg gtg acc aat cga gag cgt atg aag atc act ctc att gaa ccc aaa 451
Val Val Thr Asn Arg Glu Arg Met Lys Ile Thr Leu Ile Glu Pro Lys
                105          110          115

```

```

ggc aca tca gga cat gcc atc gac ccc caa gct ggc aag ggt tca agg 499
Gly Thr Ser Gly His Ala Ile Asp Pro Gln Ala Gly Lys Gly Ser Arg
                120          125          130

```

```

ggg ggc ttc ctc ctg gac aat ggc caa gaa gat gaa tac gac gat gtc 547
Gly Gly Phe Leu Leu Asp Asn Gly Gln Glu Asp Glu Tyr Asp Asp Val
135 140 145

gac acc gtc aca atc ccc gat gca ctc aat gtc atc ggt tac att ctt 595
Asp Thr Val Thr Ile Pro Asp Ala Leu Asn Val Ile Gly Tyr Ile Leu
150 155 160 165

acc cat gga act cca cct caa gaa ggc tgg aag gta gac gtg ttg gag 643
Thr His Gly Thr Pro Pro Gln Glu Gly Trp Lys Val Asp Val Leu Glu
170 175 180

cgt tagtcctcga tgaattcttc tcc 669
Arg

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<210> 2260

<211> 182

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2260

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Leu Val Gly Ile Ala Tyr Ala Arg Phe Pro Asp Thr Arg Asp Asp Ser
1 5 10 15

Ile Ser Arg Gly Lys Ala Arg Ser Ala Leu Glu Lys Ser Thr Gly Leu
20 25 30

Lys Glu Arg Phe Ala Arg His Phe Pro Ala Ile Ser Ile Pro Val Asp
35 40 45

Thr Gly Asp Ala Ala Asp Ile Leu Val Ser Gly Trp Trp Leu Ser Gly
50 55 60

Ser Lys Lys Lys Ile Leu Thr Ala Ala Glu Ile Gln Thr Leu Phe Ile
65 70 75 80

Asn Arg Leu Ala Thr Gly Pro Leu Ser Thr Gln Leu Glu Thr Ala Thr
85 90 95

Gly Leu Lys Leu Gln Val Val Thr Asn Arg Glu Arg Met Lys Ile Thr
100 105 110

Leu Ile Glu Pro Lys Gly Thr Ser Gly His Ala Ile Asp Pro Gln Ala
115 120 125

Gly Lys Gly Ser Arg Gly Gly Phe Leu Leu Asp Asn Gly Gln Glu Asp
130 135 140

Glu Tyr Asp Asp Val Asp Thr Val Thr Ile Pro Asp Ala Leu Asn Val
145 150 155 160

Ile Gly Tyr Ile Leu Thr His Gly Thr Pro Pro Gln Glu Gly Trp Lys
165 170 175

Val Asp Val Leu Glu Arg
180

```

<210> 2261


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<220>  
<221> CDS  
<222> (101)..(526)  
<223> RXA01475
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400> 2261																
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cgtgcacatt ggattcacac ccgtagtagt ttttggggga						atg agc atc caa ggg	115									
						Met Ser Ile Gln Gly										
						1	5									
ttt tcc gca ggt gac tat tct gca tgt ttt gaa ccg cgc atc gat gcg	163															
Phe Ser Ala Gly Asp Tyr Ser Ala Cys Phe Glu Pro Arg Ile Asp Ala																
						10	15	20								
tgg gtt gat att cgc ggt ccg cgg aag ccc gag tgg ttg gcg gaa aat	211															
Trp Val Asp Ile Arg Gly Pro Arg Lys Pro Glu Trp Leu Ala Glu Asn																
						25	30	35								
atc gat aat ccg ctg aga cac tgg ggc gat aat cct cat atc ccg gtg	259															
Ile Asp Asn Pro Leu Arg His Trp Gly Asp Asn Pro His Ile Pro Val																
						40	45	50								
tct gct gcg aaa aag gct gga aat att tac aaa gag acc ctt cga acc	307															
Ser Ala Ala Lys Lys Ala Gly Asn Ile Tyr Lys Glu Thr Leu Arg Thr																
						55	60	65								
atg aga gcc tca aca aag acc cca gac cag gat ccc tta aaa gaa acc	355															
Met Arg Ala Ser Thr Lys Thr Pro Asp Gln Asp Pro Leu Lys Glu Thr																
						70	75	80	85							
ctg cgc agc ttc atc gca agc atc aac cag ctc gcc gca aag aag aat	403															
Leu Arg Ser Phe Ile Ala Ser Ile Asn Gln Leu Ala Ala Lys Lys Asn																
						90	95	100								
ttc att gat gcc ggg gtg cgc gaa gat atc gtt gtt gcg ctg gaa aaa	451															
Phe Ile Asp Ala Gly Val Arg Glu Asp Ile Val Val Ala Leu Glu Lys																
						105	110	115								
cta tgc gaa gca gca gaa gct agc cca gaa gaa att cag cag gcg atc	499															
Leu Cys Glu Ala Ala Glu Ala Ser Pro Glu Glu Ile Gln Gln Ala Ile																
						120	125	130								
gtg atg gga gaa gaa ttc atc gag gac taacgctcca acacgtctac	546															
Val Met Gly Glu Glu Phe Ile Glu Asp																
						135	140									
ctt	549															

<400> 2262

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Met Ser Ile Gln Gly Phe Ser Ala Gly Asp Tyr Ser Ala Cys Phe Glu
  1           5           10           15

Pro Arg Ile Asp Ala Trp Val Asp Ile Arg Gly Pro Arg Lys Pro Glu
           20           25           30

Trp Leu Ala Glu Asn Ile Asp Asn Pro Leu Arg His Trp Gly Asp Asn
  35           40           45

Pro His Ile Pro Val Ser Ala Ala Lys Lys Ala Gly Asn Ile Tyr Lys
  50           55           60

Glu Thr Leu Arg Thr Met Arg Ala Ser Thr Lys Thr Pro Asp Gln Asp
  65           70           75           80

Pro Leu Lys Glu Thr Leu Arg Ser Phe Ile Ala Ser Ile Asn Gln Leu
           85           90           95

Ala Ala Lys Lys Asn Phe Ile Asp Ala Gly Val Arg Glu Asp Ile Val
  100           105           110

Val Ala Leu Glu Lys Leu Cys Glu Ala Ala Glu Ala Ser Pro Glu Glu
  115           120           125

Ile Gln Gln Ala Ile Val Met Gly Glu Glu Phe Ile Glu Asp
  130           135           140

<210> 2263
<211> 465
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(442)
<223> RXA01476

<400> 2263
atccaagaaa ttctgcacct caggagttagc gatacttcgt aaatttggga agaaggagta 60

gccacatgac gttgatcgac ctcaactgctg gagtgagcgc atg agc gat tca ccg 115
Met Ser Asp Ser Pro
1 5

tgc acc gtc gtc atc ctg aac cgc aca gct act gcg act tcc atc ctg 163
Cys Thr Val Val Ile Leu Asn Arg Thr Ala Thr Ala Thr Ser Ile Leu
10 15 20

aga gat att aaa gcc ctc acc ggt tac ggc ctg tct gag atc agg tcg 211
Arg Asp Ile Lys Ala Leu Thr Gly Tyr Gly Leu Ser Glu Ile Arg Ser
25 30 35

cgc atc gtt gcg gga ctt ccc gtc gtg atc gag gag atg ttc tca aac 259
Arg Ile Val Ala Gly Leu Pro Val Val Ile Glu Glu Met Phe Ser Asn
40 45 50

gcc tgg tac gac gaa cgc gca caa ctg ttg ctg gca ctg ctg acc aaa 307
Ala Trp Tyr Asp Glu Arg Ala Gln Leu Leu Leu Ala Leu Leu Thr Lys
55 60 65

```

```

tgg cag aac gaa gga atc aca ttc gag att cgg gaa gtc gct gag gat 355
Trp Gln Asn Glu Gly Ile Thr Phe Glu Ile Arg Glu Val Ala Glu Asp
70 75 80 85

gat ccc atc gaa gca ggg gca ttg atc tct cta gaa gtg ctg cga aac 403
Asp Pro Ile Glu Ala Gly Ala Leu Ile Ser Leu Glu Val Leu Arg Asn
90 95 100

atc att gag cca gac gat aat gaa tcg agg gac ggt atc tagtggtgaa 452
Ile Ile Glu Pro Asp Asp Asn Glu Ser Arg Asp Gly Ile
105 110

cgtaaaccoc cgg 465

```

<210> 2264

<211> 114

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2264

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Met Ser Asp Ser Pro Cys Thr Val Val Ile Leu Asn Arg Thr Ala Thr
1 5 10 15

Ala Thr Ser Ile Leu Arg Asp Ile Lys Ala Leu Thr Gly Tyr Gly Leu
20 25 30

Ser Glu Ile Arg Ser Arg Ile Val Ala Gly Leu Pro Val Val Ile Glu
35 40 45

Glu Met Phe Ser Asn Ala Trp Tyr Asp Glu Arg Ala Gln Leu Leu Leu
50 55 60

Ala Leu Leu Thr Lys Trp Gln Asn Glu Gly Ile Thr Phe Glu Ile Arg
65 70 75 80

Glu Val Ala Glu Asp Asp Pro Ile Glu Ala Gly Ala Leu Ile Ser Leu
85 90 95

Glu Val Leu Arg Asn Ile Ile Glu Pro Asp Asp Asn Glu Ser Arg Asp
100 105 110

Gly Ile

```

<210> 2265

<211> 954

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(931)

<223> RXA01488

<400> 2265

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ccttgatata gccaccggca tcgatgatgc cctgcgactt gctacgcac tgggtccacc 60

tgaactagag ctcatgtgtg tcaccaccac ctacggtaac gtg cta ctc gaa acc 115
Val Leu Leu Glu Thr

```

1

5

ggt gca gtc aat gac ctg gca ctg ctt gat ctg ttc ggt gca cca gaa	163
Gly Ala Val Asn Asp Leu Ala Leu Leu Asp Leu Phe Gly Ala Pro Glu	
10 15 20	
gta cct gtg tac ttg ggt gag cca cac gca cag acc aag gat ggc ttt	211
Val Pro Val Tyr Leu Gly Glu Pro His Ala Gln Thr Lys Asp Gly Phe	
25 30 35	
gaa gtt ctt gag atc tcc gcg ttc att cac gga caa aac ggc atc ggc	259
Glu Val Leu Glu Ile Ser Ala Phe Ile His Gly Gln Asn Gly Ile Gly	
40 45 50	
gaa gtc gag ctg cca gca agc gag tca aag gca ctc ccc ggc gca gtg	307
Glu Val Glu Leu Pro Ala Ser Glu Ser Lys Ala Leu Pro Gly Ala Val	
55 60 65	
gat ttc ctc att gat tcc gtc aac acc cac ggc gat gac ctg gtg atc	355
Asp Phe Leu Ile Asp Ser Val Asn Thr His Gly Asp Asp Leu Val Ile	
70 75 80 85	
atc gca act ggt ccc atg acc aac ctg tct gcg gca atc gca aag gat	403
Ile Ala Thr Gly Pro Met Thr Asn Leu Ser Ala Ala Ile Ala Lys Asp	
90 95 100	
cca agc ttt gct tcc aag gct cac gtg gtc atc atg ggt ggc gcc ttg	451
Pro Ser Phe Ala Ser Lys Ala His Val Val Ile Met Gly Gly Ala Leu	
105 110 115	
act gtc cca ggc aac gtc agc aca tgg gca gaa gca aac atc aac cag	499
Thr Val Pro Gly Asn Val Ser Thr Trp Ala Glu Ala Asn Ile Asn Gln	
120 125 130	
gac cca gat gca gca aac gat ctg ttc cgt tcc ggt gca gat gtc acc	547
Asp Pro Asp Ala Ala Asn Asp Leu Phe Arg Ser Gly Ala Asp Val Thr	
135 140 145	
atg atc ggt ctt gat gtc acc ctg cag acc ctt ctt acc aag aag cac	595
Met Ile Gly Leu Asp Val Thr Leu Gln Thr Leu Leu Thr Lys Lys His	
150 155 160 165	
act gcg cag tgg cgc gaa ctg ggc act cca gct gct atc gca ctg gcc	643
Thr Ala Gln Trp Arg Glu Leu Gly Thr Pro Ala Ala Ile Ala Leu Ala	
170 175 180	
gac atg act gat tac tac atc aag gca tat gag acc acc gca cca cac	691
Asp Met Thr Asp Tyr Tyr Ile Lys Ala Tyr Glu Thr Thr Ala Pro His	
185 190 195	
ctg ggc ggt tgc ggc ctg cac gac cca ctg gca gta ggc gtt gca gtg	739
Leu Gly Gly Cys Gly Leu His Asp Pro Leu Ala Val Gly Val Ala Val	
200 205 210	
gac cca agc ctg gtc act ttg ctc ccc atc aac ctc aag gta gac att	787
Asp Pro Ser Leu Val Thr Leu Leu Pro Ile Asn Leu Lys Val Asp Ile	
215 220 225	
gag ggc gag acc cgt gga cgc acc att ggc gat gaa gtc cgc ctc aac	835
Glu Gly Glu Thr Arg Gly Arg Thr Ile Gly Asp Glu Val Arg Leu Asn	
230 235 240 245	

gat cca gtg cgc acc tcc cgc gca gct gtc gcc gta gac gtg gat cgt 883
 Asp Pro Val Arg Thr Ser Arg Ala Ala Val Ala Val Asp Val Asp Arg
 250 255 260

ttc ctt tct gaa ttc atg acc cgc atc ggc cga gtc gca gca cag cag 931
 Phe Leu Ser Glu Phe Met Thr Arg Ile Gly Arg Val Ala Ala Gln Gln
 265 270 275

taaaagcagc tctggtgaag gtt 954

<210> 2266

<211> 277

<212> ERT

<213> *Corynebacterium glutamicum*

<400> 2266

Val Leu Leu Glu Thr Gly Ala Val Asn Asp Leu Ala Leu Leu Asp Leu
 1 5 10 15

Phe Gly Ala Pro Glu Val Pro Val Tyr Leu Gly Glu Pro His Ala Gln
 20 25 30

Thr Lys Asp Gly Phe Glu Val Leu Glu Ile Ser Ala Phe Ile His Gly
 35 40 45

Gln Asn Gly Ile Gly Glu Val Glu Leu Pro Ala Ser Glu Ser Lys Ala
 50 55 60

Leu Pro Gly Ala Val Asp Phe Leu Ile Asp Ser Val Asn Thr His Gly
 65 70 75 80

Asp Asp Leu Val Ile Ile Ala Thr Gly Pro Met Thr Asn Leu Ser Ala
 85 90 95

Ala Ile Ala Lys Asp Pro Ser Phe Ala Ser Lys Ala His Val Val Ile
 100 105 110

Met Gly Gly Ala Leu Thr Val Pro Gly Asn Val Ser Thr Trp Ala Glu
 115 120 125

Ala Asn Ile Asn Gln Asp Pro Asp Ala Ala Asn Asp Leu Phe Arg Ser
 130 135 140

Gly Ala Asp Val Thr Met Ile Gly Leu Asp Val Thr Leu Gln Thr Leu
 145 150 155 160

Leu Thr Lys Lys His Thr Ala Gln Trp Arg Glu Leu Gly Thr Pro Ala
 165 170 175

Ala Ile Ala Leu Ala Asp Met Thr Asp Tyr Tyr Ile Lys Ala Tyr Glu
 180 185 190

Thr Thr Ala Pro His Leu Gly Gly Cys Gly Leu His Asp Pro Leu Ala
 195 200 205

Val Gly Val Ala Val Asp Pro Ser Leu Val Thr Leu Leu Pro Ile Asn
 210 215 220

Leu Lys Val Asp Ile Glu Gly Glu Thr Arg Gly Arg Thr Ile Gly Asp

225						230						235						240
Glu	Val	Arg	Leu	Asn	Asp	Pro	Val	Arg	Thr	Ser	Arg	Ala	Ala	Val	Ala			
					245						250						255	
Val	Asp	Val	Asp	Arg	Phe	Leu	Ser	Glu	Phe	Met	Thr	Arg	Ile	Gly	Arg			
					260						265						270	
Val	Ala	Ala	Gln	Gln														
					275													

[illegible]

tcc acc acc acg att tta tat gac tgg ttt gat gcg atg tcg gtg caa 547
 Ser Thr Thr Thr Ile Leu Tyr Asp Trp Phe Asp Ala Met Ser Val Gln
 135 140 145

att act ccc gat atc gcc cac gcc ctt tat gct gga ctg ctc acc gat 595
 Ile Thr Pro Asp Ile Ala His Gly Leu Tyr Ala Gly Leu Leu Thr Asp
 150 155 160 165

acc ggg tgc ttc agg tgg ggt cga cca gtc atg cat gac atg gct aaa 643
 Thr Gly Cys Phe Arg Trp Gly Arg Pro Val Met His Asp Met Ala Lys
 170 175 180

gaa ctc atg gag ttc ggt cta gac att cgt gcc att tca tca gca ttg 691
 Glu Leu Met Glu Phe Gly Leu Asp Ile Arg Ala Ile Ser Ser Ala Leu
 185 190 195

ctt gat caa acc tcc gtg gat gat ttg cgt ctt gtt ggc cag att gtc 739
 Leu Asp Gln Thr Ser Val Asp Asp Leu Arg Leu Val Gly Gln Ile Val
 200 205 210

tct cgg atc gag ctg cgg gaa gca ggg cca tat act ctt gct gtt ctc 787
 Ser Arg Ile Glu Leu Arg Glu Ala Gly Pro Tyr Thr Leu Ala Val Leu
 215 220 225

gtg gca gac ttc gat acc atc aac gcc cgt tca cgc gcc gtt gtg gaa 835
 Val Ala Asp Phe Asp Thr Ile Asn Gly Arg Ser Arg Ala Val Val Glu
 230 235 240 245

ggc ttg atc gaa atg gtt cgc gct gtg gaa gcc gca gac ttc gga gca 883
 Gly Leu Ile Glu Met Val Arg Ala Val Glu Gly Ala Asp Phe Gly Ala
 250 255 260

gta ttc aaa gaa tat gaa cgt gcc gtc tat acc gtg tca ctg cgt tcc 931
 Val Phe Lys Glu Tyr Glu Arg Gly Val Tyr Thr Val Ser Leu Arg Ser
 265 270 275

tcc aat ttg agt gtc gct tcc ttg gca gtg cat ctt gcc ggt gcc gga 979
 Ser Asn Leu Ser Val Ala Ser Leu Ala Val His Leu Gly Gly Gly Gly
 280 285 290

cac att cct gct gca gcc tat acc gct cgt ggt acg gaa atc gaa gcc 1027
 His Ile Pro Ala Ala Gly Tyr Thr Ala Arg Gly Thr Glu Ile Glu Ala
 295 300 305

ctc gat acg ttg att gaa gca acc gtt acc ttg ggg gag tct ttg cga 1075
 Leu Asp Thr Leu Ile Glu Ala Thr Val Thr Leu Gly Glu Ser Leu Arg
 310 315 320 325

agc tcg gcg cat gtc gat gtc taacaacgac ttgagcatg agt 1119
 Ser Ser Ala His Val Asp Val
 330

<210> 2268
 <211> 332
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 2268
 Val Thr Asp Asn Ser Gln Phe His Ala Ala Ser Ala Leu Val Gln Ala
 1 5 10 15

Ala His Thr Val Ser Val Val Gly His Leu Arg Pro Asp Ala Asp Ala
 20 25 30
 Ile Gly Ser Val Ala Ala Thr Val Ala Ala Leu Gln Gln Leu Gly Lys
 35 40 45
 Asp Ala Val Gly Ala Ile Gly Gln Leu Asp Ser Met Pro Glu Asn Leu
 50 55 60
 Tyr Thr Ile Pro Gly Ala Ser Asn Ile Lys Phe Gly Asp Ser Leu Pro
 65 70 75 80
 Glu Ser Asp Leu Ile Ile Val Val Asp Cys Gly Ser Ile Glu Arg Thr
 85 90 95
 Gly Ala Phe Glu Ser Ile Ile Val Asn Asn Pro Asp Lys Val Leu Val
 100 105 110
 Val Asp His His Ala Thr Asn Pro Gly Phe Gly Ala Val Asn Leu Ile
 115 120 125
 Asp Val Glu Ala Glu Ser Thr Thr Thr Ile Leu Tyr Asp Trp Phe Asp
 130 135 140
 Ala Met Ser Val Gln Ile Thr Pro Asp Ile Ala His Gly Leu Tyr Ala
 145 150 155 160
 Gly Leu Leu Thr Asp Thr Gly Cys Phe Arg Trp Gly Arg Pro Val Met
 165 170 175
 His Asp Met Ala Lys Glu Leu Met Glu Phe Gly Leu Asp Ile Arg Ala
 180 185 190
 Ile Ser Ser Ala Leu Leu Asp Gln Thr Ser Val Asp Asp Leu Arg Leu
 195 200 205
 Val Gly Gln Ile Val Ser Arg Ile Glu Leu Arg Glu Ala Gly Pro Tyr
 210 215 220
 Thr Leu Ala Val Leu Val Ala Asp Phe Asp Thr Ile Asn Gly Arg Ser
 225 230 235 240
 Arg Ala Val Val Glu Gly Leu Ile Glu Met Val Arg Ala Val Glu Gly
 245 250 255
 Ala Asp Phe Gly Ala Val Phe Lys Glu Tyr Glu Arg Gly Val Tyr Thr
 260 265 270
 Val Ser Leu Arg Ser Ser Asn Leu Ser Val Ala Ser Leu Ala Val His
 275 280 285
 Leu Gly Gly Gly Gly His Ile Pro Ala Ala Gly Tyr Thr Ala Arg Gly
 290 295 300
 Thr Glu Ile Glu Ala Leu Asp Thr Leu Ile Glu Ala Thr Val Thr Leu
 305 310 315 320
 Gly Glu Ser Leu Arg Ser Ser Ala His Val Asp Val
 325 330


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<210> 2269
<211> 1041
<212> DNA
<213> Corvnebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1018)
<223> RXA01497
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	gccaccagaa	agacgccct	ttggcagcc	gaattag	tca	atg	gtg	ggt	aaa	ctt		115			
						Met	Val	Gly	Lys	Leu					
						1				5					
ccc atc	atg	gct	gaa	acc	aac	gaa	aat	gat	ctt	cca	gtt	atc	gac	ctt	163
Pro	Ile	Met	Ala	Glu	Thr	Asn	Glu	Asn	Asp	Leu	Pro	Val	Ile	Asp	Leu
				10					15					20	
gcc caa	atc	gaa	ggc	tat	gtt	gta	gat	gac	tcg	gat	gaa	gat	gat	cca	211
Ala	Gln	Ile	Glu	Gly	Tyr	Val	Val	Asp	Asp	Ser	Asp	Glu	Asp	Asp	Pro
			25					30					35		
gta ctt	ctg	cgt	cca	gat	gga	acc	ccc	att	gaa	acc	tgg	cgc	gaa	gac	259
Val	Leu	Leu	Arg	Pro	Asp	Gly	Thr	Pro	Ile	Glu	Thr	Trp	Arg	Glu	Asp
			40				45					50			
ttc cct	tat	gaa	gag	cgc	gtc	acc	cgc	gaa	gac	tat	gag	aag	gtc	aag	307
Phe	Pro	Tyr	Glu	Glu	Arg	Val	Thr	Arg	Glu	Asp	Tyr	Glu	Lys	Val	Lys
		55				60					65				
cgc tcc	ctc	cag	atc	gag	ctg	ctg	aag	tgg	cag	aac	tgg	acc	aag	gaa	355
Arg	Ser	Leu	Gln	Ile	Glu	Leu	Leu	Lys	Trp	Gln	Asn	Trp	Thr	Lys	Glu
				75					80					85	
act ggc	cag	cgc	cac	atc	att	ttg	ttc	gaa	ggg	cgt	gac	gcc	gct	ggc	403
Thr	Gly	Gln	Arg	His	Ile	Ile	Leu	Phe	Glu	Gly	Arg	Asp	Ala	Ala	Gly
				90					95					100	
aag ggt	ggc	acc	att	aag	cgc	ttc	aac	gaa	cac	ctg	aac	cct	cgt	ggc	451
Lys	Gly	Gly	Thr	Ile	Lys	Arg	Phe	Asn	Glu	His	Leu	Asn	Pro	Arg	Gly
			105					110				115			
gcc cgt	act	ggt	gcg	ttg	gag	aag	cca	tca	cca	cgc	gaa	tcc	acc	tca	499
Ala	Arg	Thr	Val	Ala	Leu	Glu	Lys	Pro	Ser	Pro	Arg	Glu	Ser	Thr	Ser
			120				125					130			
tgg tac	ttc	cag	cgc	tat	att	cag	cac	ttc	cca	gta	gct	ggc	gag	atc	547
Trp	Tyr	Phe	Gln	Arg	Tyr	Ile	Gln	His	Phe	Pro	Ala	Ala	Gly	Glu	Ile
		135				140				145					
gtt ttc	ttt	gac	cgc	tct	tgg	tac	aac	cgt	tcc	ggc	gtg	gag	cgc	gtc	595
Val	Phe	Phe	Asp	Arg	Ser	Trp	Tyr	Asn	Arg	Ser	Gly	Val	Glu	Arg	Val
				155					160					165	
atg ggt	ttc	tgc	acc	gaa	tca	cag	cat	gca	gag	ttc	ctg	cgt	gag	gtt	643
Met	Gly	Phe	Cys	Thr	Glu	Ser	Gln	His	Ala	Glu	Phe	Leu	Arg	Glu	Val
			170					175					180		

cca atg ctg gaa aac atg atc ctg ggc tct ggt atc agc ttg acc aag 691
 Pro Met Leu Glu Asn Met Ile Leu Gly Ser Gly Ile Ser Leu Thr Lys
 185 190 195

ttc tgg ttc tgg gtg acc cgt aaa gag cag cgc acc cgt ttt gct atc 739
 Phe Trp Phe Ser Val Thr Arg Lys Glu Gln Arg Thr Arg Phe Ala Ile
 200 205 210

cgc cag gtt gat cct gtg cgt cag tgg aag ctt tcc cca atg gac ttg 787
 Arg Gln Val Asp Pro Val Arg Gln Trp Lys Leu Ser Pro Met Asp Leu
 215 220 225

gct tca ctt gat cgc tgg gat gat tac acc cgc gct aag gaa gag cag 835
 Ala Ser Leu Asp Arg Trp Asp Asp Tyr Thr Arg Ala Lys Glu Glu Gln
 230 235 240 245

ttc cgt tac acc gac act gat gag tcc cgc tgg atc acc atc aag tgc 883
 Phe Arg Tyr Thr Asp Thr Asp Glu Ser Pro Trp Ile Thr Ile Lys Ser
 250 255 260

aat gac aag aag cgt gcg cgt atc aac gcg atg cgt tat gta ttg tcc 931
 Asn Asp Lys Lys Arg Ala Arg Ile Asn Ala Met Arg Tyr Val Leu Ser
 265 270 275

aag ttt gat tac acc gac aag gat tac gag ctg gtt ggt gag cct gac 979
 Lys Phe Asp Tyr Thr Asp Lys Asp Tyr Glu Leu Val Gly Glu Pro Asp
 280 285 290

cct aag gtt gtg ctt cgt ggg cgc gac cag atc ggt gac tagtactag 1028
 Pro Lys Val Val Leu Arg Gly Arg Asp Gln Ile Gly Asp
 295 300 305

gcgggcatga aaa 1041

<210> 2270
 <211> 306
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2270
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Pro Val Ile Asp Leu Ala Gln Ile Glu Gly Tyr Val Val Asp Asp Ser
 20 25 30

Asp Glu Asp Asp Pro Val Leu Leu Arg Pro Asp Gly Thr Pro Ile Glu
 35 40 45

Thr Trp Arg Glu Asp Phe Pro Tyr Glu Glu Arg Val Thr Arg Glu Asp
 50 55 60

Tyr Glu Lys Val Lys Arg Ser Leu Gln Ile Glu Leu Leu Lys Trp Gln
 65 70 75 80

Asn Trp Thr Lys Glu Thr Gly Gln Arg His Ile Ile Leu Phe Glu Gly
 85 90 95

Arg Asp Ala Ala Gly Lys Gly Gly Thr Ile Lys Arg Phe Asn Glu His

100	105	110
Leu Asn Pro Arg Gly Ala Arg Thr Val Ala Leu Glu Lys Pro Ser Pro		
115	120	125
Arg Glu Ser Thr Ser Trp Tyr Phe Gln Arg Tyr Ile Gln His Phe Pro		
130	135	140
Ala Ala Gly Glu Ile Val Phe Phe Asp Arg Ser Trp Tyr Asn Arg Ser		
145	150	155
Gly Val Glu Arg Val Met Gly Phe Cys Thr Glu Ser Gln His Ala Glu		
165	170	175
Phe Leu Arg Glu Val Pro Met Leu Glu Asn Met Ile Leu Gly Ser Gly		
180	185	190
Ile Ser Leu Thr Lys Phe Trp Phe Ser Val Thr Arg Lys Glu Gln Arg		
195	200	205
Thr Arg Phe Ala Ile Arg Gln Val Asp Pro Val Arg Gln Trp Lys Leu		
210	215	220
Ser Pro Met Asp Leu Ala Ser Leu Asp Arg Trp Asp Asp Tyr Thr Arg		
225	230	235
Ala Lys Glu Glu Gln Phe Arg Tyr Thr Asp Thr Asp Glu Ser Pro Trp		
245	250	255
Ile Thr Ile Lys Ser Asn Asp Lys Lys Arg Ala Arg Ile Asn Ala Met		
260	265	270
Arg Tyr Val Leu Ser Lys Phe Asp Tyr Thr Asp Lys Asp Tyr Glu Leu		
275	280	285
Val Gly Glu Pro Asp Pro Lys Val Val Leu Arg Gly Arg Asp Gln Ile		
290	295	300
Gly Asp		
305		

<210> 2271

<211> 411

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(388)

<223> RXA01501

<400> 2271

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actatttcaa gaatttattc aacaaaggag ttcttcacaa atg aag gaa gta gca	115
Met Lys Glu Val Ala	
1	5

gtc aac gaa gtc cca gca ggc gca cag ttg atc gat gtc cgc gag acc	163
Val Asn Glu Val Pro Ala Gly Ala Gln Leu Ile Asp Val Arg Glu Thr	

	10	15	20	
gat gaa tac gca gag gtt cga gca cag ggt gcc gtc aac att cct atg				211
Asp Glu Tyr Ala Glu Val Arg Ala Gln Gly Ala Val Asn Ile Pro Met	25	30	35	
agc gag ttc gtt ggc cgc atc gat gag atc gat ctg gac cgc gac att				259
Ser Glu Phe Val Gly Arg Ile Asp Glu Ile Asp Leu Asp Arg Asp Ile	40	45	50	
tat gtc att tgc aag ctg ggt gga cgc tca gct cag gtt gcc gaa tac				307
Tyr Val Ile Cys Lys Leu Gly Gly Arg Ser Ala Gln Val Ala Glu Tyr	55	60	65	
ctt gag cag cgc gga att gaa gcc atc aac gta aac ggt ggc acc gac				355
Leu Glu Gln Arg Gly Ile Glu Ala Ile Asn Val Asn Gly Gly Thr Asp	70	75	80	85
ggc tgg gtt gct gca gga ttg cca acc gag gca taagaaccgc cgcgaaga				408
Gly Trp Val Ala Ala Gly Leu Pro Thr Glu Ala	90	95		
tcc				411
<210> 2272				
<211> 96				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 2272				
Met Lys Glu Val Ala Val Asn Glu Val Pro Ala Gly Ala Gln Leu Ile				
1 5 10 15				
Asp Val Arg Glu Thr Asp Glu Tyr Ala Glu Val Arg Ala Gln Gly Ala				
20 25 30				
Val Asn Ile Pro Met Ser Glu Phe Val Gly Arg Ile Asp Glu Ile Asp				
35 40 45				
Leu Asp Arg Asp Ile Tyr Val Ile Cys Lys Leu Gly Gly Arg Ser Ala				
50 55 60				
Gln Val Ala Glu Tyr Leu Glu Gln Arg Gly Ile Glu Ala Ile Asn Val				
65 70 75 80				
Asn Gly Gly Thr Asp Gly Trp Val Ala Ala Gly Leu Pro Thr Glu Ala				
85 90 95				

<210> 2273

<211> 732

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> {101}..(709)

<223> RXA01504

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ttggctcgta ccgaacttag aaaaactcatg ggagtttcgc atg aat atc acg tgg 115
Met Asn Ile Thr Trp
1 5

ctt atc ctg gcc ggt gtt tta gcc atc atc gct gtc gtg ttc ttt tat 163
Leu Ile Leu Ala Gly Val Leu Ala Ile Ile Ala Val Val Phe Phe Tyr
10 15 20

ctt tca gca cag aag aaa aag agc gaa ccg cag cct cct cgt cag cgt 211
Leu Ser Ala Gln Lys Lys Lys Ser Glu Pro Gln Pro Pro Arg Gln Arg
25 30 35

caa gat cct ctg aaa ttt gcc gac gga tcc gac act ttt aat gcc cgc 259
Gln Asp Pro Leu Lys Phe Ala Asp Gly Ser Asp Thr Phe Asn Ala Arg
40 45 50

att ttg ggt cct gga gca att att tcc cgc ggt ggc gtg gat tat gtc 307
Ile Leu Gly Pro Gly Ala Ile Ile Ser Arg Gly Gly Val Asp Tyr Val
55 60 65

tgc cgc gga gcc atc cag ttc cgt caa ggc caa tac att tgg cac gag 355
Cys Arg Gly Ala Ile Gln Phe Arg Gln Gly Gln Tyr Ile Trp His Glu
70 75 80 85

tat cta ctc gac ggt ggc aaa ggc agt gag tac ctg agc gtg gaa tac 403
Tyr Leu Leu Asp Gly Gly Lys Gly Ser Glu Tyr Leu Ser Val Glu Tyr
90 95 100

gat gag ggc caa ctc aac ctc gga tgg tgg att acc cgc cct gac ctg 451
Asp Glu Gly Gln Leu Asn Leu Gly Trp Trp Ile Thr Arg Pro Asp Leu
105 110 115

gca caa cag ccc gca cat gat gtc acc gtg gag ggc gtt cgc tac cgt 499
Ala Gln Gln Pro Ala His Asp Val Thr Val Glu Gly Val Arg Tyr Arg
120 125 130

aaa acc gaa tct ggc gtg ggc acc ttc acc tcc gaa ggc acc acc ggc 547
Lys Thr Glu Ser Gly Val Gly Thr Phe Thr Ser Glu Gly Thr Thr Gly
135 140 145

gtg gct gat caa ggt gaa ttt gaa tac tgg gat ctc gcc gaa gtt ggc 595
Val Ala Asp Gln Gly Glu Phe Glu Tyr Trp Asp Leu Ala Glu Val Gly
150 155 160 165

gga aac agg ttg ctc agt ttt gaa cgc tac ggc aaa gac agt cca ttt 643
Gly Asn Arg Leu Leu Ser Phe Glu Arg Tyr Gly Lys Asp Ser Pro Phe
170 175 180

gaa gta tgc ctc ggg tgg acg gtg ctg ccc ggc gaa ctc acc gtt tac 691
Glu Val Ser Leu Gly Trp Thr Val Leu Pro Gly Glu Leu Thr Val Tyr
185 190 195

cca gca cca gag gcc tca tgattcatca catcgattgc atg 732
Pro Ala Pro Glu Ala Ser
200

<210> 2274
 <211> 203
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 2274
 Met Asn Ile Thr Trp Leu Ile Leu Ala Gly Val Leu Ala Ile Ile Ala
 1 5 10 15
 Val Val Phe Phe Tyr Leu Ser Ala Gln Lys Lys Lys Ser Glu Pro Gln
 20 25 30
 Pro Pro Arg Gln Arg Gln Asp Pro Leu Lys Phe Ala Asp Gly Ser Asp
 35 40 45
 Thr Phe Asn Ala Arg Ile Leu Gly Pro Gly Ala Ile Ile Ser Arg Gly
 50 55 60
 Gly Val Asp Tyr Val Cys Arg Gly Ala Ile Gln Phe Arg Gln Gly Gln
 65 70 75 80
 Tyr Ile Trp His Glu Tyr Leu Leu Asp Gly Gly Lys Gly Ser Glu Tyr
 85 90 95
 Leu Ser Val Glu Tyr Asp Glu Gly Gln Leu Asn Leu Gly Trp Trp Ile
 100 105 110
 Thr Arg Pro Asp Leu Ala Gln Gln Pro Ala His Asp Val Thr Val Glu
 115 120 125
 Gly Val Arg Tyr Arg Lys Thr Glu Ser Gly Val Gly Thr Phe Thr Ser
 130 135 140
 Glu Gly Thr Thr Gly Val Ala Asp Gln Gly Glu Phe Glu Tyr Trp Asp
 145 150 155 160
 Leu Ala Glu Val Gly Gly Asn Arg Leu Leu Ser Phe Glu Arg Tyr Gly
 165 170 175
 Lys Asp Ser Pro Phe Glu Val Ser Leu Gly Trp Thr Val Leu Pro Gly
 180 185 190
 Glu Leu Thr Val Tyr Pro Ala Pro Glu Ala Ser
 195 200

<210> 2275
 <211> 621
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(598)
 <223> RXA01505

<400> 2275
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Met Ile His His Ile
1 5

gat tgc atg cct aca gat gtc tcc gcc gaa gcg ctc ggc gtg agc tgg 163
Asp Cys Met Pro Thr Asp Val Ser Ala Glu Ala Leu Gly Val Ser Trp
10 15 20

aat ggg gaa tcg ccg gag gtg ctc gtc gat aag ctt atc gac gca tcc 211
Asn Gly Glu Ser Pro Glu Val Leu Val Asp Asp Lys Leu Ile Asp Ala Ser
25 30 35

cca cac ccc agc acc tgc cat tta gcg gtg att ggc ggc tcg cat gtg 259
Pro His Pro Ser Thr Cys His Leu Ala Val Ile Gly Gly Ser His Val
40 45 50

gtt acc gtt gaa acg ccc gat ggg cgt ttc cgg gaa gaa att tcc tgc 307
Val Thr Val Glu Thr Pro Asp Gly Arg Phe Arg Glu Glu Ile Ser Cys
55 60 65

cat gca caa gaa gcg gaa gat tcc cgc tgg ccg ctg ccc gac agc atc 355
His Ala Gln Glu Ala Glu Asp Ser Arg Trp Pro Leu Pro Asp Ser Ile
70 75 80 85

acg cgg gaa aac tac ctg ctg caa acc aac gtc gcc gtg ctg tct gag 403
Thr Arg Glu Asn Tyr Leu Leu Gln Thr Asn Val Ala Val Leu Ser Glu
90 95 100

gaa gat ttt gcc cgc gca gcc gaa gaa atc tcc aac ggc gac gac gac 451
Glu Asp Phe Ala Arg Ala Ala Glu Glu Ile Ser Asn Gly Asp Asp Asp
105 110 115

tgg ttg atc gcc agt ttc ccc ggc gcc ggc gaa cac cac ctc acc gcg 499
Trp Leu Ile Ala Ser Phe Pro Gly Ala Gly Glu His His Leu Thr Ala
120 125 130

ctg acc gca gaa ttt ctg gaa gac gta tgg gaa tgg ttt agc cac cac 547
Leu Thr Ala Glu Phe Leu Glu Asp Val Trp Glu Trp Phe Ser His His
135 140 145

ctc tac cca gaa gag ctc acc atc gtg agc acg agg agc att tac aaa 595
Leu Tyr Pro Glu Glu Leu Thr Ile Val Ser Thr Arg Ser Ile Tyr Lys
150 155 160 165

cca tgagctcccg aaactaccga agc 621
Pro

<210> 2276

<211> 166

<212> PRT

<213> Corynebacterium glutamicum

<400> 2276

Met Ile His His Ile Asp Cys Met Pro Thr Asp Val Ser Ala Glu Ala
1 5 10 15

Leu Gly Val Ser Trp Asn Gly Glu Ser Pro Glu Val Leu Val Asp Lys
20 25 30

Leu Ile Asp Ala Ser Pro His Pro Ser Thr Cys His Leu Ala Val Ile

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35              40              45
Gly Gly Ser His Val Val Thr Val Glu Thr Pro Asp Gly Arg Phe Arg
50              55              60
Glu Glu Ile Ser Cys His Ala Gln Glu Ala Glu Asp Ser Arg Trp Pro
65              70              75              80
Leu Pro Asp Ser Ile Thr Arg Glu Asn Tyr Leu Leu Gln Thr Asn Val
85              90              95
Ala Val Leu Ser Glu Glu Asp Phe Ala Arg Ala Ala Glu Glu Ile Ser
100             105             110
Asn Gly Asp Asp Asp Trp Leu Ile Ala Ser Phe Pro Gly Ala Gly Glu
115             120             125
His His Leu Thr Ala Leu Thr Ala Glu Phe Leu Glu Asp Val Trp Glu
130             135             140
Trp Phe Ser His His Leu Tyr Pro Glu Glu Leu Thr Ile Val Ser Thr
145             150             155             160
Arg Ser Ile Tyr Lys Pro
165
<210> 2277
<211> 534
<212> DNA
<213> Corynebacterium glutamicum
<220>
<221> CDS
<222> (101)..(511)
<223> RXA01506
<400> 2277
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aagagctcac catcgtgagc acgaggagca ttacaaacc atg agc tcc cga aac 115
Met Ser Ser Arg Asn
1 5
tac cga agc ata gga ttc atc ctg ctg ttt tta gca gtg ttg tgc ctg 163
Tyr Arg Ser Ile Gly Phe Ile Leu Leu Phe Leu Ala Val Leu Cys Leu
10 15 20
ttc gct gcg gtt ttt gcc aag cct gcg gtg gga agc caa gtc tcc gac 211
Phe Ala Ala Val Phe Ala Lys Pro Ala Val Gly Ser Gln Val Ser Asp
25 30 35
cgc tgg ccc gga aac aac ggc acc tac tca tgc gct ggc gaa agt ggg 259
Arg Trp Pro Gly Asn Asn Gly Thr Tyr Ser Cys Ala Gly Glu Ser Gly
40 45 50
gtg gtg gat gaa atc gtg aac atg tcc acc cca acc gac cgc gcc acc 307
Val Val Asp Glu Ile Val Asn Met Ser Thr Pro Thr Asp Arg Ala Thr
55 60 65
gac ccc gca act ggc gat act tac ctg cga tac agc aaa aac ctg atc 355

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Asp Pro Ala Thr Gly Asp Thr Tyr Leu Arg Tyr Ser Lys Asn Leu Ile
 70          75          80          85

atc atc tca ggt gaa ggc acg ccg gaa tgc acc atc acc gtc gaa ggc   403
Ile Ile Ser Gly Glu Gly Thr Pro Glu Cys Thr Ile Thr Val Glu Gly
          90          95          100

ctt gac cgc gtc aac agt ggt gcg ttc atc tgg ctc ggc ggc ggt ttc   451
Leu Asp Arg Val Asn Ser Gly Ala Phe Ile Trp Leu Gly Gly Gly Phe
          105          110          115

ggc cca tcc tca cca agc agt tcc agc ggc gga tcc tcc ggt tcc ggc   499
Gly Pro Ser Ser Pro Ser Ser Ser Ser Gly Gly Ser Ser Gly Ser Gly
          120          125          130

ggt ggc gtg aaa tagaagaac actatgagtc aat   534
Gly Gly Val Lys
          135

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<210> 2278

<211> 137

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2278

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Met Ser Ser Arg Asn Tyr Arg Ser Ile Gly Phe Ile Leu Leu Phe Leu
 1          5          10          15

Ala Val Leu Cys Leu Phe Ala Ala Val Phe Ala Lys Pro Ala Val Gly
          20          25          30

Ser Gln Val Ser Asp Arg Trp Pro Gly Asn Asn Gly Thr Tyr Ser Cys
          35          40          45

Ala Gly Glu Ser Gly Val Val Asp Glu Ile Val Asn Met Ser Thr Pro
          50          55          60

Thr Asp Arg Ala Thr Asp Pro Ala Thr Gly Asp Thr Tyr Leu Arg Tyr
          65          70          75          80

Ser Lys Asn Leu Ile Ile Ile Ser Gly Glu Gly Thr Pro Glu Cys Thr
          85          90          95

Ile Thr Val Glu Gly Leu Asp Arg Val Asn Ser Gly Ala Phe Ile Trp
          100          105          110

Leu Gly Gly Gly Phe Gly Pro Ser Pro Ser Ser Ser Ser Gly Gly
          115          120          125

Ser Ser Gly Ser Gly Gly Gly Val Lys
          130          135

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<210> 2279

<211> 546

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(523)

<223> RXA01507

<400> 2279

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Met Ser Gln Tyr Leu
1 5

gtc gac gga gtg ctc gcc acc ctt tca tat ttc gtg ttg gcc gca gtg 163
Val Asp Gly Val Leu Gly Thr Leu Ser Tyr Phe Val Leu Ala Ala Val
10 15 20

atc ctc gtg gtc ggt ttt gtg att ttg gac ttg atc acc cca ggt aaa 211
Ile Leu Val Val Gly Phe Val Ile Leu Asp Leu Ile Thr Pro Gly Lys
25 30 35

ctg cat gaa ctc gtg ttt gtg cac cat ctg ccc aac gcc gct gtg atc 259
Leu His Glu Leu Val Phe Val His His Leu Pro Asn Ala Ala Val Ile
40 45 50

acc gtg gcg cag cag gtt tcc atc gga atc atc gtg gtc act gct gtg 307
Thr Val Ala Gln Gln Val Ser Ile Gly Ile Ile Val Val Thr Ala Val
55 60 65

ctg acc tcc tca gat att ttg agt gaa ggt ttg ctg gag act gca gtg 355
Leu Thr Ser Ser Asp Ile Leu Ser Glu Gly Leu Leu Glu Thr Ala Val
70 75 80 85

ttc ggt gcc ctt ggt ctg gtt atc caa gtg gtg gtc atg gcg gtg ttg 403
Phe Gly Ala Leu Gly Leu Val Ile Gln Val Val Val Met Ala Val Leu
90 95 100

gaa gct gtc att ccg gga cgt ttc cgt gat ctc gtg gaa gat ccc aaa 451
Glu Ala Val Ile Pro Gly Arg Phe Arg Asp Leu Val Glu Asp Pro Lys
105 110 115

ctc cgt tcc ggt gcc gtc gtg gcc gcc gtc atc ttg atc gtg gtg gga 499
Leu Arg Ser Gly Ala Val Val Ala Ala Val Ile Leu Ile Val Val Gly
120 125 130

acc gta aac gct gca tgt ctg att taggacccat ctggcgctgg ctg 546
Thr Val Asn Ala Ala Cys Leu Ile
135 140

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<210> 2280

<211> 141

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2280

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Met Ser Gln Tyr Leu Val Asp Gly Val Leu Gly Thr Leu Ser Tyr Phe
1 5 10 15

Val Leu Ala Ala Val Ile Leu Val Val Gly Phe Val Ile Leu Asp Leu
20 25 30

Ile Thr Pro Gly Lys Leu His Glu Leu Val Phe Val His His Leu Pro
35 40 45

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Asn Ala Ala Val Ile Thr Val Ala Gln Gln Val Ser Ile Gly Ile Ile
 50 55 60
 Val Val Thr Ala Val Leu Thr Ser Ser Asp Ile Leu Ser Glu Gly Leu
 65 70 75 80
 Leu Glu Thr Ala Val Phe Gly Ala Leu Gly Leu Val Ile Gln Val Val
 85 90 95
 Val Met Ala Val Leu Glu Ala Val Ile Pro Gly Arg Phe Arg Asp Leu
 100 105 110
 Val Glu Asp Pro Lys Leu Arg Ser Gly Ala Val Val Ala Ala Val Ile
 115 120 125
 Leu Ile Val Val Gly Thr Val Asn Ala Ala Cys Leu Ile
 130 135 140

<210> 2281

<211> 870

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(847)

<223> RXA01519

<400> 2281

ctgggcggaa tcgcaactctc agctgcgcga ctttatcttag agcgaagctg tgaggctccg 60

cctccccaat ctggcgaagc gatcagctag attggaattc atg aat caa gac ctg 115
 Met Asn Gln Asp Leu 5

tca cac gag gat tcc ggc gac ggc aat tct gtc gac cgt gga cag att 163
 Ser His Glu Asp Ser Gly Asp Gly Asn Ser Val Asp Arg Gly Gln Ile 10 15 20

ctg cta gca gta ctc att gga ctt gcc ctg att gcc agc gtc atc atg 211
 Leu Leu Ala Val Leu Ile Gly Leu Ala Leu Ile Ala Ser Val Ile Met 25 30 35

ctg ctg gcc aac agt gac ggc gcc atg aaa ata gca ctt ctt gca gcg 259
 Leu Leu Ala Asn Ser Asp Gly Ala Met Lys Ile Ala Leu Leu Ala Ala 40 45 50

ctg tgg gcg gca atc atc gga ttc ttc ctt gtt tat cgg tcc cgc aaa 307
 Leu Trp Ala Ala Ile Ile Gly Phe Phe Leu Val Tyr Arg Ser Arg Lys 55 60 65

caa gtc gaa gct gct gcg cgg gag aag gaa acc ctc gaa tac gca cac 355
 Gln Val Glu Ala Ala Ala Arg Glu Lys Glu Thr Leu Glu Tyr Ala His 70 75 80 85

caa tct gaa ctc aac cga cta gaa gct gaa ctc gtc caa gaa aaa atg 403
 Gln Ser Glu Leu Asn Arg Leu Glu Ala Glu Leu Val Gln Glu Lys Met 90 95 100

gag att tct gaa tcc cgt cgt gca cgc gat cag gaa acc ctt gag gaa 451
 Glu Ile Ser Glu Ser Arg Arg Ala Arg Asp Gln Glu Thr Leu Glu Glu
 105 110 115

 atc aaa ctt caa ctg gag gaa atg cgc acc cag ctg tct gag ctt tct 499
 Ile Lys Leu Glu Gln Leu Glu Glu Met Arg Thr Gln Leu Ser Glu Leu Ser
 120 125 130

 ggc cgt gaa tgg ggc tat gag cca acc atg ctg cgt gcc gaa gcc cga 547
 Gly Arg Glu Trp Gly Tyr Glu Pro Thr Met Leu Arg Ala Glu Ala Arg
 135 140 145

 cga atc ctt gag ttg gaa tcc cag cag ctt tcc cag cag ttc cag gca 595
 Arg Ile Leu Glu Leu Glu Ser Gln Gln Leu Ser Gln Gln Phe Gln Ala
 150 155 160 165

 ccg cag cca gaa gtc ccg gag cct gtt gca gtt cca gag cca atg ccg 643
 Pro Gln Pro Glu Val Pro Glu Pro Val Ala Val Pro Glu Pro Met Pro
 170 175 180

 gaa cct gca ccg gtg ccg gaa cca gta cca gaa cct gag cca gtt gaa 691
 Glu Pro Ala Pro Val Pro Glu Pro Val Pro Glu Pro Glu Pro Val Glu
 185 190 195

 gtt gct gtc gaa gct gag gaa gaa cca gca cca ggt cgc aga agg cgt 739
 Val Ala Val Glu Ala Glu Glu Glu Pro Ala Pro Gly Arg Arg Arg Arg
 200 205 210

 agg cac gca gct ccc gaa gaa act ggc gga cgc cga cgc aaa gat gaa 787
 Arg His Ala Ala Pro Glu Glu Thr Gly Gly Arg Arg Arg Lys Asp Glu
 215 220 225

 cgc caa ggc ggt ttg agc gtg gct gat ctt ctg gca gca gca agg aaa 835
 Arg Gln Gly Gly Leu Ser Val Ala Asp Leu Leu Ala Ala Ala Arg Lys
 230 235 240 245

 aag gaa aac aac taatgcaggc tctcgcctt cgc 870
 Lys Glu Asn Asn

<210> 2282

<211> 249

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2282

Met Asn Gln Asp Leu Ser His Glu Asp Ser Gly Asp Gly Asn Ser Val
 1 5 10 15

Asp Arg Gly Gln Ile Leu Leu Ala Val Leu Ile Gly Leu Ala Leu Ile
 20 25 30

Ala Ser Val Ile Met Leu Leu Ala Asn Ser Asp Gly Ala Met Lys Ile
 35 40 45

Ala Leu Leu Ala Ala Leu Trp Ala Ala Ile Ile Gly Phe Phe Leu Val
 50 55 60

Tyr Arg Ser Arg Lys Gln Val Glu Ala Ala Ala Arg Glu Lys Glu Thr
 65 70 75 80

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Leu Glu Tyr  Ala His  Gln Ser  Glu Leu  Asn Arg  Leu Glu  Ala  Glu Leu
                   85                      90                      95

Val  Gln Glu  Lys Met  Glu Ile  Ser Glu  Ser Arg  Arg Ala  Arg Asp  Gln
                   100                   105                   110

Glu Thr Leu  Glu Glu  Ile Lys  Leu Gln  Leu Glu  Glu Met  Arg Thr  Gln
                   115                   120                   125

Leu Ser Glu  Leu Ser  Gly Arg  Glu Trp  Gly Tyr  Glu  Pro  Thr Met  Leu
                   130                   135                   140

Arg Ala Glu  Ala Arg  Arg Ile  Leu Glu  Leu Glu  Ser  Gln  Gln Leu  Ser
                   145                   150                   155                   160

Gln Gln Phe  Gln Ala  Pro Gln  Pro Glu  Val  Pro  Glu  Pro  Val Ala  Val
                   165                   170                   175

Pro Glu Pro  Met  Pro  Glu Pro  Ala  Pro  Val  Pro  Glu  Pro  Val  Pro  Glu
                   180                   185                   190

Pro Glu Pro  Val Glu  Val Ala  Val Glu  Ala Glu  Glu Glu  Pro Ala  Pro
                   195                   200                   205

Gly Arg Arg  Arg Arg  Arg His  Ala Ala  Pro Glu  Glu Thr  Gly Gly  Arg
                   210                   215                   220

Arg Arg Lys  Asp Glu  Arg Gln  Gly Gly  Leu Ser  Val Ala  Asp Leu  Leu
                   225                   230                   235                   240

Ala Ala Ala  Arg Lys  Lys Glu  Asn Asn
                   245

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<210> 2283

<211> 507

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(484)

<223> RXA01520

<400> 2283

ctgcataacct cgctcacgca cggcatcaact gtgatgggac cgctgcagac gtcgggcagg 60

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catcgtgatg tctgcgcacc cgattgggtca ggaccggtgg  gtg gcg tcc gcg ttg    115
                                     Val Ala Ser Ala Leu
                                     1                      5

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gat gag ttg ggg gag acc atc gtg ggg ctt ttg gtg ggg gag ctc ggt    163
Asp Glu Leu Gly Glu Thr Ile Val Gly Leu Leu Val Gly Glu Leu Gly
                   10                      15                      20

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```

ggc tcg att gtc gag atc gcc gat gac aag cgc gca cag ttg gct gca    211
Gly Ser Ile Val Glu Ile Ala Asp Asp Lys Arg Ala Gln Leu Ala Ala
                   25                      30                      35

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gcg ctg acc tat gcc gga ttt tta agc acc ttg cag cgc gat gcg tcg    259

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Ala Leu Thr Tyr Ala Gly Phe Leu Ser Thr Leu Gln Arg Asp Ala Ser
    40                      45                      50
tat ttc ctg gat gaa ttt ctt ggc gat ccc gat gtg acc tct gac atc 307
Tyr Phe Leu Asp Glu Phe Leu Gly Asp Pro Asp Val Thr Ser Asp Ile
    55                      60                      65
gtt atg gat tcc gca cag caa ttc cag gca ctg cct tcg ttg gat gag 355
Val Met Asp Ser Ala Gln Gln Phe Gln Ala Leu Pro Ser Leu Asp Glu
    70                      75                      80
gtc att gcc cag tac gat tcg att aac aac ccc ggc agg caa cgc ctt 403
Val Ile Ala Gln Tyr Asp Ser Ile Asn Asn Pro Gly Arg Gln Arg Leu
    90                      95                      100
ttc cgg gat ttg gcg cgc agg cag gca gag att tcc cgc gcg caa gat 451
Phe Arg Asp Leu Ala Arg Arg Gln Ala Glu Ile Ser Arg Ala Gln Asp
    105                      110                      115
att gag ctg tgg gca att cag aag gag gac cgt tgagtttcac gcatggtcag 504
Ile Glu Leu Trp Ala Ile Gln Lys Glu Asp Arg
    120                      125

ggc 507

<210> 2284
<211> 128
<212> PRT
<213> Corynebacterium glutamicum

<400> 2284
Val Ala Ser Ala Leu Asp Glu Leu Gly Glu Thr Ile Val Gly Leu Leu
    1                      5                      10
Val Gly Glu Leu Gly Gly Ser Ile Val Glu Ile Ala Asp Asp Lys Arg
    20                      25                      30
Ala Gln Leu Ala Ala Ala Leu Thr Tyr Ala Gly Phe Leu Ser Thr Leu
    35                      40                      45
Gln Arg Asp Ala Ser Tyr Phe Leu Asp Glu Phe Leu Gly Asp Pro Asp
    50                      55                      60
Val Thr Ser Asp Ile Val Met Asp Ser Ala Gln Gln Phe Gln Ala Leu
    65                      70                      75                      80
Pro Ser Leu Asp Glu Val Ile Ala Gln Tyr Asp Ser Ile Asn Asn Pro
    85                      90                      95
Gly Arg Gln Arg Leu Phe Arg Asp Leu Ala Arg Arg Gln Ala Glu Ile
    100                      105                      110
Ser Arg Ala Gln Asp Ile Glu Leu Trp Ala Ile Gln Lys Glu Asp Arg
    115                      120                      125

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<210> 2285

<211> 1074
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1051)
 <223> RXA01523

<400> 2285
 aatcctccaa accctgtggat agaacaatct atccacagggt ttctcagtttt ctgcacaaagtt 60
 catccttggc ttcttatgcc ttccgatcca tagtgagggtc atg aaa aac tgg caa 115
 Met Lys Asn Trp Gln
 1 5
 gaa gaa ttc caa cta gtc aat ctg acg aaa ctt ctg cat agc gat acc 163
 Glu Glu Phe Gln Leu Val Asn Leu Thr Lys Leu Leu His Ser Asp Thr
 10 15 20
 gag act tct gcg gca atc agt aat ggt caa atg att aaa ctg act cat 211
 Glu Thr Ser Ala Ala Ile Ser Asn Gly Gln Met Ile Lys Leu Thr His
 25 30 35
 gaa gtc gca atc aat gct gaa aag tac cga agc ctt cct gca tgg gat 259
 Glu Val Ala Ile Asn Ala Glu Lys Tyr Arg Ser Leu Pro Ala Trp Asp
 40 45 50
 aaa gca gcc gcc cga gct ttt gca gtg ggt atg act gtg gac aaa gca 307
 Lys Ala Ala Ala Arg Ala Phe Ala Val Gly Met Thr Val Asp Lys Ala
 55 60 65
 gtg gta gcg ggg cag tct gcg gcg agg tta tgg gga tac caa act ttg 355
 Val Val Ala Gly Gln Ser Ala Ala Arg Leu Trp Gly Tyr Gln Thr Leu
 70 75 80 85
 act gtt gag aaa acc gcg ttg tgt ctg ttg ccg gaa agg cta cgt tca 403
 Thr Val Glu Lys Thr Val Leu Cys Leu Leu Pro Glu Arg Leu Arg Ser
 90 95 100
 aaa tcc tcc aag cat tgg ccg tcc ggg atg cga tat aaa gat cgt tac 451
 Lys Ser Ser Lys His Trp Pro Ser Gly Met Arg Tyr Lys Asp Arg Tyr
 105 110 115
 ctg tcg tcg cgt gat att cga gag gtt cat ggg atc cga gtt acg gga 499
 Leu Ser Ser Arg Asp Ile Arg Glu Val His Gly Ile Arg Val Thr Gly
 120 125 130
 gcg ttc cgc aca ttt ttg gac atc gct ttg gat gat ggg gtg gtg gcg 547
 Ala Phe Arg Thr Phe Leu Asp Ile Ala Leu Asp Asp Gly Val Val Ala
 135 140 145
 gct gtg gtc act att gat tca gct cga aga cag aat cca tcg ctt acg 595
 Ala Val Val Thr Ile Asp Ser Ala Arg Arg Gln Asn Pro Ser Leu Thr
 150 155 160 165
 cgt gag aag tta atg cac agt gcg gaa agt ttc ccg agg cat cgg ggt 643
 Arg Glu Lys Leu Met His Ser Ala Glu Ser Phe Pro Arg His Arg Gly
 170 175 180
 gtg aag gcg tat ccg cag gcg att gag ttg tcg att ccc aat tcg gat 691

Val Lys Ala Tyr Arg Gln Ala Ile Glu Leu Ser Ile Pro Asn Ser Asp
 185 190 195

agt gct cag gag acg agg gct cgg tta atc ctt cgg gag gcc aag ctc 739
 Ser Ala Gln Glu Thr Arg Ala Arg Leu Ile Leu Arg Glu Ala Lys Leu
 200 205 210

ccg gaa atc cag tca gtg aag gtg cag gcc cgt ttc gat caa tcg cac 787
 Pro Glu Ile Gln Ser Val Lys Val Gln Ala Arg Phe Asp Gln Ser His
 215 220 225

aac aag tat ttc ctc gtc gat ttc ttg atc aat gag tgg atc atc gtg 835
 Asn Lys Tyr Phe Leu Val Asp Phe Leu Ile Asn Glu Trp Ile Ile Val
 230 235 240 245

gag att gat gga cgt tcg aaa tat gat tcc ccg gag ctc aat gag gtg 883
 Glu Ile Asp Gly Arg Ser Lys Tyr Asp Ser Pro Glu Leu Asn Glu Val
 250 255 260

ctc atg gct gaa cgc gat cgg gag aaa ttc ttc ctc aat cag ggc tat 931
 Leu Met Ala Glu Arg Asp Arg Glu Lys Phe Phe Leu Asn Gln Gly Tyr
 265 270 275

gcg gtc tta aga atc gat ccg aaa cag tta gac ctc aac caa gat ggg 979
 Ala Val Leu Arg Ile Asp Pro Lys Gln Leu Asp Leu Asn Gln Asp Gly
 280 285 290

gag tgt gag ttc atc gga atc ctc aaa aac act ttg cag aag acc cca 1027
 Glu Cys Glu Phe Ile Gly Ile Leu Lys Asn Thr Leu Gln Lys Thr Pro
 295 300 305

cct gag cac ctc aag caa gcc gcc taaacactcc aagaaccacc att 1074
 Pro Glu His Leu Lys Gln Ala Ala
 310 315

<210> 2286
 <211> 317
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 2286
 Met Lys Asn Trp Gln Glu Glu Phe Gln Leu Val Asn Leu Thr Lys Leu
 1 5 10 15

Leu His Ser Asp Thr Glu Thr Ser Ala Ala Ile Ser Asn Gly Gln Met
 20 25 30

Ile Lys Leu Thr His Glu Val Ala Ile Asn Ala Glu Lys Tyr Arg Ser
 35 40 45

Leu Pro Ala Trp Asp Lys Ala Ala Ala Arg Ala Phe Ala Val Gly Met
 50 55 60

Thr Val Asp Lys Ala Val Val Ala Gly Gln Ser Ala Ala Arg Leu Trp
 65 70 75 80

Gly Tyr Gln Thr Leu Thr Val Glu Lys Thr Val Leu Cys Leu Leu Pro
 85 90 95

Glu Arg Leu Arg Ser Lys Ser Ser Lys His Trp Pro Ser Gly Met Arg


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100              105              110
Tyr Lys Asp Arg Tyr Leu Ser Ser Arg Asp Ile Arg Glu Val His Gly
115              120
Ile Arg Val Thr Gly Ala Phe Arg Thr Phe Leu Asp Ile Ala Leu Asp
130              135              140
Asp Gly Val Val Ala Ala Val Val Thr Ile Asp Ser Ala Arg Arg Gln
145              150              155              160
Asn Pro Ser Leu Thr Arg Glu Lys Leu Met His Ser Ala Glu Ser Phe
165              170              175
Pro Arg His Arg Gly Val Lys Ala Tyr Arg Gln Ala Ile Glu Leu Ser
180              185              190
Ile Pro Asn Ser Asp Ser Ala Gln Glu Thr Arg Ala Arg Leu Ile Leu
195              200              205
Arg Glu Ala Lys Leu Pro Glu Ile Gln Ser Val Lys Val Gln Ala Arg
210              215              220
Phe Asp Gln Ser His Asn Lys Tyr Phe Leu Val Asp Phe Leu Ile Asn
225              230              235              240
Glu Trp Ile Ile Val Glu Ile Asp Gly Arg Ser Lys Tyr Asp Ser Pro
245              250              255
Glu Leu Asn Glu Val Leu Met Ala Glu Arg Asp Arg Glu Lys Phe Phe
260              265              270
Leu Asn Gln Gly Tyr Ala Val Leu Arg Ile Asp Pro Lys Gln Leu Asp
275              280              285
Leu Asn Gln Asp Gly Glu Cys Glu Phe Ile Gly Ile Leu Lys Asn Thr
290              295              300
Leu Gln Lys Thr Pro Pro Glu His Leu Lys Gln Ala Ala
305              310              315

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<210> 2287

<211> 1845

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1822)

<223> RXA01525

<400> 2287

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tagggaggcg tcgacaagca tctttaagta gctttgaagc atg cgt tcc ttt caa 115
Met Arg Ser Phe Gln
1
5

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tcg atc ctt gac ctg gta aat tca gca tcc gag gtg gct acc aaa att 163
Ser Ile Leu Asp Leu Val Asn Ser Ala Ser Glu Val Ala Thr Lys Ile

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	10	15	20	
	gtg ttg aag cgc ttc gaa aaa cgg ata acc agc gaa act gac tgg gta	211		
	Val Leu Lys Arg Phe Glu Lys Arg Ile Thr Ser Glu Thr Asp Trp Val			
	25 30 35			
	cgc tat cag cgg ttt agt ctt tgg tcg gtt ggt tct cgc cta acg atc	259		
	Pro Tyr Gln Arg Phe Ser Leu Trp Ser Val Gly Ser Pro Leu Thr Ile			
	40 45 50			
	gaa cgc aaa ggc ccc gat gtg cgt gtg agc aag gac aac act gcc gtt	307		
	Glu Arg Lys Gly Pro Asp Val Arg Val Ser Lys Asp Asn Thr Ala Val			
	55 60 65			
	ctt cag cgc tat caa aga cgc gaa gca gaa gga ctg atc agc tac ttc	355		
	Leu Gln Arg Tyr Gln Arg Pro Glu Ala Glu Gly Leu Ile Ser Tyr Phe			
	70 75 80 85			
	atg gat cca aag cca tgg ata act gaa ttg gca ggc ctg aat ctg gac	403		
	Met Asp Pro Lys Pro Trp Ile Thr Glu Leu Ala Gly Leu Asn Leu Asp			
	90 95 100			
	gat gtt tcc gaa gat aca gtt gca ggt cgc aca gta tta gtg gtt ccc	451		
	Asp Val Ser Glu Asp Thr Val Ala Gly Arg Thr Val Leu Val Val Pro			
	105 110 115			
	cta tcc aat gtc att ctc agc atc gat gcg gaa ttt ggg atg att cta	499		
	Leu Ser Asn Val Ile Leu Ser Ile Asp Ala Glu Phe Gly Met Ile Leu			
	120 125 130			
	act gcg gaa aac gac ata gaa aag atc cac gca ata tct gtc gaa ctc	547		
	Thr Ala Glu Asn Asp Ile Glu Lys Ile His Ala Ile Ser Val Glu Leu			
	135 140 145			
	tta gaa aaa tgg aga tca tcc cat tac cct gag cgc cat ttt cct gca	595		
	Leu Glu Lys Trp Arg Ser Ser His Tyr Pro Glu Pro His Phe Pro Ala			
	150 155 160 165			
	gcg gtt ctc cca cct gcg tcg act gga aac cgc aac ctc cga gtt cta	643		
	Ala Val Leu Pro Pro Ala Ser Thr Gly Asn Arg Asp Leu Arg Val Leu			
	170 175 180			
	tgc cct gag ttt tcc att cca agt gtc aac gtt ggt gat cag gtt tta	691		
	Cys Pro Glu Phe Ser Ile Pro Ser Val Asn Val Gly Asp Gln Val Leu			
	185 190 195			
	cta ttt tta aca ttt gat caa acc ctg cca cca gta gat cag ctt gaa	739		
	Leu Phe Leu Thr Phe Asp Gln Thr Leu Pro Pro Val Asp Gln Leu Glu			
	200 205 210			
	act act cgc cgc gga tac act gat cca atc cag ctt gac tac gac cac	787		
	Thr Thr Arg Arg Gly Tyr Thr Asp Pro Ile Gln Leu Asp Tyr Asp His			
	215 220 225			
	cgc caa tac agg ttt cac gcc gac ggt tgg gat gcc atc atc tcc acg	835		
	Arg Gln Tyr Arg Phe His Ala Asp Gly Trp Asp Ala Ile Ile Ser Thr			
	230 235 240 245			
	gtg gag cca cta cac gac gaa gaa gaa ctc aca ggt tac ttc ctg cac	883		
	Val Glu Pro Leu His Asp Glu Glu Glu Leu Thr Gly Tyr Phe Leu His			
	250 255 260			

cgc ctt gac cca gat agc gcg tac cca acc att gca gtc gtt aca gca 931
 Arg Leu Asp Pro Asp Ser Ala Tyr Pro Thr Ile Ala Val Thr Thr Ala
 265 270 275

gcg cac tac cac ggt acg gac gca att atc gac gtg acc cta gat ggt 979
 Ala His Tyr His Gly Thr Asp Ala Ile Ile Asp Val Thr Leu Asp Gly
 280 285 290

gtg cat cca ccc aaa aac caa gaa act ctt gaa ggc atc agc act agt 1027
 Val His Pro Pro Lys Asn Gln Glu Thr Leu Glu Gly Ile Ser Thr Ser
 295 300 305

acc agt gac ggt gac ata ttt tgg ctc tcc gat gaa agc ttg cct ttc 1075
 Thr Ser Asp Gly Asp Ile Phe Thr Trp Leu Ser Asp Glu Ser Leu Pro Phe
 310 315 320 325

gtc cgt gga ttc agc gtg tca aca ggc gaa cta tta cac gag atc tcc 1123
 Val Arg Gly Phe 330 Ser Val Ser Thr Gly Glu Leu Leu His Glu Ile Ser
 335 340

atc ccc acg ttc caa gag atc gtc ctc gat tcc gct aat aga gcc cgc 1171
 Ile Pro Thr Phe Gln Glu Ile Val Leu Asp Ser Ala Asn Arg Ala Arg
 345 350 355

gta aaa caa aag caa tgg cct cac gat ttc agt gat tgc aag gga aaa 1219
 Val Lys Gln Lys Gln Trp Pro His Asp Phe Ser Asp Cys Lys Gly Lys
 360 365 370

aca tgg gag ctt ccg gat ctt aaa gaa gta ttc gaa gct gtc cct tcg 1267
 Thr Trp Glu Leu Pro Asp Leu Lys Glu Val Phe Glu Ala Val Pro Ser
 375 380 385

att cca gca ggt tgg aga ttg tta gac agc ttc ggg aaa aac ttg cac 1315
 Ile Pro Ala Gly Trp Arg Leu Leu Asp Ser Phe Gly Lys Asn Leu His
 390 395 400 405

aat gtc aca cgc gaa aac cct cgt ctt aat gac aac ttt tgg ctt caa 1363
 Asn Val Thr Arg Glu Asn Pro Arg Leu Asn Asp Asn Phe Trp Leu Gln
 410 415 420

aca atc ctt agg ctt aaa cca ttt aaa gca gta gat ctt gat atc ggc 1411
 Thr Ile Leu Arg Leu Lys Pro Phe Lys Ala Val Asp Leu Asp Ile Gly
 425 430 435

cga tcg ata atc aca gca att tac cca tac ggt gat cga att tac tta 1459
 Arg Ser Ile Thr Ala Ile Tyr Pro Tyr Gly Asp Arg Ile Tyr Leu
 440 445 450

cgc gct agt aac cac cac atc acg ttt aac cag gac ctc gag att ctc 1507
 Arg Ala Ser Asn His His Ile Thr Phe Asn Gln Asp Leu Glu Ile Leu
 455 460 465

aac gta gaa gtc ttt ggc gac cct gag gtt ccc gaa tct ggt cta att 1555
 Asn Val Glu Val Phe Gly Asp Pro Glu Val Pro Glu Ser Gly Leu Ile
 470 475 480 485

tat ctt cca cct ggg gat tct cca aca ctc ggt ttt ccc acc gga aca 1603
 Tyr Leu Pro Pro Gly Asp Ser Pro Thr Leu Gly Phe Pro Thr Gly Thr
 490 495 500

ctc atg atg ttt cat gag caa gaa ggc aca tat gct ttc cac gac cct 1651
 Leu Met Met Phe His Glu Gln Glu Gly Thr Tyr Ala Phe His Asp Pro
 505 510 515

gaa aca aca gaa caa ata aca act gtg aac tta gac agg aat agt ttt 1699
 Glu Thr Thr Glu Gln Ile Thr Thr Val Asn Leu Asp Arg Asn Ser Phe
 520 525 530

tca gtg gca tat tct tcc cga acc aaa att gtt att tca ctg aaa aac 1747
 Ser Val Ala Tyr Ser Ser Arg Thr Lys Ile Val Ile Ser Leu Lys Asn
 535 540 545

cca gaa agc cga cct acc aac aag ctg ttg gtg tgg gaa cca caa acc 1795
 Pro Glu Ser Arg Pro Thr Asn Lys Leu Leu Val Trp Glu Pro Gln Thr
 550 555 560 565

ggg tgg cga gaa cag aac ctg gag cgc tgagcacgct taaggtgagg 1842
 Gly Trp Arg Glu Gln Asn Leu Glu Arg
 570

tgg 1845

<210> 2288
 <211> 574
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 2288
 Met Arg Ser Phe Gln Ser Ile Leu Asp Leu Val Asn Ser Ala Ser Glu
 1 5 10 15

Val Ala Thr Lys Ile Val Leu Lys Arg Phe Glu Lys Arg Ile Thr Ser
 20 25 30

Glu Thr Asp Trp Val Pro Tyr Gln Arg Phe Ser Leu Trp Ser Val Gly
 35 40 45

Ser Pro Leu Thr Ile Glu Arg Lys Gly Pro Asp Val Arg Val Ser Lys
 50 55 60

Asp Asn Thr Ala Val Leu Gln Arg Tyr Gln Arg Pro Glu Ala Glu Gly
 65 70 75 80

Leu Ile Ser Tyr Phe Met Asp Pro Lys Pro Trp Ile Thr Glu Leu Ala
 85 90 95

Gly Leu Asn Leu Asp Asp Val Ser Glu Asp Thr Val Ala Gly Arg Thr
 100 105 110

Val Leu Val Val Pro Leu Ser Asn Val Ile Leu Ser Ile Asp Ala Glu
 115 120 125

Phe Gly Met Ile Leu Thr Ala Glu Asn Asp Ile Glu Lys Ile His Ala
 130 135 140

Ile Ser Val Glu Leu Leu Glu Lys Trp Arg Ser Ser His Tyr Pro Glu
 145 150 155 160

Pro His Phe Pro Ala Ala Val Leu Pro Pro Ala Ser Thr Gly Asn Arg
 165 170 175

Asn Leu Arg Val Leu Cys Pro Glu Phe Ser Ile Pro Ser Val Asn Val
 180 185 190
 Gly Asp Gln Val Leu Leu Phe Leu Thr Phe Asp Gln Thr Leu Pro Pro
 195 200 205
 Val Asp Gln Leu Glu Thr Thr Arg Arg Gly Tyr Thr Asp Pro Ile Gln
 210 215 220
 Leu Asp Tyr Asp His Arg Gln Tyr Arg Phe His Ala Asp Gly Trp Asp
 225 230 235 240
 Ala Ile Ile Ser Thr Val Glu Pro Leu His Asp Glu Glu Glu Leu Thr
 245 250 255
 Gly Tyr Phe Leu His Arg Leu Asp Pro Asp Ser Ala Tyr Pro Thr Ile
 260 265 270
 Ala Val Val Thr Ala Ala His Tyr His Gly Thr Asp Ala Ile Ile Asp
 275 280 285
 Val Thr Leu Asp Gly Val His Pro Pro Lys Asn Gln Glu Thr Leu Glu
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 Gly Ile Ser Thr Ser Thr Ser Asp Gly Asp Ile Phe Trp Leu Ser Asp
 305 310 315 320
 Glu Ser Leu Pro Phe Val Arg Gly Phe Ser Val Ser Thr Gly Glu Leu
 325 330 335
 Leu His Glu Ile Ser Ile Pro Thr Phe Gln Glu Ile Val Leu Asp Ser
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 Ala Asn Arg Ala Arg Val Lys Gln Lys Gln Trp Pro His Asp Phe Ser
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 Asp Cys Lys Gly Lys Thr Trp Glu Leu Pro Asp Leu Lys Glu Val Phe
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 Glu Ala Val Pro Ser Ile Pro Ala Gly Trp Arg Leu Leu Asp Ser Phe
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 Gly Lys Asn Leu His Asn Val Thr Arg Glu Asn Pro Arg Leu Asn Asp
 405 410 415
 Asn Phe Trp Leu Gln Thr Ile Leu Arg Leu Lys Pro Phe Lys Ala Val
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 Asp Leu Asp Ile Gly Arg Ser Ile Ile Thr Ala Ile Tyr Pro Tyr Gly
 435 440 445
 Asp Arg Ile Tyr Leu Arg Ala Ser Asn His His Ile Thr Phe Asn Gln
 450 455 460
 Asp Leu Glu Ile Leu Asn Val Glu Val Phe Gly Asp Pro Glu Val Pro
 465 470 475 480
 Glu Ser Gly Leu Ile Tyr Leu Pro Pro Gly Asp Ser Pro Thr Leu Gly
 485 490 495

Phe Pro Thr Gly Thr Leu Met Met Phe His Glu Gln Glu Gly Thr Tyr
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 Ala Phe His Asp Pro Glu Thr Thr Glu Gln Ile Thr Thr Val Asn Leu
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 Asp Arg Asn Ser Phe Ser Val Ala Tyr Ser Ser Arg Thr Lys Ile Val
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 Ile Ser Leu Lys Asn Pro Glu Ser Arg Pro Thr Asn Lys Leu Leu Val
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<211> 2634

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(2611)

<223> RXA01527

<400> 2289

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 Val Ile Pro Asn Pro 5
 aac ccg aac ccc aaa gcc aaa act ctt cgc ctc gtt tca gcg ctg acc 163
 Asn Pro Asn Pro Lys Ala Lys Thr Leu Arg Leu Val Ser Ala Leu Thr 20
 10 15
 gcc atc act gtg gtg ggt ttt agc gct tca cct gtt cat gcg ttg ccg 211
 Ala Ile Thr Val Val Gly Phe Ser Ala Ser Pro Val His Ala Leu Pro 35
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 att ccg ttg gat cct tct gat ccg gcg gtg tcg gag ttg tgg gtg aat 259
 Ile Pro Leu Asp Pro Ser Asp Pro Ala Val Ser Glu Leu Trp Val Asn 50
 40 45
 ccg aat gcg cggtgat gat gag ctt tct ggt gtg gat gta gag atc 307
 Pro Asn Ala Arg Ala Asp Asp Glu Leu Ser Gly Val Asp Val Glu Ile 60
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 Ser Asp Phe Val Met Pro Asn Ser Asn Leu Thr Val Gln Val Gly Thr 85
 70 75 80
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 Ser Phe Lys Ala Gln Val Arg Val Thr Asn Arg Ser Ser Glu Thr Leu 100
 90 95
 agc aat att acg ttg cag gcg cgt cgt gcg gag gcg tcg ttt gat atg 451
 Ser Asn Ile Thr Leu Gln Ala Arg Arg Ala Glu Ala Ser Phe Asp Met 110
 105 110

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gcg atg gtg act ctt gat gat gag ttg gag cgg ggg gag agt gtt gag Ala Met Val Thr Leu Asp Asp Glu Leu Glu Pro Gly Glu Ser Val Glu	547
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act gag gtg gag att tct acc gat agt ttg tgg att tct cag cgg ggt Thr Glu Val Glu Ile Ser Thr Asp Ser Leu Ser Ile Ser Gln Pro Gly	595
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cag cat ttg gat tgg cag cgt ttc ctt ctg cca gtc etc agc gat aca Gln His Leu Asp Ser Gln Arg Phe Leu Leu Pro Val Leu Ser Asp Thr	691
185 190 195	
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215 220 225	
gag cgg cct ttg ctg gtc agt tcc gac gcg ctt gcg ggc gag ttg gat Glu Pro Pro Leu Leu Val Ser Ser Asp Ala Leu Ala Gly Glu Leu Asp	835
230 235 240 245	
gag ggc ggt cgt ttg caa aag ctt atc gac gcc tac ctc cag tct tca Glu Gly Gly Arg Leu Gln Lys Leu Ile Asp Ala Tyr Leu Gln Ser Ser	883
250 255 260	
ccc gcc gtg cag caa gcc acg tgc ctt gct att gat cgg cag ctt ctt Pro Ala Val Gln Gln Ala Thr Cys Leu Ala Ile Asp Pro Gln Leu Leu	931
265 270 275	
gat gtg gtg gat cgc atg acc ggc ggt tac acc gtg acc gat act cgt Asp Val Val Asp Arg Met Thr Gly Gly Tyr Thr Val Thr Asp Thr Arg	979
280 285 290	
ccc agt acg gtg cgg cag aat cag cgg ctt cgt gag ttg tgg act gcc Pro Ser Thr Val Arg Gln Asn Gln Arg Leu Arg Gly Leu Trp Thr Ala	1027
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330 335 340	
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345 350 355	
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Phe	Glu	Glu	Val	Leu	Gly	Val	Ile	Pro	Glu	Ser	Asn	Val	Val	Ile	Pro	
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gga	aat	ggt	ttt	gtg	gag	ccc	tcc	acc	gtg	ggt	gat	ctc	gga	tggt	gcg	1315
Gly	Asn	Gly	Phe	Val	Glu	Pro	Ser	Thr	Val	Gly	Asp	Leu	Gly	Trp	Ala	
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gaa	gta	acg	ctt	aat	cgc	gat	cag	gcg	tggt	gag	gtg	cag	tca	gag	gag	1363
Glu	Val	Thr	Leu	Asn	Pro	Asp	Gln	Ala	Trp	Glu	Val	Gln	Ser	Glu	Glu	
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ttg	gtt	gct	gcc	cct	gat	gcc	aca	gag	caa	agc	gca	ttg	gat	aac	cct	1411
Leu	Val	Ala	Ala	Pro	Asp	Ala	Thr	Glu	Gln	Ser	Ala	Leu	Asp	Asn	Pro	
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aag	cca	acg	cca	ggc	acg	gtg	acg	cgc	cca	acc	cct	atg	tca	acg	gtg	1459
Lys	Pro	Thr	Pro	Gly	Thr	Val	Thr	Pro	Pro	Thr	Pro	Met	Ser	Thr	Val	
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Ser	Val	Leu	Val	Ser	Asp	Asn	Thr	Val	Trp	Arg	Thr	Thr	Ser	Ala	Asp	
	455					460					465					
cgc	ttc	cac	tct	ttg	gct	cgc	gga	ata	act	ggg	gtg	tgc	tat	cag	gga	1555
Arg	Phe	His	Ser	Leu	Ala	Pro	Gly	Ile	Thr	Gly	Val	Ser	Tyr	Gln	Gly	
	470				475					480				485		
tgc	tta	tgc	gca	acc	ttg	gct	acc	ttg	gga	caa	aac	cct	gag	act	gtg	1603
Ser	Leu	Ser	Ala	Thr	Leu	Ala	Thr	Leu	Gly	Gln	Asn	Pro	Glu	Thr	Val	
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ggc	tat	tcc	aat	cgc	gat	tgc	cgt	tat	gac	tac	gcc	atg	gat	tct	gag	1651
Gly	Tyr	Ser	Asn	Pro	Asp	Ser	Arg	Tyr	Asp	Tyr	Ala	Met	Asp	Ser	Glu	
			505					510					515			
agc	gcc	cgc	aat	ctc	acc	ggc	cag	gcg	gcg	ctg	cgc	ttg	acg	gtg	gac	1699
Ser	Ala	Arg	Asn	Leu	Thr	Gly	Gln	Ala	Ala	Leu	Arg	Leu	Thr	Val	Asp	
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aac	ggc	gat	gaa	gac	tct	ccc	gtg	ttg	atc	atg	cgc	agc	gcg	gtg	ctg	1747
Asn	Gly	Asp	Glu	Asp	Ser	Pro	Val	Leu	Ile	Met	Pro	Ser	Ala	Val	Leu	
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ggc	gcc	gaa	gac	ggc	gcg	atg	ttg	ctt	gag	acc	acc	ggg	gct	ttg	ctt	1795
Gly	Ala	Glu	Asp	Gly	Ala	Met	Leu	Leu	Glu	Thr	Thr	Gly	Ala	Leu	Leu	
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gcc	gac	ggc	tcc	gcc	cga	cct	ttt	tcc	ctg	cag	caa	tat	gtc	act	gcc	1843
Ala	Asp	Gly	Ser	Ala	Arg	Pro	Phe	Ser	Leu	Gln	Gln	Tyr	Val	Thr	Ala	
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aat	gcg	gaa	caa	aga	aat	act	ttg	gcc	aca	gca	aca	act	cca	ccg	gat	1891
Asn	Ala	Glu	Gln	Arg	Asn	Thr	Leu	Ala	Thr	Ala	Thr	Thr	Pro	Pro	Asp	
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gac	act	gct	ttt	ggt	gca	ccc	tac	gac	gat	cct	gcg	tca	ttg	acg	gaa	1939
Asp	Thr	Ala	Phe	Gly	Ala	Pro	Tyr	Asp	Asp	Pro	Ala	Ser	Leu	Thr	Glu	

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Thr Gly Ile Met Ser Asn Asp Pro Ser Ile Ala Leu Thr Arg Tyr Gly			
630	635	640	645
ttt aca gca ccg ctg cgg caa gat ctg ctg cgc gcg ttg agt atc agt	2083		
Phe Thr Ala Pro Leu Arg Gln Asp Leu Leu Arg Ala Leu Ser Ile Ser			
650	655	660	
gag cgt cgt tgc tta gct cgc cac acc cag gca acc tct gct gcc gat	2131		
Glu Arg Arg Ser Leu Ala Arg His Thr Gln Ala Thr Ser Ala Ala Asp			
665	670	675	
aaa tta ctt aat cgc aac cgc gat act ctg cag aag ctg cgt agc tct	2179		
Lys Leu Leu Asn Arg Asn Arg Asp Thr Leu Gln Lys Leu Arg Ser Ser			
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gtg gcg ttg ttg ccg ccg gga aat gtg tat acc cga acc tgc gaa tgc	2227		
Val Ala Leu Leu Pro Pro Gly Asn Val Tyr Thr Arg Thr Ser Glu Ser			
695	700	705	
tct ccg ttg ttg att gtg gcg caa aac ggt ttg cca ttg ccc gcg gag	2275		
Ser Pro Leu Leu Ile Val Ala Gln Asn Gly Leu Pro Leu Pro Ala Glu			
710	715	720	725
act cag att ttg tat tcc gga aat cag gat gcg cac atc aat act ccg	2323		
Thr Gln Ile Leu Tyr Ser Gly Asn Gln Asp Ala His Ile Asn Thr Pro			
730	735	740	
ggc gtg gtt cgt att ccg gcg cag ggt tcc atc acc ttg cag atg act	2371		
Gly Val Val Arg Ile Pro Ala Gln Gly Ser Ile Thr Leu Gln Met Thr			
745	750	755	
gcg gat ttg ccc gat gac aat ctg cgc act gat ctc acg ttg tgg ttg	2419		
Ala Asp Leu Pro Asp Asp Asn Leu Arg Thr Asp Leu Thr Leu Trp Leu			
760	765	770	
gca tcc cca gat ggg gcc acc att agt gaa cct gtg gaa att act gtc	2467		
Ala Ser Pro Asp Gly Ala Thr Ile Ser Glu Pro Val Glu Ile Thr Val			
775	780	785	
cag cct cgc ccg aat ttg ggc acc acg ctg ttt ttc gtg gca gcg ggc	2515		
Gln Pro Arg Pro Asn Leu Gly Thr Thr Leu Phe Val Ala Ala Gly			
790	795	800	805
att ctg gca gta gga ggg ttg ttg ttt ata cgg aag aaa cga aac gtc	2563		
Ile Leu Ala Val Gly Gly Leu Leu Phe Ile Arg Lys Lys Arg Asn Val			
810	815	820	
gaa aag cgc tgc ccc ggt acg gga tgc ccc aaa ccg cca cca acc cac	2611		
Glu Lys Arg Ser Pro Gly Thr Gly Ser Pro Lys Pro Pro Pro Thr His			
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taacgtatcg catagttatt ttc	2634		

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<211> 837

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2290

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Val	His	Ala	Leu	Pro	Ile	Pro	Leu	Asp	Pro	Ser	Asp	Pro	Ala	Val	Ser
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Glu	Leu	Trp	Val	Asn	Pro	Asn	Ala	Arg	Ala	Asp	Asp	Glu	Leu	Ser	Gly
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Val	Asp	Val	Glu	Ile	Ser	Asp	Phe	Val	Met	Pro	Asn	Ser	Asn	Leu	Thr
	65				70					75				80	

Val	Gln	Val	Gly	Glu	Ser	Phe	Lys	Ala	Gln	Val	Arg	Val	Thr	Asn	Arg
				85					90					95	

Ser	Ser	Glu	Thr	Leu	Ser	Asn	Ile	Thr	Leu	Gln	Ala	Arg	Arg	Ala	Glu
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Ala	Ser	Phe	Asp	Met	Ala	Ser	Ala	Arg	Val	Ala	Ala	Thr	Asp	Asn	Asn
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Tyr	Gly	Tyr	Phe	Gly	Ala	Met	Val	Thr	Leu	Asp	Asp	Glu	Leu	Glu	Pro
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Gly	Glu	Ser	Val	Glu	Thr	Glu	Val	Glu	Ile	Ser	Thr	Asp	Ser	Leu	Ser
	145				150					155				160	

Ile	Ser	Gln	Pro	Gly	Ser	Tyr	Pro	Thr	Met	Leu	Ala	Leu	Ser	Gly	Gln
			165						170					175	

Leu	Asp	Gly	Val	Ala	Gln	His	Leu	Asp	Ser	Gln	Arg	Phe	Leu	Leu	Pro
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Val	Leu	Ser	Asp	Thr	Thr	Asp	Thr	Glu	Asp	Thr	Ala	Thr	Pro	Thr	Thr
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Met	Ile	Tyr	Pro	Ile	Ser	Ala	Gln	Thr	Asn	Val	Leu	Gly	Gly	Glu	Thr
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Gly	Glu	Ala	Pro	Glu	Glu	Pro	Pro	Leu	Leu	Val	Ser	Ser	Asp	Ala	Leu
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Ala	Gly	Glu	Leu	Asp	Glu	Gly	Gly	Arg	Leu	Gln	Lys	Leu	Ile	Asp	Ala
			245					250					255		

Tyr	Leu	Gln	Ser	Ser	Pro	Ala	Val	Gln	Gln	Ala	Thr	Cys	Leu	Ala	Ile
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Asp	Pro	Gln	Leu	Leu	Asp	Val	Val	Asp	Arg	Met	Thr	Gly	Gly	Tyr	Thr
		275					280					285			

Val	Thr	Asp	Thr	Arg	Pro	Ser	Thr	Val	Arg	Gln	Asn	Gln	Arg	Leu	Arg
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290	295	300
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Gly Ala Glu Asn Ala	Ile Phe Leu Glu Lys	Leu Arg Gln Ala Thr
	325	330
Ala Thr Ser Cys Thr	Val Ala Leu Pro Trp	Ala Asn Ala Asp Leu Asn
	340	345
Ala Val Ser Gln Thr	Gly Asn Gln Trp Leu	Met Arg Glu Ala Leu Gln
	355	360
Arg Gly Val Thr Thr	Phe Glu Glu Val Leu	Gly Val Ile Pro Glu Ser
	370	375
Asn Val Val Ile Pro	Gly Asn Gly Phe Val	Glu Pro Ser Thr Val Gly
	385	390
Asp Leu Gly Trp Ala	Glu Val Thr Leu Asn	Pro Asp Gln Ala Trp Glu
	405	410
Val Gln Ser Glu Glu	Leu Val Ala Ala Pro	Asp Ala Thr Glu Gln Ser
	420	425
Ala Leu Asp Asn Pro	Lys Pro Thr Pro Gly	Thr Val Thr Pro Pro Thr
	435	440
Pro Met Ser Thr Val	Ser Val Leu Val Ser	Asp Asn Thr Val Trp Arg
	450	455
Thr Thr Ser Ala Asp	Arg Phe His Ser Leu	Ala Pro Gly Ile Thr Gly
	465	470
Val Ser Tyr Gln Gly	Ser Leu Ser Ala Thr	Leu Ala Thr Leu Gly Gln
	485	490
Asn Pro Glu Thr Val	Gly Tyr Ser Asn Pro	Asp Ser Arg Tyr Asp Tyr
	500	505
Ala Met Asp Ser Glu	Ser Ala Arg Asn Leu	Thr Gly Gln Ala Ala Leu
	515	520
Arg Leu Thr Val Asp	Asn Gly Asp Glu Asp	Ser Pro Val Leu Ile Met
	530	535
Pro Ser Ala Val Leu	Gly Ala Glu Asp Gly	Ala Met Leu Leu Glu Thr
	545	550
Thr Gly Ala Leu Leu	Ala Asp Gly Ser Ala	Arg Pro Phe Ser Leu Gln
	565	570
Gln Tyr Val Thr Ala	Asn Ala Glu Gln Arg	Asn Thr Leu Ala Thr Ala
	580	585
Thr Thr Pro Pro Asp	Asp Thr Ala Phe Gly	Ala Pro Tyr Asp Asp Pro
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Ala Ser Leu Thr Glu	Thr Glu Ile Leu Arg	Thr Thr Gln Gln Ala Glu
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		620

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Tyr Ile Asp Asp Leu Thr Gly Ile Met Ser Asn Asp Pro Ser Ile Ala
625                               630                               635                               640

Leu Thr Arg Tyr Gly Phe Thr Ala Pro Leu Arg Gln Asp Leu Leu Arg
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Ala Leu Ser Ile Ser Glu Arg Arg Ser Leu Ala Arg His Thr Gln Ala
660                               665                               670

Thr Ser Ala Ala Asp Lys Leu Leu Asn Arg Asn Arg Asp Thr Leu Gln
675                               680                               685

Lys Leu Arg Ser Ser Val Ala Leu Leu Pro Pro Gly Asn Val Tyr Thr
690                               695                               700

Arg Thr Ser Glu Ser Ser Pro Leu Leu Ile Val Ala Gln Asn Gly Leu
705                               710                               715                               720

Pro Leu Pro Ala Glu Thr Gln Ile Leu Tyr Ser Gly Asn Gln Asp Ala
725                               730                               735

His Ile Asn Thr Pro Gly Val Val Arg Ile Pro Ala Gln Gly Ser Ile
740                               745                               750

Thr Leu Gln Met Thr Ala Asp Leu Pro Asp Asp Asn Leu Arg Thr Asp
755                               760                               765

Leu Thr Leu Trp Leu Ala Ser Pro Asp Gly Ala Thr Ile Ser Glu Pro
770                               775                               780

Val Glu Ile Thr Val Gln Pro Arg Pro Asn Leu Gly Thr Thr Leu Phe
785                               790                               795                               800

Phe Val Ala Ala Gly Ile Leu Ala Val Gly Gly Leu Leu Phe Ile Arg
805                               810                               815

Lys Lys Arg Asn Val Glu Lys Arg Ser Pro Gly Thr Gly Ser Pro Lys
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Pro Pro Pro Thr His
835

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<210> 2291

<211> 1365

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1342)

<223> RXA01536

<400> 2291

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Met Ala Phe Gly Phe

1

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Phe Ser Arg Arg Lys Lys Lys Asn Lys Asp Lys Asn Pro Asn Glu Asn	
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tca gca gtg ccc gca cac tct gaa gat tca cct cag gag gtt ttt gag	211
Ser Ala Val Pro Ala His Ser Glu Asp Ser Pro Gln Glu Val Phe Glu	
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ggt aat ggt cgt cag gta ggc gac ccc att gaa cag cag gtt gat cga	259
Gly Asn Gly Arg Gln Val Gly Asp Pro Ile Glu Gln Gln Val Asp Arg	
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gat gct aaa ggt cgt ctc aca gcg gcg gat ttc ttg ccg gac gct gat	307
Asp Ala Lys Gly Arg Leu Thr Ala Ala Asp Phe Leu Pro Asp Ala Asp	
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Leu Pro Gln Leu Asn Arg Ser Arg Ala Asn Met Leu Arg Arg Glu Leu	
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gag tac cgt ttt tca ctc cag aat gcc cac att aat atc gat gga aac	403
Glu Tyr Arg Phe Ser Leu Gln Asn Ala His Ile Asn Ile Asp Gly Asn	
90 95 100	
acg gcc atg att cag cgt tca gat gcc ggg gca gca cat gtc tcg ttg	451
Thr Ala Met Ile Gln Arg Ser Asp Gly Gly Ala Ala His Val Ser Leu	
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cgc acc ctc gcg atg aat gca gct gcc ctt gat aac ttt gat caa ctc	499
Arg Thr Leu Ala Met Asn Ala Ala Gly Leu Asp Asn Phe Asp Gln Leu	
120 125 130	
cct gaa ctg gtg gaa agc ttc gtt cac gcc acg ctg gcc gat gca aca	547
Pro Glu Leu Val Glu Ser Phe Val His Gly Thr Leu Ala Asp Ala Thr	
135 140 145	
tta aac gat ctt tct act gct gac ctg tat aaa gca ctg cgc ctt cgc	595
Leu Asn Asp Leu Ser Thr Ala Asp Leu Tyr Lys Ala Leu Arg Leu Arg	
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ctg ctg cca aca cct gcc gaa gcc gac gat cta gtt gag cat gga ctc	643
Leu Leu Pro Thr Pro Gly Glu Gly Asp Asp Leu Val Glu His Gly Leu	
170 175 180	
gac cgg gaa agc cag atc cgc gac gat tca atc ctg cgc acc ttc acc	691
Asp Arg Glu Ser Gln Ile Arg Asp Asp Ser Ile Leu Arg Thr Phe Thr	
185 190 195	
tct gac atg tcg atc gcg ctg gtg ctc gat acc gag cat gcc atc cgc	739
Ser Asp Met Ser Ile Ala Leu Val Leu Asp Thr Glu His Ala Ile Arg	
200 205 210	
atc cag cca ctc aaa gag ctc gag gag ttc gat gac ctc agc gcc cta	787
Ile Gln Pro Leu Lys Glu Leu Glu Glu Phe Asp Asp Leu Ser Ala Leu	
215 220 225	
gag cgg gct gcg gac cgc aat acc tgg caa gag ctt tac gac gca aac	835
Glu Arg Ala Ala Asp Arg Asn Thr Trp Gln Glu Leu Tyr Asp Ala Asn	
230 235 240 245	
ggt gac gct tcc ttc gtc gac gct gaa tca gac agc gaa ggg tca tca	883

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Val Asp Ala Ser Phe Val Asp Ala Glu Ser Asp Ser Glu Gly Ser Ser
250 255 260

ttt tgg gct ttc gaa tct aac tcg tac tac ttg ggt agt gca cca ctg 931
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265 270 275

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Phe Leu Asn Asp Leu Leu Ala Lys Trp Ala Pro Asp Leu Asp Gln Ser
280 285 290

gat ggc gtc atc ttt gct gtc cct gat cgt gat ctg ttg att gcg cgt 1027
Asp Gly Val Ile Phe Ala Val Pro Asp Arg Asp Leu Leu Ile Ala Arg
295 300 305

cct gtg acc acc ggc gaa gat ctg atg aac gga atc acc gcg atg gtg 1075
Pro Val Thr Thr Gly Glu Asp Leu Met Asn Gly Ile Thr Ala Met Val
310 315 320

agg atc gcg atg cgc ttt ggc ctc ggg aac ccg acg tcg ata agc ccg 1123
Arg Ile Ala Met Arg Phe Gly Leu Gly Asn Pro Thr Ser Ile Ser Pro
330 335 340

cgc ctg cac ctg ctg cgc gac aac cag gtg acc acc ttc acc gac ttc 1171
Arg Leu His Leu Leu Arg Asp Asn Gln Val Thr Thr Phe Thr Asp Phe
345 350 355

cgc gtc gtc tct cct gaa atg gaa gct gaa tgg gaa gac agc gcg ttt 1219
Arg Val Val Ser Pro Glu Met Glu Ala Glu Trp Glu Asp Ser Ala Phe
360 365 370

gac gcg cca ccg gcc ggc ggc atc ggc att gag gtg cgc cca gat ccg 1267
Asp Ala Pro Pro Ala Gly Ala Ile Gly Ile Glu Val Arg Pro Asp Pro
375 380 385

tat ctg atg gag cgc ctc caa cag ggc ggc ttt ggt gat ttc gga gat 1315
Tyr Leu Met Glu Arg Leu Gln Gln Gly Gly Phe Gly Asp Phe Gly Asp
390 395 400

ttc ggc aag ccc cgc gat cta gat atg tagcgaaaaa gggaccttca 1362
Phe Gly Lys Pro Arg Asp Leu Asp Met
410

ctt 1365

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<210> 2292

<211> 414

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2292

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Met Ala Phe Gly Phe Phe Ser Arg Arg Lys Lys Lys Asn Lys Asp Lys
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Asn Pro Asn Glu Asn Ser Ala Val Pro Ala His Ser Glu Asp Ser Pro
20 25 30

Gln Glu Val Phe Glu Gly Asn Gly Arg Gln Val Gly Asp Pro Ile Glu
35 40 45

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Gln Gln Val Asp Arg Asp Ala Lys Gly Arg Leu Thr Ala Ala Asp Phe
 50 55 60
 Leu Pro Asp Ala Asp Leu Pro Gln Leu Asn Arg Ser Arg Ala Asn Met
 65 70 75 80
 Leu Arg Arg Glu Leu Glu Tyr Arg Phe Ser Leu Gln Asn Ala His Ile
 85 90 95
 Asn Ile Asp Gly Asn Thr Ala Met Ile Gln Arg Ser Asp Gly Gly Ala
 100 105 110
 Ala His Val Ser Leu Arg Thr Leu Ala Met Asn Ala Ala Gly Leu Asp
 115 120 125
 Asn Phe Asp Gln Leu Pro Glu Leu Val Glu Ser Phe Val His Gly Thr
 130 135 140
 Leu Ala Asp Ala Thr Leu Asn Asp Leu Ser Thr Ala Asp Leu Tyr Lys
 145 150 155 160
 Ala Leu Arg Leu Arg Leu Leu Pro Thr Pro Gly Glu Gly Asp Asp Leu
 165 170 175
 Val Glu His Gly Leu Asp Arg Glu Ser Gln Ile Arg Asp Asp Ser Ile
 180 185 190
 Leu Arg Thr Phe Thr Ser Asp Met Ser Ile Ala Leu Val Leu Asp Thr
 195 200 205
 Glu His Ala Ile Arg Ile Gln Pro Leu Lys Glu Leu Glu Glu Phe Asp
 210 215 220
 Asp Leu Ser Ala Leu Glu Arg Ala Ala Asp Arg Asn Thr Trp Gln Glu
 225 230 235 240
 Leu Tyr Asp Ala Asn Val Asp Ala Ser Phe Val Asp Ala Glu Ser Asp
 245 250 255
 Ser Glu Gly Ser Ser Phe Trp Ala Phe Glu Ser Asn Ser Tyr Tyr Leu
 260 265 270
 Gly Ser Ala Pro Leu Phe Leu Asn Asp Leu Leu Ala Lys Trp Ala Pro
 275 280 285
 Asp Leu Asp Gln Ser Asp Gly Val Ile Phe Ala Val Pro Asp Arg Asp
 290 295 300
 Leu Leu Ile Ala Arg Pro Val Thr Thr Gly Glu Asp Leu Met Asn Gly
 305 310 315 320
 Ile Thr Ala Met Val Arg Ile Ala Met Arg Phe Gly Leu Gly Asn Pro
 325 330 335
 Thr Ser Ile Ser Pro Arg Leu His Leu Leu Arg Asp Asn Gln Val Thr
 340 345 350
 Thr Phe Thr Asp Phe Arg Val Val Ser Pro Glu Met Glu Ala Glu Trp
 355 360 365
 Glu Asp Ser Ala Phe Asp Ala Pro Pro Ala Gly Ala Ile Gly Ile Glu

370 375 380

Val Arg Pro Asp Pro Tyr Leu Met Glu Arg Leu Gln Gln Gly Gly Phe
 385 390 395 400

Gly Asp Phe Gly Asp Phe Gly Lys Pro Arg Asp Leu Asp Met
 405 410

<210> 2293
 <211> 825
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(802)
 <223> RXA01540

<400> 2293
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gaaacaccca cacactcatc acaagaaagt aggtctcacc atg act ttt gca gaa 115
 Met Thr Phe Ala Glu 5

ctt agc tca ccg cgt acc atc atc gct ttt aat ggc cgt gcc gaa tct 163
 Leu Ser Ser Pro Arg Thr Ile Ile Ala Phe Asn Gly Arg Ala Glu Ser 20

ggc aaa gat act gca gca cag tat ctc acc cat atg cac agt ttt cac 211
 Gly Lys Asp Thr Ala Ala Gln Tyr Leu Thr His Met His Ser Phe His 35

cgc atc gcc ttt gcc gat ggt gtc cgt gac gca ctc tat gcg ctt aac 259
 Arg Ile Ala Phe Ala Asp Gly Val Arg Asp Ala Leu Tyr Ala Leu Asn 40 45 50

cca ctg gtc tgt gtg gag cag gct atc acc aca cat ggt gcc att tat 307
 Pro Leu Val Cys Val Glu Gln Ala Ile Thr Thr His Gly Ala Ile Tyr 55 60 65

gac cgc gtg gcc act gtt gtg gac aca ctt ggt tgg gat acc gca aag 355
 Asp Arg Val Ala Thr Val Val Asp Thr Leu Gly Trp Asp Thr Ala Lys 70 75 80 85

caa atc ccc gac atc cgc gca ctt atg cag cgt att ggt acc gaa gct 403
 Gln Ile Pro Asp Ile Arg Ala Leu Met Gln Arg Ile Gly Thr Gln Ala 90 95 100

ggt tgg cgc atc cac ggc gag cat ctg tgg gtc aat ctt gct atc aaa 451
 Gly Trp Arg Ile His Gly Glu His Leu Trp Val Asn Leu Ala Ile Lys 105 110 115

aag atc aat gaa ctg ccc gct gac cac gcc att gtc atc act gat ttg 499
 Lys Ile Asn Glu Leu Pro Ala Asp His Ala Ile Val Ile Thr Asp Leu 120 125 130

cga ttc ccc aat gag att gag tgg ttg aac agc ctc aaa gcc aac ccg 547
 Arg Phe Pro Asn Glu Ile Glu Trp Leu Asn Ser Leu Lys Ala Asn Pro 135 140 145

atg aac acc att cag acc gtc aaa gtc atc cga cca gat cat gaa tcg 595
 Met Asn Thr Ile Gln Thr Val Lys Val Ile Arg Pro Asp His Glu Ser
 150 155 160 165

acc ttg act gca gga tca ttc ggt act acc tca cat att tcc gaa agc 643
 Thr Leu Thr Ala Gly Ser Phe Gly Thr Thr Ser His Ile Ser Glu Ser
 170 175 180

ttt aat ctc act acc gac act gtg ctc cgc aac gat ggc acc att gac 691
 Phe Asn Leu Thr Thr Asp Thr Val Leu Arg Asn Asp Gly Thr Ile Asp
 185 190 195

gat ttg cac tca aag ctg gct gat ttt ttg agc act tcc ccg cag ccc 739
 Asp Leu His Ser Lys Leu Ala Asp Phe Leu Ser Thr Ser Pro Gln Pro
 200 205 210

gtg ctc tct cgt aac gcc cct gta cca aaa cac aac gca ccg gca cca 787
 Val Leu Ser Arg Asn Ala Pro Val Pro Lys His Asn Ala Pro Ala Pro
 215 220 225

acc act gat gcc atg taaataaccc ccgtatcaag atc 825
 Thr Thr Asp Ala Met
 230

<210> 2294
 <211> 234
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2294
 Met Thr Phe Ala Glu Leu Ser Ser Pro Arg Thr Ile Ile Ala Phe Asn
 1 5 10 15
 Gly Arg Ala Glu Ser Gly Lys Asp Thr Ala Ala Gln Tyr Leu Thr His
 20 25 30
 Met His Ser Phe His Arg Ile Ala Phe Ala Asp Gly Val Arg Asp Ala
 35 40 45
 Leu Tyr Ala Leu Asn Pro Leu Val Cys Val Glu Gln Ala Ile Thr Thr
 50 55 60
 His Gly Ala Ile Tyr Asp Arg Val Ala Thr Val Val Asp Thr Leu Gly
 65 70 75 80
 Trp Asp Thr Ala Lys Gln Ile Pro Asp Ile Arg Ala Leu Met Gln Arg
 85 90 95
 Ile Gly Thr Glu Ala Gly Trp Arg Ile His Gly Glu His Leu Trp Val
 100 105 110
 Asn Leu Ala Ile Lys Lys Ile Asn Glu Leu Pro Ala Asp His Ala Ile
 115 120 125
 Val Ile Thr Asp Leu Arg Phe Pro Asn Glu Ile Glu Trp Leu Asn Ser
 130 135 140
 Leu Lys Ala Asn Pro Met Asn Thr Ile Gln Thr Val Lys Val Ile Arg
 145 150 155 160

```

Pro Asp His Glu Ser Thr Leu Thr Ala Gly Ser Phe Gly Thr Thr Ser
                165                      170                      175

His Ile Ser Glu Ser Phe Asn Leu Thr Thr Asp Thr Val Leu Arg Asn
                180                      185                      190

Asp Gly Thr Ile Asp Asp Leu His Ser Lys Leu Ala Asp Phe Leu Ser
                195                      200                      205

Thr Ser Pro Gln Pro Val Leu Ser Arg Asn Ala Pro Val Pro Lys His
                210                      215                      220

Asn Ala Pro Ala Pro Thr Thr Asp Ala Met
225                      230

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<210> 2295

<211> 2889

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2866)

<223> RXA01543

<400> 2295

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ggggcgctgt tgtttagt aaagaaagag cgggtgggaaa atg agt ttg aaa caa 115
                Met Ser Leu Lys Gln
                1                      5

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```

gcc att atc gtg cgc aat gaa tat acg att aag cag gca aat gcc aaa 163
Ala Ile Ile Val Arg Asn Glu Tyr Thr Ile Lys Gln Ala Asn Gly Lys
                10                      15                      20

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ggt tca cga gga tca tcg cca ggt aaa tat atc tct gcc tat atg gca 211
Gly Ser Arg Gly Ser Ser Pro Gly Lys Tyr Ile Ser Gly Tyr Met Ala
                25                      30                      35

```

```

cgc agc gat cgc gta gaa gca gta gca cct att gtg cgc aat aaa tta 259
Arg Ser Asp Ala Val Glu Ala Val Ala Pro Ile Val Arg Asn Lys Leu
                40                      45                      50

```

```

gat gat ttc atc atg cgg tat atg gca cgt gat agt gcc gtg gag cag 307
Asp Asp Phe Ile Met Arg Tyr Met Ala Arg Asp Ser Ala Val Glu Gln
                55                      60                      65

```

```

ctc acc acg gac agt aac gca gac tat gac cag caa cct gaa atg aac 355
Leu Thr Thr Asp Ser Asn Ala Asp Tyr Asp Gln Gln Pro Glu Met Asn
                70                      75                      80                      85

```

```

tct cgt cgt gcc cgg caa ggt cgc cgc gcg acc ttg aaa caa cgt cgt 403
Ser Arg Arg Gly Arg Gln Gly Arg Arg Ala Thr Leu Lys Gln Arg Arg
                90                      95                      100

```

```

gca gaa cgc agc gcc cgg cga gca gca ttg cga cgc gcc gtg aat aca 451
Ala Glu Arg Ser Ala Arg Arg Ala Ala Leu Arg Ala Gly Val Asn Thr
                105                      110                      115

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gac tcc gac acc acc aac cca tca caa cct gtg cac ccg agg gaa ctc Asp Ser Asp Thr Thr Asn Pro Ser Gln Pro Val His Pro Arg Glu Leu 120 125 130	499
gcg gaa ttt act acc cag gat ggg cag cgc gtt cat gat ctc atg ctg Ala Glu Phe Thr Thr Gln Asp Gly Gln Arg Val His Asp Leu Met Leu 135 140 145	547
agg gct cag ggt aat ggg gga gtg gcc ttt ggg tat ggc gat gtc tcg Arg Ala Gln Gly Asn Gly Gly Val Ala Phe Gly Tyr Gly Asp Val Ser 150 155 160 165	595
ctg tca cat gat gat ctt cat gca gca agt aat aac gtc caa gag ctc Leu Ser His Asp Asp Leu His Ala Ala Ser Asn Asn Val Gln Glu Leu 170 175 180	643
tat gaa aat agg cat acc gtg atg aaa gtg gtc cta tct ttt acc cag Tyr Glu Asn Arg His Thr Val Met Lys Val Val Leu Ser Phe Thr Gln 185 190 195	691
gat tac ctg acc gcg cat ggc ctt att cca gag gat ctc gat att aag Asp Tyr Leu Thr Ala His Gly Leu Ile Pro Glu Asp Leu Asp Ile Lys 200 205 210	739
cgt gct ggt gat tat cgc gcc cag gtt gac caa atg aag cta cgc atg Arg Ala Gly Asp Tyr Arg Gly Gln Val Asp Gln Met Lys Leu Arg Met 215 220 225	787
gct gtc atg cat ggt gtg gat cgt cta gcc cag cgt cat tat gat gat Ala Val Met His Gly Val Asp Arg Leu Ala Gln Arg His Tyr Asp Asp 230 235 240 245	835
ttg cgc tat gtc gcc gtg att cag gtt gat acg aag cat gtg cac gcc Leu Arg Tyr Val Gly Val Ile Gln Val Asp Thr Lys His Val His Ala 250 255 260	883
cac ttg acc atg gtg gat gct ggt tat gga cac ccg gct gct gat ggt His Leu Thr Met Val Asp Ala Gly Tyr Gly His Arg Ala Ala Asp Gly 265 270 275	931
acg caa aaa gcc aaa atc aat aag cca ggt aag gct att ttg cgg cgt Thr Gln Lys Gly Lys Ile Asn Lys Pro Gly Lys Ala Ile Leu Arg Arg 280 285 290	979
ggt att gac gcc tgg ctt gat cag cat cag cat atg gcg cac ttg tca Gly Ile Asp Ala Trp Leu Asp Gln His Gln His Met Ala His Leu Ser 295 300 305	1027
gca gca gtg ggg tat gaa aaa cgc aat gtc acc agc tac gtc aag cgc Ala Ala Val Gly Tyr Glu Lys Arg Asn Val Thr Ser Tyr Val Lys Arg 310 315 320 325	1075
tgg gcg ttt cat cag ctc acc caa gaa agt gct gcg caa ttt gtg gtc Trp Ala Phe His Gln Leu Thr Gln Glu Ser Ala Ala Gln Phe Val Val 330 335 340	1123
gct tgt ttg cca gag gat aag cga ctg tgg cgt gca tcg acc aat gcc Ala Cys Leu Pro Glu Asp Lys Arg Leu Trp Arg Ala Ser Thr Asn Ala 345 350 355	1171

aag gaa atg gat aag ccg aat aga tta gtg cgc gag ttg gtg gag gcg Lys Glu Met Asp Lys Pro Asn Arg Leu Val Arg Glu Leu Val Glu Ala 360 365 370	1219
cga ctt ggt gag act gat tca ccg atg ccg gca gca ctg tcg cag gtc Arg Leu Gly Glu Thr Asp Ser Pro Met Pro Ala Ala Leu Ser Gln Val 375 380 385	1267
tat cag tat cgc caa aaa cgc cgc gtt aaa gaa ggt tta agc aag cag Tyr Gln Tyr Ala Gln Lys Arg Arg Val Lys Glu Gly Leu Ser Lys Gln 390 395 400 405	1315
gac acc cag cgt ttg att gat aat ggc cgc gaa aag atc att gag cag Asp Thr Gln Arg Leu Ile Asp Asn Gly Arg Glu Lys Ile Ile Glu Gln 410 415 420	1363
gcc atg aac ggt gtc tac agt gtc cta tcc gcg att tcc gat gag caa Ala Met Asn Gly Val Tyr Ser Val Leu Ser Ala Ile Ser Asp Glu Gln 425 430 435	1411
cgc gat gtc tct acg gcc atg ttg aca gtc atg cgt caa gac tat gag Arg Asp Val Ser Thr Ala Met Leu Thr Val Met Arg Gln Asp Tyr Glu 440 445 450	1459
gat ttg ctc gat ggt att gcg ccg aag aag agc aag gat cta gac gag Asp Leu Leu Asp Gly Ile Ala Arg Lys Lys Ser Lys Asp Leu Asp Glu 455 460 465	1507
cag ggt agt agt gga tca caa gag gtg ggg aaa gaa gag cct gag cca Gln Gly Ser Ser Gly Ser Gln Glu Val Gly Lys Glu Glu Pro Glu Pro 470 475 480 485	1555
agt att gag gaa ttt ggg ctg cgt ttg ccg tgc tat tca gca cgc ttg Ser Ile Glu Glu Phe Gly Leu Arg Leu Arg Ser Tyr Ser Ala Arg Leu 490 495 500	1603
aat cat cac cga gaa caa cga gaa gcc ttt gcc gtg aaa aaa cgc tgc Asn His His Arg Glu Gln Arg Glu Ala Phe Ala Val Lys Lys Arg Ser 505 510 515	1651
tgg gag gac gct aac tct caa ggt ttg gct gat ccc acc tca cag gta Trp Glu Asp Ala Asn Ser Gln Gly Leu Ala Asp Pro Thr Ser Gln Val 520 525 530	1699
atg tgg agt ttt tat gac act gag gag cag tat cat gcg atg tgc caa Met Trp Ser Phe Tyr Asp Thr Glu Glu Gln Tyr His Ala Met Cys Gln 535 540 545	1747
tcc aag tac cag cac ttt ttg acc ttt gcc cca cct gtc ggt cag tgg Ser Lys Tyr Gln His Phe Leu Thr Phe Ala Pro Pro Val Gly Gln Trp 550 555 560 565	1795
gag aag caa tgg gct gag gtt gct gat tac ggt aaa agg gtt gtg ggt Glu Lys Gln Trp Ala Glu Val Ala Asp Tyr Gly Lys Arg Val Val Gly 570 575 580	1843
ctg cgt gca ctg ccg gca gat cgt tct ttg gca cgc atg agc gat gaa Leu Arg Ala Leu Arg Ala Asp Arg Ser Leu Ala Arg Met Ser Asp Glu 585 590 595	1891
cgt gca gct gaa gct ttg ggt ccg caa ctt tat gac caa ccc ggt ggt	1939

Arg	Ala	Ala	Glu	Ala	Leu	Gly	Arg	Gln	Leu	Tyr	Asp	Gln	Pro	Gly	Gly		
	600						605					610					
ggg	tta	ttg	gct	cga	aca	ggc	gct	gag	ggg	aaa	gct	ggg	cgt	gcg	gtc	1987	
Gly	Leu	Leu	Ala	Arg	Thr	Gly	Ala	Glu	Gly	Lys	Ala	Gly	Arg	Ala	Val		
	615					620					625						
ctg	gat	ggc	cga	att	gag	cgc	atg	atg	gtg	acc	tat	cag	caa	aaa	att	2035	
Leu	Asp	Gly	Arg	Ile	Glu	Arg	Met	Met	Val	Thr	Tyr	Gln	Gln	Lys	Ile		
	630					635					640				645		
gat	gat	ttg	cga	cga	gaa	tgg	gca	cag	ctc	ggg	gca	cgt	tta	gag	gtt	2083	
Asp	Asp	Leu	Arg	Arg	Glu	Trp	Ala	Gln	Leu	Gly	Ala	Arg	Leu	Glu	Val		
					650				655					660			
gaa	ggg	gat	gct	gta	ttg	atg	gat	gca	gca	gat	cta	cgt	gaa	tct	ggg	2131	
Glu	Gly	Asp	Gly	Ala	Val	Leu	Met	Asp	Ala	Ala	Asp	Leu	Arg	Glu	Ser	Gly	
			665					670						675			
gga	gag	ggg	gca	gat	gaa	cgc	cag	ata	cag	cag	caa	aca	att	gag	ttg	2179	
Gly	Glu	Gly	Ala	Asp	Glu	Arg	Gln	Ile	Gln	Gln	Gln	Gln	Ile	Glu	Leu		
			680				685						690				
ccg	gtc	gct	gat	gta	tct	gat	tct	gtg	cgc	aca	tac	ctt	gac	gaa	gag	2227	
Pro	Val	Ala	Asp	Val	Ser	Asp	Ser	Val	Arg	Thr	Tyr	Leu	Asp	Glu	Glu		
	695					700					705						
tta	cgt	gat	agt	cgt	gat	gtg	agc	gct	cat	gat	cca	gtg	cac	acc	ttg	2275	
Leu	Arg	Asp	Ser	Arg	Asp	Val	Ser	Ala	His	Asp	Pro	Val	His	Thr	Leu		
	710					715				720					725		
cgt	ggc	agg	ttt	cag	gtc	gtg	ttt	cga	ccg	gag	cat	gat	ttt	gag	cag	2323	
Arg	Gly	Arg	Phe	Gln	Val	Val	Phe	Arg	Pro	Glu	His	Asp	Phe	Glu	Gln		
				730				735						740			
gtg	ggg	ggc	cct	gac	ctg	cgc	gat	ctt	cac	tat	gcc	tgg	ttt	agc	gat	2371	
Val	Gly	Gly	Pro	Asp	Leu	Arg	Asp	Leu	His	Tyr	Ala	Trp	Phe	Ser	Asp		
			745					750						755			
cag	aag	gtc	agt	cag	ccc	att	gtg	tgt	agt	tac	ggg	gag	tta	gtc	acc	2419	
Gln	Lys	Val	Ser	Gln	Pro	Ile	Val	Cys	Ser	Tyr	Gly	Glu	Leu	Val	Thr		
		760					765						770				
cag	cga	cgt	tat	gct	ttt	gaa	cgc	gct	ccg	gag	tgg	atg	atc	agt	tcg	2467	
Gln	Arg	Arg	Tyr	Ala	Phe	Glu	Arg	Ala	Arg	Glu	Trp	Met	Ile	Ser	Ser		
	775					780					785						
cag	cag	gaa	cca	gaa	gca	gtg	gca	gaa	gag	ctt	gat	cat	gcc	ggc	gcg	2515	
Gln	Gln	Glu	Pro	Glu	Ala	Val	Ala	Glu	Glu	Leu	Asp	His	Ala	Gly	Ala		
	790				795					800				805			
gac	ata	act	cgc	atg	gaa	gca	acc	agt	agt	gag	gta	tcc	cgt	aca	ggg	2563	
Asp	Ile	Thr	Arg	Met	Glu	Ala	Thr	Ser	Ser	Glu	Val	Ser	Arg	Thr	Gly		
				810				815						820			
att	ttg	cgt	agt	gcc	atg	ctt	gcc	aga	att	aga	gag	cag	gcg	cga	caa	2611	
Ile	Leu	Arg	Ser	Ala	Met	Leu	Ala	Arg	Ile	Arg	Glu	Gln	Ala	Arg	Gln		
			825					830					835				
cgc	gct	cag	cgt	gca	gcg	gaa	gag	cag	gct	cgt	cgt	gag	cgt	gag	ttg	2659	
Arg	Ala	Gln	Arg	Ala	Ala	Glu	Glu	Gln	Ala	Arg	Arg	Glu	Arg	Glu	Leu		

840	845	850	
gta gca cag cga caa caa gaa att gat cag gag acc acg caa cca gcg			2707
Val Ala Gln Arg Gln Gln Glu Ile Asp Gln Glu Thr Thr Gln Pro Ala			
855	860	865	
ttc gag gtg gtg caa cga cat gta caa ccg gag tcg gtg cag att aag			2755
Phe Glu Val Val Gln Arg His Val Gln Pro Glu Ser Val Gln Ile Lys			
870	875	880	885
cgg ggt aga aca gtt gcg cta gat aag cga gtg cag cca ctg att cgt			2803
Arg Gly Arg Thr Val Ala Leu Asp Lys Arg Val Gln Pro Leu Ile Arg			
890	895	900	
gat gct gtg gat cga gct gtg ctg gat tca cag ctg ccg agt acc cgt			2851
Asp Ala Val Asp Arg Ala Val Leu Asp Ser Gln Leu Arg Ser Thr Arg			
905	910	915	
gat ggt gga ttg ggg taggcggttg attaaaaaaaa aag			2889
Asp Gly Gly Leu Gly			
920			

<210> 2296

<211> 922

<212> PRT

<213> Corynebacterium glutamicum

<400> 2296

Met	Ser	Leu	Lys	Gln	Ala	Ile	Ile	Val	Arg	Asn	Glu	Tyr	Thr	Ile	Lys
1				5					10					15	

Gln	Ala	Asn	Gly	Lys	Gly	Ser	Arg	Gly	Ser	Ser	Pro	Gly	Lys	Tyr	Ile
			20					25					30		

Ser	Gly	Tyr	Met	Ala	Arg	Ser	Asp	Ala	Val	Glu	Ala	Val	Ala	Pro	Ile
		35					40					45			

Val	Arg	Asn	Lys	Leu	Asp	Phe	Ile	Met	Arg	Tyr	Met	Ala	Arg	Asp	
	50				55					60					

Ser	Ala	Val	Glu	Gln	Leu	Thr	Thr	Asp	Ser	Asn	Ala	Asp	Tyr	Asp	Gln
	65				70					75					80

Gln	Pro	Glu	Met	Asn	Ser	Arg	Arg	Gly	Arg	Gln	Gly	Arg	Arg	Ala	Thr
			85					90						95	

Leu	Lys	Gln	Arg	Arg	Ala	Glu	Arg	Ser	Ala	Arg	Arg	Ala	Ala	Leu	Arg
		100					105						110		

Ala	Gly	Val	Asn	Thr	Asp	Ser	Asp	Thr	Thr	Asn	Pro	Ser	Gln	Pro	Val
		115					120					125			

His	Pro	Arg	Glu	Leu	Ala	Glu	Phe	Thr	Thr	Gln	Asp	Gly	Gln	Arg	Val
	130					135					140				

His	Asp	Leu	Met	Leu	Arg	Ala	Gln	Gly	Asn	Gly	Gly	Val	Ala	Phe	Gly
	145				150				155						160

Tyr	Gly	Asp	Val	Ser	Leu	Ser	His	Asp	Asp	Leu	His	Ala	Ala	Ser	Asn
				165					170						175

Asn Val Gln Glu Leu Tyr Glu Asn Arg His Thr Val Met Lys Val Val
 180 185 190
 Leu Ser Phe Thr Gln Asp Tyr Leu Thr Ala His Gly Leu Ile Pro Glu
 195 200 205
 Asp Leu Asp Ile Lys Arg Ala Gly Asp Tyr Arg Gly Gln Val Asp Gln
 210 215 220
 Met Lys Leu Arg Met Ala Val Met His Gly Val Asp Arg Leu Ala Gln
 225 230 235 240
 Arg His Tyr Asp Asp Leu Arg Tyr Val Gly Val Ile Gln Val Asp Thr
 245 250 255
 Lys His Val His Ala His Leu Thr Met Val Asp Ala Gly Tyr Gly His
 260 265 270
 Arg Ala Ala Asp Gly Thr Gln Lys Gly Lys Ile Asn Lys Pro Gly Lys
 275 280 285
 Ala Ile Leu Arg Arg Gly Ile Asp Ala Trp Leu Asp Gln His Gln His
 290 295 300
 Met Ala His Leu Ser Ala Ala Val Gly Tyr Glu Lys Arg Asn Val Thr
 305 310 315 320
 Ser Tyr Val Lys Arg Trp Ala Phe His Gln Leu Thr Gln Glu Ser Ala
 325 330 335
 Ala Gln Phe Val Val Ala Cys Leu Pro Glu Asp Lys Arg Leu Trp Arg
 340 345 350
 Ala Ser Thr Asn Ala Lys Glu Met Asp Lys Pro Asn Arg Leu Val Arg
 355 360 365
 Glu Leu Val Glu Ala Arg Leu Gly Glu Thr Asp Ser Pro Met Pro Ala
 370 375 380
 Ala Leu Ser Gln Val Tyr Gln Tyr Ala Gln Lys Arg Arg Val Lys Glu
 385 390 395 400
 Gly Leu Ser Lys Gln Asp Thr Gln Arg Leu Ile Asp Asn Gly Arg Glu
 405 410 415
 Lys Ile Ile Glu Gln Ala Met Asn Gly Val Tyr Ser Val Leu Ser Ala
 420 425 430
 Ile Ser Asp Glu Gln Arg Asp Val Ser Thr Ala Met Leu Thr Val Met
 435 440 445
 Arg Gln Asp Tyr Glu Asp Leu Leu Asp Gly Ile Ala Arg Lys Lys Ser
 450 455 460
 Lys Asp Leu Asp Glu Gln Gly Ser Ser Gly Ser Gln Glu Val Gly Lys
 465 470 475 480
 Glu Glu Pro Glu Pro Ser Ile Glu Glu Phe Gly Leu Arg Leu Arg Ser
 485 490 495

Tyr Ser Ala Arg Leu Asn His His Arg Glu Gln Arg Glu Ala Phe Ala
 500 505 510
 Val Lys Lys Arg Ser Trp Glu Asp Ala Asn Ser Gln Gly Leu Ala Asp
 515 520 525
 Pro Thr Ser Gln Val Met Trp Ser Phe Tyr Asp Thr Glu Glu Gln Tyr
 530 535 540
 His Ala Met Cys Gln Ser Lys Tyr Gln His Phe Leu Thr Phe Ala Pro
 545 550 555 560
 Pro Val Gly Gln Trp Glu Lys Gln Trp Ala Glu Val Ala Asp Tyr Gly
 565 570 575
 Lys Arg Val Val Gly Leu Arg Ala Leu Arg Ala Asp Arg Ser Leu Ala
 580 585 590
 Arg Met Ser Asp Glu Arg Ala Ala Glu Ala Leu Gly Arg Gln Leu Tyr
 595 600 605
 Asp Gln Pro Gly Gly Gly Leu Leu Ala Arg Thr Gly Ala Glu Gly Lys
 610 615 620
 Ala Gly Arg Ala Val Leu Asp Gly Arg Ile Glu Arg Met Met Val Thr
 625 630 635 640
 Tyr Gln Gln Lys Ile Asp Asp Leu Arg Arg Glu Trp Ala Gln Leu Gly
 645 650 655
 Ala Arg Leu Glu Val Glu Gly Asp Ala Val Leu Met Asp Ala Ala Asp
 660 665 670
 Leu Arg Glu Ser Gly Gly Glu Gly Ala Asp Glu Arg Gln Ile Gln Gln
 675 680 685
 Gln Thr Ile Glu Leu Pro Val Ala Asp Val Ser Asp Ser Val Arg Thr
 690 695 700
 Tyr Leu Asp Glu Glu Leu Arg Asp Ser Arg Asp Val Ser Ala His Asp
 705 710 715 720
 Pro Val His Thr Leu Arg Gly Arg Phe Gln Val Val Phe Arg Pro Glu
 725 730 735
 His Asp Phe Glu Gln Val Gly Gly Pro Asp Leu Arg Asp Leu His Tyr
 740 745 750
 Ala Trp Phe Ser Asp Gln Lys Val Ser Gln Pro Ile Val Cys Ser Tyr
 755 760 765
 Gly Glu Leu Val Thr Gln Arg Arg Tyr Ala Phe Glu Arg Ala Arg Glu
 770 775 780
 Trp Met Ile Ser Ser Gln Gln Glu Pro Glu Ala Val Ala Glu Glu Leu
 785 790 795 800
 Asp His Ala Gly Ala Asp Ile Thr Arg Met Glu Ala Thr Ser Ser Glu
 805 810 815
 Val Ser Arg Thr Gly Ile Leu Arg Ser Ala Met Leu Ala Arg Ile Arg

820	825	830
Glu Gln Ala Arg Gln Arg Ala Gln Arg Ala Ala	Glu Gln Ala Arg	
835	840	845
Arg Glu Arg Glu Leu Val Ala Gln Arg Gln Gln	Glu Ile Asp Gln Glu	
850	855	860
Thr Thr Gln Pro Ala Phe Glu Val Val Gln Arg	His Val Gln Pro Glu	
865	870	875
Ser Val Gln Ile Lys Arg Gly Arg Thr Val Ala Leu Asp Lys Arg Val		
885	890	895
Gln Pro Leu Ile Arg Asp Ala Val Asp Arg Ala Val Leu Asp Ser Gln		
900	905	910
Leu Arg Ser Thr Arg Asp Gly Gly Leu Gly		
915	920	
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	Val Lys Leu Asp Asp	5
	1	
gct atg gtc atg atc gaa cag cgc ctg gtc aaa ggt cgc ggc gca acc	163	
Ala Met Val Met Ile Glu Gln Arg Leu Val Lys Gly Arg Gly Ala Thr		
	10	15
		20
aag acg caa cta gca ccc tat gag cat atc cag cgc aat att gca gcc	211	
Lys Thr Gln Leu Ala Pro Tyr Glu His Ile Gln Arg Asn Ile Ala Ala		
	25	30
		35
cga ggg ttg aga gcc gat gac gga ggc tgc tgc ttc ggt tat ggg gat	259	
Arg Gly Leu Arg Ala Asp Asp Gly Gly Ser Cys Phe Gly Tyr Gly Asp		
	40	45
		50
gcg tgc ctg agt aat gac gat gta gca act gct gca gaa gat att cag	307	
Ala Ser Leu Ser Asn Asp Asp Val Ala Thr Ala Ala Glu Asp Ile Gln		
	55	60
		65
gat ttg ttt gcg tgc ggg cat acg gtt atc tca gcg att gtc gtt ttt	355	
Asp Leu Phe Ala Cys Gly His Thr Val Ile Ser Ala Ile Val Val Phe		
	70	75
		80
		85
gat aag agc tat ctc agt gag cat gga atc atg agc ttt gat cgg aac	403	
Asp Lys Ser Tyr Leu Ser Glu His Gly Ile Met Ser Phe Asp Pro Asn		
	90	95
		100

tat ttt ggt cag gat att tat gcg gac acc cat cca gag att gat ctc 451
 Tyr Phe Gly Gln Asp Ile Tyr Ala Asp Thr His Pro Glu Ile Asp Leu
 105 110 115

atg gaa ttg cgt tta gcc gtg atg aat ggg ctc ttg ggg ctt gag gga 499
 Met Glu Leu Arg Leu Ala Val Met Asn Gly Leu Leu Gly Leu Glu Gly
 120 125 130

acg ttt ttt gag gat atg cgt tat gtc gca tct atc gag gtg agc cgg 547
 Thr Phe Phe Glu Asp Met Arg Tyr Val Ala Ser Ile Glu Val Ser Arg
 135 140 145

agc tat gtc tat gcg cac ata atg atg gcg gat gca gcc gtt gac gat 595
 Ser Tyr Val Tyr Ala His Ile Met Met Ala Asp Ala Gly Val Asp Asp
 150 155 160 165

gca cgc ggt aat gca cag gtg aag att acg gac acc gaa cga gtg ctg 643
 Ala Arg Gly Asn Ala Gln Val Lys Ile Thr Asp Thr Glu Arg Val Leu
 170 175 180

ttt aga cgt ggt gtt gaa tcc cgg ttt gtg gag caa gag gca cgc aac 691
 Phe Arg Arg Gly Val Glu Ser Arg Phe Val Glu Gln Glu Ala Arg Asn
 185 190 195

gtc gtg ctt tagccaaggt gaggcacaa gag 723
 Val Val Leu
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<210> 2298

<211> 200

<212> PRT

<213> Corynebacterium glutamicum

<400> 2298

Val Lys Leu Asp Asp Ala Met Val Met Ile Glu Gln Arg Leu Val Lys
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Gly Arg Gly Ala Thr Lys Thr Gln Leu Ala Pro Tyr Glu His Ile Gln
 20 25 30

Arg Asn Ile Ala Ala Arg Gly Leu Arg Ala Asp Asp Gly Gly Ser Cys
 35 40 45

Phe Gly Tyr Gly Asp Ala Ser Leu Ser Asn Asp Asp Val Ala Thr Ala
 50 55 60

Ala Glu Asp Ile Gln Asp Leu Phe Ala Cys Gly His Thr Val Ile Ser
 65 70 75 80

Ala Ile Val Val Phe Asp Lys Ser Tyr Leu Ser Glu His Gly Ile Met
 85 90 95

Ser Phe Asp Pro Asn Tyr Phe Gly Gln Asp Ile Tyr Ala Asp Thr His
 100 105 110

Pro Glu Ile Asp Leu Met Glu Leu Arg Leu Ala Val Met Asn Gly Leu
 115 120 125

Leu Gly Leu Glu Gly Thr Phe Phe Glu Asp Met Arg Tyr Val Ala Ser

130 135 140
 Ile Glu Val Ser Arg Ser Tyr Val Tyr Ala His Ile Met Met Ala Asp
 145 150 155 160
 Ala Gly Val Asp Asp Ala Arg Gly Asn Ala Gln Val Lys Ile Thr Asp
 165 170 175
 Thr Glu Arg Val Leu Phe Arg Arg Gly Val Glu Ser Arg Phe Val Glu
 180 185 190
 Gln Glu Ala Arg Asn Val Val Leu
 195 200

 <210> 2299
 <211> 1374
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
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 <222> (101)..(1351)
 <223> RXA01545

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 Met Lys Leu Ala Gly
 1 5
 ttt aac acc aat tca ccc gca gcg cag cgg gtt gcc gaa cag ggt gaa 163
 Phe Asn Thr Asn Ser Pro Ala Ala Gln Arg Val Ala Glu Gln Gly Glu
 10 15 20
 aag gta cag ctc gat gca cgg gtg tac gcg gtg ttt acc cca gat gtt 211
 Lys Val Gln Leu Asp Ala Pro Val Tyr Ala Val Phe Thr Pro Asp Val
 25 30 35
 gtt gaa gtt gag ttt att ggc acg cag cat gag ccg gta ttg cac gtt 259
 Val Glu Val Glu Phe Ile Gly Thr Gln His Glu Pro Val Leu His Val
 40 45 50
 gag ggt gcc atc gac agc gtg act gca ttg tgc cag cta ccg tac gac 307
 Glu Gly Ala Ile Asp Ser Val Thr Ala Leu Ser Gln Leu Pro Tyr Asp
 55 60 65
 att caa aaa att acg ttt gat tca gaa aac caa cag cgt ttt agt gga 355
 Ile Gln Lys Ile Thr Phe Asp Ser Glu Asn Gln Gln Arg Phe Ser Gly
 70 75 80 85
 ttt tat aaa ttc agt cca cag cag cat aaa gag ctc att gat aaa ggt 403
 Phe Tyr Lys Phe Ser Pro Gln Gln His Lys Glu Leu Ile Asp Lys Gly
 90 95 100
 ctg tat cta gaa ggt ttc cag cca ccg cgc gag atg atg acg agc ctg 451
 Leu Tyr Leu Glu Gly Phe Gln Pro Pro Arg Glu Met Met Thr Ser Leu
 105 110 115
 ccg tgg gaa cta ccc atg aat gcc gat gtc act gtc gtg gca cca gag 499

Pro Trp	Glu	Leu	Pro	Met	Asn	Ala	Asp	Val	Thr	Val	Val	Ala	Pro	Glu		
120						125				130						
tcg	cag	gat	gcg	cca	ccg	att	gtg	ctt	gtg	ggc	tta	tct	gag	att	cat	547
Ser	Gln	Asp	Ala	Pro	Pro	Ile	Val	Leu	Val	Gly	Leu	Ser	Glu	Ile	His	
135						140				145						
ggc	gtg	gat	ttt	agt	caa	gaa	tcc	tct	ggc	tat	gag	ctc	acc	agc	atg	595
Gly	Val	Asp	Phe	Ser	Gln	Glu	Ser	Ser	Gly	Tyr	Glu	Leu	Thr	Ser	Met	
150					155				160					165		
ttt	gag	gac	tac	cgt	agc	cag	cgt	gaa	gcg	ggc	gag	gcg	gac	aag	gat	643
Phe	Glu	Asp	Tyr	Arg	Ser	Gln	Arg	Glu	Ala	Gly	Glu	Ala	Asp	Lys	Asp	
				170				175						180		
ttc	tct	gag	tca	att	tct	cgt	gca	gag	att	gaa	ggc	aaa	gat	att	ttc	691
Phe	Ser	Glu	Ser	Ile	Ser	Arg	Ala	Glu	Ile	Glu	Gly	Lys	Asp	Ile	Phe	
				185			190						195			
gct	gat	gct	aac	cgc	acc	cgt	acc	ggc	gtc	agt	gca	cat	gca	cag	cgc	739
Ala	Asp	Ala	Asn	Arg	Thr	Arg	Thr	Gly	Val	Ser	Ala	His	Ala	Gln	Arg	
			200				205				210					
ctt	gag	cag	gag	cga	gcg	ctg	agc	gca	gca	cag	ttg	atg	gcg	aaa	ctt	787
Leu	Glu	Gln	Glu	Arg	Ala	Leu	Ser	Ala	Ala	Gln	Leu	Met	Ala	Lys	Leu	
			215			220					225					
gct	ggc	att	tcc	ttc	cag	act	gaa	ccc	gtg	ctt	gtt	ggc	gcg	gaa	gag	835
Ala	Gly	Ile	Ser	Phe	Gln	Thr	Glu	Pro	Val	Leu	Val	Gly	Ala	Glu	Glu	
230					235				240					245		
agc	ttt	gat	gct	gag	caa	ttc	ctc	gcc	cat	gat	ctt	gat	gac	acc	gct	883
Ser	Phe	Asp	Ala	Glu	Gln	Phe	Leu	Ala	His	Asp	Leu	Asp	Asp	Thr	Ala	
				250				255						260		
ggc	atg	agt	gag	tgg	gag	cgc	gag	gtt	acc	gag	ttc	tac	aac	gag	aag	931
Gly	Met	Ser	Glu	Trp	Glu	Arg	Glu	Val	Thr	Glu	Phe	Tyr	Asn	Glu	Lys	
			265				270						275			
att	cgc	gcc	cag	gag	cct	gtg	gtg	gag	cgg	gag	gct	gag	cgg	gat	agc	979
Ile	Arg	Ala	Gln	Glu	Pro	Val	Val	Glu	Arg	Glu	Ala	Glu	Arg	Asp	Ser	
			280			285						290				
gat	att	gag	act	gag	gtt	gat	gca	gca	cca	act	gtc	agt	gct	gca	gag	1027
Asp	Ile	Glu	Thr	Glu	Val	Asp	Ala	Ala	Pro	Thr	Val	Ser	Ala	Ala	Glu	
			295			300					305					
att	aac	gat	gtt	att	cat	gat	ctt	gat	gag	ctt	gaa	ttc	gat	gac	gtg	1075
Ile	Asn	Asp	Val	Ile	His	Asp	Leu	Asp	Glu	Leu	Glu	Phe	Asp	Asp	Val	
310					315				320					325		
att	gat	ctt	gat	gca	gat	gat	gtt	gtc	aat	acc	gcc	gag	gta	gag	gcg	1123
Ile	Asp	Leu	Asp	Ala	Asp	Asp	Val	Val	Asn	Thr	Ala	Glu	Val	Glu	Ala	
				330				335						340		
cca	gca	agt	gtc	agt	gct	gca	gag	att	tct	gcg	aca	gag	ctt	gat	ttt	1171
Pro	Ala	Ser	Val	Ser	Ala	Ala	Glu	Ile	Ser	Ala	Thr	Glu	Leu	Asp	Phe	
			345				350						355			
gat	cgc	gag	tca	cgg	gct	aag	acc	gcg	cag	cga	gaa	gcc	agc	cga	cgt	1219
Asp	Arg	Glu	Ser	Arg	Ala	Lys	Thr	Ala	Gln	Arg	Glu	Ala	Ser	Arg	Arg	

360	365	370	
gtt gca cag aag att cag act caa gaa tct gtg cgt gag gca tat att			1267
Val Ala Gln Lys Ile Gln Thr Gln Glu Ser Val Arg Glu Ala Tyr Ile			
375	380	385	
cgc gag caa aag cat ggc tat gac gca tca cct gcg gag ggg cgc aag			1315
Arg Glu Gln Lys His Gly Tyr Asp Ala Ser Pro Ala Glu Gly Arg Lys			
390	395	400	405
ttt gat gag aaa att gca gaa cgc ggg cta gat cta taacgaggat			1361
Phe Asp Glu Lys Ile Ala Glu Arg Gly Leu Asp Leu			
410	415		
cggcgtact tta			1374

<210> 2300

<211> 417

<212> PRT

<213> Corynebacterium glutamicum

<400> 2300

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Phe Thr Pro Asp Val Val Glu Val Glu Phe Ile Gly Thr Gln His Glu			
35	40	45	
Pro Val Leu His Val Glu Gly Ala Ile Asp Ser Val Thr Ala Leu Ser			
50	55	60	
Gln Leu Pro Tyr Asp Ile Gln Lys Ile Thr Phe Asp Ser Glu Asn Gln			
65	70	75	80
Gln Arg Phe Ser Gly Phe Tyr Lys Phe Ser Pro Gln Gln His Lys Glu			
85	90	95	
Leu Ile Asp Lys Gly Leu Tyr Leu Glu Gly Phe Gln Pro Pro Arg Glu			
100	105	110	
Met Met Thr Ser Leu Pro Trp Glu Leu Pro Met Asn Ala Asp Val Thr			
115	120	125	
Val Val Ala Pro Glu Ser Gln Asp Ala Pro Pro Ile Val Leu Val Gly			
130	135	140	
Leu Ser Glu Ile His Gly Val Asp Phe Ser Gln Glu Ser Ser Gly Tyr			
145	150	155	160
Glu Leu Thr Ser Met Phe Glu Asp Tyr Arg Ser Gln Arg Glu Ala Gly			
165	170	175	
Glu Ala Asp Lys Asp Phe Ser Glu Ser Ile Ser Arg Ala Glu Ile Glu			
180	185	190	
Gly Lys Asp Ile Phe Ala Asp Ala Asn Arg Thr Arg Thr Gly Val Ser			
195	200	205	

Ala His Ala Gln Arg Leu Glu Gln Glu Arg Ala Leu Ser Ala Ala Gln
210 215 220

Leu Met Ala Lys Leu Ala Gly Ile Ser Phe Gln Thr Glu Pro Val Leu
225 230 235 240

Val Gly Ala Glu Glu Ser Phe Asp Ala Glu Gln Phe Leu Ala His Asp
245 250 255

Leu Asp Asp Thr Ala Gly Met Ser Glu Trp Glu Arg Glu Val Thr Glu
260 265 270

Phe Tyr Asn Glu Lys Ile Arg Ala Gln Glu Pro Val Val Glu Arg Glu
275 280 285

Ala Glu Arg Asp Ser Asp Ile Glu Thr Glu Val Asp Ala Ala Pro Thr
290 295 300

Val Ser Ala Ala Glu Ile Asn Asp Val Ile His Asp Leu Asp Glu Leu
305 310 315 320

Glu Phe Asp Asp Val Ile Asp Leu Asp Ala Asp Asp Val Val Asn Thr
325 330 335

Ala Glu Val Glu Ala Pro Ala Ser Val Ser Ala Ala Glu Ile Ser Ala
340 345 350

Thr Glu Leu Asp Phe Asp Arg Glu Ser Arg Ala Lys Thr Ala Gln Arg
355 360 365

Glu Ala Ser Arg Arg Val Ala Gln Lys Ile Gln Thr Gln Glu Ser Val
370 375 380

Arg Glu Ala Tyr Ile Arg Glu Gln Lys His Gly Tyr Asp Ala Ser Pro
385 390 395 400

Ala Glu Gly Arg Lys Phe Asp Glu Lys Ile Ala Glu Arg Gly Leu Asp
405 410 415

Leu

<210> 2301

<211> 819

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(796)

<223> RXA01546

<400> 2301

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acaacatac ttgcattaaa aaggaattga gataggcact atg gca cga gcg aaa 115
Met Ala Arg Ala Lys
1 5

aat aag aaa cag cgt caa ttg cag cac gct cat gat gca gca cag gct 163
 Asn Lys Lys Gln Arg Gln Leu Gln His Ala His Asp Ala Ala Gln Ala
 10 15 20

gag att gca gaa gcg gta gcg gtt aac acg gtt gaa cca att aat gca 211
 Glu Ile Ala Glu Ala Val Ala Val Asn Thr Val Glu Pro Ile Asn Ala
 25 30 35

cgc acc ggt gga tgg cct tcg tgg gtc gat aag gtc tgg aag ctc act 259
 Arg Thr Gly Gly Trp Pro Ser Trp Val Asp Lys Val Trp Lys Leu Thr
 40 45 50

ggt tca ctt ggt ggt tgg ttt gct ttc ctg gtt ttt gcc atc gcc gtg 307
 Gly Ser Leu Gly Gly Trp Phe Ala Phe Leu Val Phe Ala Ile Ala Val
 55 60 65

tgg ccg gta gcg atc ctt gca gct ggc act gtg gtc acc atc atc ggt 355
 Trp Pro Val Ala Ile Leu Ala Ala Gly Thr Val Thr Ile Ile Gly
 70 75 80 85

acg tgg gga gta tca gta ctg cca agt ctg gtt att tcc agc atc gcc 403
 Thr Trp Gly Val Ser Val Leu Pro Ser Leu Val Ile Ser Ser Ile Gly
 90 95 100

gct tct gct ggt gtg att atc tcc act act gat ggg ttc ctc ttt agc 451
 Ala Ser Ala Gly Val Ile Ile Ser Thr Thr Asp Gly Phe Leu Phe Ser
 105 110 115

tgg gtc atc ccg gtg ctg ttt ctc atg att gtg ctg gca ctg gtg gtc 499
 Trp Val Ile Pro Val Leu Phe Leu Met Ile Val Leu Ala Leu Val Val
 120 125 130

atg aaa gtg ctc aat ctt att ttt ggt gca ttg tgg cgc ttc acc atg 547
 Met Lys Val Leu Asn Leu Ile Phe Gly Ala Leu Trp Arg Phe Thr Met
 135 140 145

act ttg cga cag ggg tta tac gca ggt cgt gaa aag att tct cgc gac 595
 Thr Leu Arg Gln Gly Leu Tyr Ala Gly Arg Glu Lys Ile Ser Arg Asp
 150 155 160 165

gac gcg aag cgc gca cga gca gaa aag aag ctg act aag cag cag gct 643
 Asp Ala Lys Arg Ala Arg Ala Glu Lys Lys Leu Thr Lys Gln Gln Ala
 170 175 180

aaa gaa gcc aaa aag cag cgc aaa ctt gat gcc att tac tcg gct caa 691
 Lys Glu Ala Lys Lys Gln Arg Lys Leu Asp Ala Ile Tyr Ser Ala Gln
 185 190 195

cag gct gaa gag act ctg gcg caa cag gca cag tct gag cca gaa gag 739
 Gln Ala Glu Thr Leu Ala Gln Gln Ala Gln Ser Glu Pro Glu Glu
 200 205 210

tca gac gat aag aac cga cac gac gcc ctc aac gac gct gtt gca gca 787
 Ser Asp Asp Lys Asn Arg His Asp Ala Leu Asn Asp Ala Val Ala Ala
 215 220 225

gct cgc aac tagctagtta ccacgcctga cac 819
 Ala Arg Asn
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<210> 2302

<211> 232

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2302

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 20 25 30

Glu Pro Ile Asn Ala Arg Thr Gly Gly Trp Pro Ser Trp Val Asp Lys
 35 40 45

Val Trp Lys Leu Thr Gly Ser Leu Gly Gly Trp Phe Ala Phe Leu Val
 50 55 60

Phe Ala Ile Ala Val Trp Pro Val Ala Ile Leu Ala Ala Gly Thr Val
 65 70 75 80

Val Thr Ile Ile Gly Thr Trp Gly Val Ser Val Leu Pro Ser Leu Val
 85 90 95

Ile Ser Ser Ile Gly Ala Ser Ala Gly Val Ile Ile Ser Thr Thr Asp
 100 105 110

Gly Phe Leu Phe Ser Trp Val Ile Pro Val Leu Phe Leu Met Ile Val
 115 120 125

Leu Ala Leu Val Val Met Lys Val Leu Asn Leu Ile Phe Gly Ala Leu
 130 135 140

Trp Arg Phe Thr Met Thr Leu Arg Gln Gly Leu Tyr Ala Gly Arg Glu
 145 150 155 160

Lys Ile Ser Arg Asp Asp Ala Lys Arg Ala Arg Ala Glu Lys Lys Leu
 165 170 175

Thr Lys Gln Gln Ala Lys Glu Ala Lys Lys Gln Arg Lys Leu Asp Ala
 180 185 190

Ile Tyr Ser Ala Gln Gln Ala Glu Glu Thr Leu Ala Gln Gln Ala Gln
 195 200 205

Ser Glu Pro Glu Glu Ser Asp Asp Lys Asn Arg His Asp Ala Leu Asn
 210 215 220

Asp Ala Val Ala Ala Ala Arg Asn
 225 230

<210> 2303

<211> 786

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(763)

<223> RXA01547


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aaatgtagat aaccagagtg gtgtaactga ggacgagccg  atg ttc gat cag gtc 115
              Met Phe Asp Gln Val
              1                      5

aag cgc ttt ttt gtt cgc aat atc gtc atg atc att gcg ttg atc ttg 163
Lys Arg Phe Phe Val Arg Asn Ile Val Met Ile Ile Ala Leu Ile Leu
              10                      15                      20

gca gtg gtg gtc att att gtt gcc acc agc acc tct gcg gat cga cat 211
Ala Val Val Val Ile Ile Val Ala Thr Ser Thr Ser Ala Asp Arg His
              25                      30                      35

gct gta ctt aag cgt caa act ggt gag att atg gcc ttg caa cag gaa 259
Ala Val Leu Lys Arg Gln Thr Gly Glu Ile Met Ala Leu Gln Gln Glu
              40                      45                      50

cgt gat gca tta aac agt aag ctt gag ggc caa ctt gag cag gtg gtg 307
Arg Asp Ala Leu Asn Ser Lys Leu Glu Gly Gln Leu Glu Gln Val Val
              55                      60                      65

cgt gac gct acc ggt ggt atg gat att gaa cac aag gct gca gat gat 355
Arg Asp Ala Thr Gly Gly Met Asp Ile Glu His Lys Ala Ala Asp Asp
              70                      75                      80                      85

gct gtt gtt cga gaa ttt ttg tcc atg gcg ctg acg tgg gac agc gtg 403
Ala Val Val Arg Glu Phe Leu Ser Met Ala Leu Thr Trp Asp Ser Val
              90                      95                      100

cgc gac tac ctt gat gtg cgc gag caa gtg atg cgg gtt tat gac ctg 451
Arg Asp Tyr Leu Asp Val Arg Glu Gln Val Met Arg Val Tyr Asp Leu
              105                      110                      115

gat gaa gaa tca cag ttt atg tgg gtg ttt atg cct ggt gaa atg gcg 499
Asp Glu Glu Ser Gln Phe Met Ser Val Phe Met Pro Gly Glu Met Ala
              120                      125                      130

ggc att gct cgc acc gat cca act ggc gaa gtg cac tat gcc tat gat 547
Gly Ile Ala Arg Thr Asp Pro Thr Gly Glu Val His Tyr Ala Tyr Asp
              135                      140                      145

gca gat ctg tcc aac cgc ttt agc agc tta gaa tcc gtg gtt act cgc 595
Ala Asp Leu Ser Asn Arg Phe Ser Ser Leu Glu Ser Val Val Thr Arg
              150                      155                      160                      165

att aat ggt aca gag tac agc tat gta tcc acg gtg acg atg aag tgg 643
Ile Asn Gly Thr Glu Tyr Ser Tyr Val Ser Thr Val Thr Met Lys Ser
              170                      175                      180

aag cgc tct ggt ggt gag gca gaa aca acc tct acc tca cgc ctt gcc 691
Lys Arg Ser Gly Gly Glu Ala Glu Thr Thr Ser Thr Ser Arg Leu Ala
              185                      190                      195

tat gac gtg atc gac ggc aaa att cgt aac ctc gaa gca cgt act gtc 739
Tyr Asp Val Ile Asp Gly Lys Ile Arg Asn Leu Glu Ala Arg Thr Val
              200                      205                      210

ccc ggt ggt gtg aaa tac tgg ggc taaaagtctc tggggcaacc ccc 786

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Pro Gly Gly Val Lys Tyr Ser Gly
215 220

<210> 2304

<211> 221

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2304

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Ser Ala Asp Arg His Ala Val Leu Lys Arg Gln Thr Gly Glu Ile Met
35 40 45

Ala Leu Gln Gln Glu Arg Asp Ala Leu Asn Ser Lys Leu Glu Gly Gln
50 55 60

Leu Glu Gln Val Val Arg Asp Ala Thr Gly Gly Met Asp Ile Glu His
65 70 75 80

Lys Ala Ala Asp Asp Ala Val Val Arg Glu Phe Leu Ser Met Ala Leu
85 90 95

Thr Trp Asp Ser Val Arg Asp Tyr Leu Asp Val Arg Glu Gln Val Met
100 105 110

Arg Val Tyr Asp Leu Asp Glu Glu Ser Gln Phe Met Ser Val Phe Met
115 120 125

Pro Gly Glu Met Ala Gly Ile Ala Arg Thr Asp Pro Thr Gly Glu Val
130 135 140

His Tyr Ala Tyr Asp Ala Asp Leu Ser Asn Arg Phe Ser Ser Leu Glu
145 150 155 160

Ser Val Val Thr Arg Ile Asn Gly Thr Glu Tyr Ser Tyr Val Ser Thr
165 170 175

Val Thr Met Lys Ser Lys Arg Ser Gly Gly Glu Ala Glu Thr Thr Ser
180 185 190

Thr Ser Arg Leu Ala Tyr Asp Val Ile Asp Gly Lys Ile Arg Asn Leu
195 200 205

Glu Ala Arg Thr Val Pro Gly Gly Val Lys Tyr Ser Gly
210 215 220

<210> 2305

<211> 1131

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1108)

<223> RXA01548

<400> 2305

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agaaacttca ataacttagt aactttaaaa ggggtttaat atg gct gag aat aat 115
                               Met Ala Glu Asn Asn
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ggc ggg tcg gat gac ctt aag ccc atc tct gtc gat ggg gtc gtc aat 163
Gly Gly Ser Asp Asp Leu Lys Pro Ile Ser Val Asp Gly Val Val Asn
                               10                               15                               20

ggg gaa gtg cgc agc gac aaa gaa aag cag gcg ttc gag aag att acc 211
Gly Glu Val Arg Ser Asp Lys Glu Lys Gln Ala Phe Glu Lys Ile Thr
                               25                               30                               35

ggt gat gat ctg cgt cgt cgt gca gaa caa atc cgt aaa cgt cgt tta 259
Gly Asp Asp Leu Arg Arg Arg Ala Glu Gln Ile Arg Lys Arg Arg Leu
                               40                               45                               50

gca aaa gcg caa gaa gat gca cgt aag cgt aag cca ttg ttt ggt ttg 307
Ala Lys Ala Gln Glu Asp Ala Arg Lys Arg Lys Pro Leu Phe Gly Leu
                               55                               60                               65

ggt cgt atc gct gtc aca gta ctg gct ggc gcc gta ttt att ggt aca 355
Gly Arg Ile Ala Val Thr Val Leu Ala Gly Ala Val Phe Ile Gly Thr
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acg ttg tgg atc agt acc acc tcg ggc ggc ttt gac gac aag gtg agt 403
Thr Leu Trp Ile Ser Thr Thr Ser Gly Gly Phe Asp Asp Lys Val Ser
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gca aac aat gag cag att gtc act ctg cgt aat gaa gtc aac gac tta 451
Ala Asn Asn Glu Gln Ile Val Thr Leu Arg Asn Glu Val Asn Asp Leu
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aaa aac act gca gag aca atg ccc aaa aaa gag act ctt gct agt caa 499
Lys Asn Thr Ala Glu Thr Met Pro Lys Lys Glu Thr Leu Ala Ser Gln
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ttt gac gca gca acc tca cgt gca cag aat gtg gct gac tta cag aat 547
Phe Asp Ala Ala Thr Ser Arg Ala Gln Asn Val Ala Asp Leu Gln Asn
                               135                               140                               145

cag tta gcc ggc att att acc agt gtt gat gat gat gcc gcg acc gag 595
Gln Leu Ala Gly Ile Ile Thr Ser Val Asp Asp Asp Ala Ala Thr Glu
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cag ttc aag aca att gtt gat gag ctg aaa ccg aaa ttc acg gtc tct 643
Gln Phe Lys Thr Ile Val Asp Glu Leu Lys Pro Lys Phe Thr Val Ser
                               170                               175                               180

gct ggt acg aca ggt gaa ttt cct gcg gcg ggt cgt tgg tac cag cca 691
Ala Gly Thr Thr Gly Glu Phe Pro Ala Ala Gly Arg Trp Tyr Gln Pro
                               185                               190                               195

caa gaa gtt gtt gtc gga gat aac aac cga ccc acc tgg gcg ccg atg 739
Gln Glu Val Val Val Gly Asp Asn Asn Arg Pro Thr Trp Ala Pro Met
                               200                               205                               210

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215 220 225

gat acc gag cac gtt gtg gtg atg tgg gag gcc cgc ttg acc gga ggt 835
Asp Thr Glu His Val Val Val Met Trp Glu Ala Arg Leu Thr Gly Gly
230 235 240 245

gag cgt tac ggt gcg ctg ttg gcg tgg gtg aca gcc gat tac aac atc 883
Glu Arg Tyr Gly Ala Leu Leu Ala Trp Val Thr Ala Asp Tyr Asn Ile
250 255 260

aac acc gcc gtg ttt agc tcg ctg gcg ttg gcg cat acc tat gaa gga 931
Asn Thr Gly Val Phe Ser Ser Leu Ala Leu Ala His Thr Tyr Glu Gly
265 270 275

cac cag cgt att ggt gca acc acc tca cca agt gaa ttt ggt gcc cac 979
His Gln Arg Ile Gly Ala Thr Thr Ser Pro Ser Glu Phe Gly Ala His
280 285 290

ggc aca aat gca gag gcg agc gct gca cgt gct ggc agt gaa ggc ggg 1027
Gly Thr Asn Ala Glu Ala Ser Ala Ala Arg Ala Gly Ser Glu Gly Gly
295 300 305

ggg ctt gag gcc gag gct att ttc gtt gat gag ctg cag cgg gca cta 1075
Gly Leu Glu Gly Glu Ala Ile Phe Val Asp Glu Leu Gln Arg Ala Leu
310 315 320 325

gag atc gct cag ctg aac aaa cag gag aac aga taatgacgac acgaaatgta 1128
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330 335

gat 1131

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<212> PRT
<213> Corynebacterium glutamicum

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35 40 45
Arg Lys Arg Arg Leu Ala Lys Ala Gln Glu Asp Ala Arg Lys Arg Lys
50 55 60
Pro Leu Phe Gly Leu Gly Arg Ile Ala Val Thr Val Leu Ala Gly Ala
65 70 75 80
Val Phe Ile Gly Thr Thr Leu Trp Ile Ser Thr Thr Ser Gly Gly Phe
85 90 95
Asp Asp Lys Val Ser Ala Asn Asn Glu Gln Ile Val Thr Leu Arg Asn
100 105 110

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Glu Val Asn Asp Leu Lys Asn Thr Ala Glu Thr Met Pro Lys Lys Glu
 115 120 125
 Thr Leu Ala Ser Gln Phe Asp Ala Ala Thr Ser Arg Ala Gln Asn Val
 130 135 140
 Ala Asp Leu Gln Asn Gln Leu Ala Gly Ile Ile Thr Ser Val Asp Asp
 145 150 155 160
 Asp Ala Ala Thr Glu Gln Phe Lys Thr Ile Val Asp Glu Leu Lys Pro
 165 170 175
 Lys Phe Thr Val Ser Ala Gly Thr Thr Gly Glu Phe Pro Ala Ala Gly
 180 185 190
 Arg Trp Tyr Gln Pro Gln Glu Val Val Val Gly Asp Asn Asn Arg Pro
 195 200 205
 Thr Trp Ala Pro Met Gly Ala Glu Ser Trp Gly Trp Thr Val Thr Pro
 210 215 220
 Thr Leu Ser Met Ser Asp Thr Glu His Val Val Val Met Trp Glu Ala
 225 230 235 240
 Arg Leu Thr Gly Gly Glu Arg Tyr Gly Ala Leu Leu Ala Trp Val Thr
 245 250 255
 Ala Asp Tyr Asn Ile Asn Thr Gly Val Phe Ser Ser Leu Ala Leu Ala
 260 265 270
 His Thr Tyr Glu Gly His Gln Arg Ile Gly Ala Thr Thr Ser Pro Ser
 275 280 285
 Glu Phe Gly Ala His Gly Thr Asn Ala Glu Ala Ser Ala Ala Arg Ala
 290 295 300
 Gly Ser Glu Gly Gly Gly Leu Glu Gly Glu Ala Ile Phe Val Asp Glu
 305 310 315 320
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<211> 1101

<212> DNA

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<220>

<221> CDS

<222> (101)..(1078)

<223> RXA01552

<400> 2307

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Lys Glu Asp Ser Leu Ala Pro Pro Gln Asn Arg Phe Glu Ser His Lys						
	10				20	
act gtc ttt tcc cta aaa cag aaa aac atc cca att aag gat gct gct						211
Thr Val Phe Ser Leu Lys Gln Lys Asn Ile Pro Ile Lys Asp Ala Ala						
	25				35	
aaa tct gat cag gtg aat ctc act tgg cat gat tat cca ggt gaa tgg						259
Lys Ser Asp Gln Val Asn Leu Thr Trp His Asp Tyr Pro Gly Glu Trp						
	40				50	
ttt gag ggt gga gct gta acg gac tcg gaa aag cag gat aaa gtt gaa						307
Phe Glu Gly Gly Ala Val Thr Asp Ser Glu Lys Gln Asp Lys Val Glu						
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acg ttt aga aac ctg ctg ggc tca gat gta gcg cta ttt tta gtt gac						355
Thr Phe Arg Asn Leu Leu Gly Ser Asp Val Ala Leu Phe Leu Val Asp						
	70				80	85
ggt caa aag ctg cat gat tac gcc aat gaa gag gag cgc tat ctt agc						403
Gly Gln Lys Leu His Asp Tyr Ala Asn Glu Glu Glu Arg Tyr Leu Ser						
	90				95	100
tat tta ttt gat gga ttc att gaa aac cta aat cag atc aaa gat gca						451
Tyr Leu Phe Asp Gly Phe Ile Glu Asn Leu Asn Gln Ile Lys Asp Ala						
	105				110	115
atc ctg gag ggt ggg aaa cag ctc caa cag ttc cca cga att tgg gta						499
Ile Leu Glu Gly Gly Lys Gln Leu Gln Gln Phe Pro Arg Ile Trp Val						
	120				125	130
att gct tta tcc aaa gct gat cta tgg cca gat ctc caa gta aaa gat						547
Ile Ala Leu Ser Lys Ala Asp Leu Trp Pro Asp Leu Gln Val Lys Asp						
	135				140	145
ttt gag aat cta ctt aat aag aaa gct ggc aat gaa att att gcg ctg						595
Phe Glu Asn Leu Leu Asn Lys Lys Ala Gly Asn Glu Ile Ile Ala Leu						
	150				155	160
cgt tca aag ctt ttg gag ttt atc gat aac gac gaa gct ttc tcc ttc						643
Arg Ser Lys Leu Leu Glu Phe Ile Asp Asn Asp Glu Ala Phe Ser Phe						
	170				175	180
ggt aaa gat ttc ctt ttg ctc tct tcg gcg aag ttc act cca ggc cat						691
Gly Lys Asp Phe Leu Leu Ser Ser Ala Lys Phe Thr Pro Gly His						
	185				190	195
att gat ata agc cag cgc aag ggt gtt gat gtc ctc ctc ccg ttg gct						739
Ile Asp Ile Ser Gln Arg Lys Gly Val Asp Val Leu Pro Leu Ala						
	200				205	210
tgt gta ttg ccc atg caa cgc cat ttg tgg tgg cag gag ctg aaa gtt						787
Cys Val Leu Pro Met Gln Arg His Leu Trp Trp Gln Glu Leu Lys Val						
	215				220	225
ttg cca att aac ctg gct gat ata ctt ttg gga aat gaa att gcc caa						835
Leu Pro Ile Asn Leu Ala Asp Ile Leu Leu Gly Asn Glu Ile Ala Gln						

230	235	240	245	
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Met Gly Phe Lys Ile Val Ser Lys Val Leu Lys Asn Lys Val Ser Gly	250	255	260	
aca aat aac aag gcg atg gcg gca ttg gtt ttc gct gaa ctt gtg agg				931
Thr Asn Asn Lys Ala Met Ala Ala Leu Val Phe Ala Glu Leu Val Arg	265	270	275	
gat atg gtt gat cag cca act gaa ttg ctt cag aag gct cgt gag gaa				979
Asp Met Val Asp Gln Pro Thr Glu Leu Leu Gln Lys Ala Arg Glu Glu	280	285	290	
gcc gtc gga agg cgt gaa ttc ctt aaa gcg att act gca gaa ttc acc				1027
Ala Val Gly Arg Arg Glu Phe Leu Lys Ala Ile Thr Ala Glu Phe Thr	295	300	305	
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Arg Lys Leu Asn Gln Ala Glu Ala Asp Gln Val Leu Val Arg Asp Phe	310	315	320	325
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Ile Lys Asp Ala Ala Lys Ser Asp Gln Val Asn Leu Thr Trp His Asp	35	40	45	
Tyr Pro Gly Glu Trp Phe Glu Gly Ala Val Thr Asp Ser Glu Lys	50	55	60	
Gln Asp Lys Val Glu Thr Phe Arg Asn Leu Leu Gly Ser Asp Val Ala	65	70	75	80
Leu Phe Leu Val Asp Gly Gln Lys Leu His Asp Tyr Ala Asn Glu Glu	85	90	95	
Glu Arg Tyr Leu Ser Tyr Leu Phe Asp Gly Phe Ile Glu Asn Leu Asn	100	105	110	
Gln Ile Lys Asp Ala Ile Leu Glu Gly Gly Lys Gln Leu Gln Gln Phe	115	120	125	
Pro Arg Ile Trp Val Ile Ala Leu Ser Lys Ala Asp Leu Trp Pro Asp	130	135	140	
Leu Gln Val Lys Asp Phe Glu Asn Leu Leu Asn Lys Lys Ala Gly Asn				

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145              150              155              160
Glu Ile Ile Ala Leu Arg Ser Lys Leu Leu Glu Phe Ile Asp Asn Asp
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Glu Ala Phe Ser Phe Gly Lys Asp Phe Leu Leu Leu Ser Ser Ala Lys
              180              185              190
Phe Thr Pro Gly His Ile Asp Ile Ser Gln Arg Lys Gly Val Asp Val
              195              200              205
Leu Leu Pro Leu Ala Cys Val Leu Pro Met Gln Arg His Leu Trp Trp
              210              215              220
Gln Glu Leu Lys Val Leu Pro Ile Asn Leu Ala Asp Ile Leu Leu Gly
225              230              235              240
Asn Glu Ile Ala Gln Met Gly Phe Lys Ile Val Ser Lys Val Leu Lys
              245              250              255
Asn Lys Val Ser Gly Thr Asn Asn Lys Ala Met Ala Ala Leu Val Phe
              260              265              270
Ala Glu Leu Val Arg Asp Met Val Asp Gln Pro Thr Glu Leu Leu Gln
              275              280              285
Lys Ala Arg Glu Glu Ala Val Gly Arg Arg Glu Phe Leu Lys Ala Ile
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Leu Val Arg Asp Phe Ala
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<213> Corynebacterium glutamicum

<220>
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<222> (101)..(2242)
<223> RXA01554

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              Leu Lys Lys His Val
              1              5
acc tca gcc gtt acc gcc gtg gtg acg gct ttt tca acg gct gcg ctt 163
Thr Ser Ala Val Thr Ala Val Val Thr Ala Phe Ser Thr Ala Ala Leu
              10              15              20
ggt tta agt att gcc gtt tct cct gct gtt gcc caa gtg gct aat cca 211
Gly Leu Ser Ile Ala Val Ser Pro Ala Val Ala Gln Val Ala Asn Pro
              25              30              35

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Ala Pro Asp Leu Ser Ala Pro Tyr Thr Trp Val Glu Phe Asp Ser	
40 45 50	
gag gat gct ctc aaa ggg tgg aac att ttc cgc cag cca gat tat ggc	307
Glu Asp Ala Leu Lys Gly Trp Asn Ile Phe Arg Gln Pro Asp Tyr Gly	
55 60 65	
agc gac aaa gtt ctc tat acc gaa gat gct tta agt atc gaa gat ggc	355
Ser Asp Lys Val Leu Tyr Thr Glu Asp Ala Leu Ser Ile Glu Asp Gly	
70 75 80 85	
aag ctc acc atc acc act cag cgc cac tgc gtt gac gaa gac ttc gcg	403
Lys Leu Thr Ile Thr Thr Gln Arg His Cys Val Asp Glu Asp Phe Ala	
90 95 100	
atc agt gat cct gtc aac cgc gga aag ctc aat gac agc acc gcg caa	451
Ile Ser Asp Pro Val Asn Arg Gly Lys Leu Asn Asp Ser Thr Ala Gln	
105 110 115	
gtt gaa cct tgt gct cca ggt cag ttt gaa aag ttc acc agt gcg cgc	499
Val Glu Pro Cys Ala Pro Gly Gln Phe Glu Lys Phe Thr Ser Ala Arg	
120 125 130	
atc gtc act ccg aaa att gct cgt gga gag ttc gac ctt tct gtc act	547
Ile Val Thr Pro Lys Ile Ala Arg Gly Glu Phe Asp Leu Ser Val Thr	
135 140 145	
gca act ctt aac acc ggt ggc gtc gaa ggt gtc cga agt gcc att tgg	595
Ala Thr Leu Asn Thr Gly Gly Val Glu Gly Val Arg Ser Ala Ile Trp	
150 155 160 165	
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Met Gln Asn Gly Glu Gln Ala Cys Ser Ser Ala Thr Asn Asn Gly Leu	
170 175 180	
tac gga gaa cta gac ctg gta gag cac ttt tct tac gat ctt gcg tcg	691
Tyr Gly Glu Leu Asp Leu Val Glu His Phe Ser Tyr Asp Leu Arg Ser	
185 190 195	
cca tgg tct cca tca aac acc cac ttg ggt tgt gat cct gaa agt gtc	739
Pro Trp Ser Pro Ser Asn Thr His Leu Gly Cys Asp Pro Glu Ser Val	
200 205 210	
aac ggc acc aac cgt gca cct cgt gaa ctt aaa cta gat gag tca ctc	787
Asn Gly Thr Asn Arg Ala Pro Arg Glu Leu Lys Leu Asp Glu Ser Leu	
215 220 225	
gat ggc gtg gag cac acc tgg act gtg agc acc acc cgc gac ggc gtt	835
Asp Gly Val Glu His Thr Trp Thr Val Ser Thr Thr Arg Asp Gly Val	
230 235 240 245	
gag tac ttc att gat gat gag gcg att aac cgc cag tca tgg cgc aac	883
Glu Tyr Phe Ile Asp Asp Glu Ala Ile Asn Arg Gln Ser Trp Arg Asn	
250 255 260	
gat gtc act ttg ggg cat gcc gaa att gat gat ttc ggg atc tcc gcg	931
Asp Val Thr Leu Gly His Ala Glu Ile Asp Asp Phe Gly Ile Ser Ala	
265 270 275	
cag acg ttt gat gag atc gtc gac cgc gaa tgg act ctc act ctt aat	979

Gln Thr Phe Asp Glu Ile Val Asp Arg Glu Trp Thr Leu Thr Leu Asn	
280 285 290	
caa aag gta gaa agc gcc gac tgg gca aaa cca cgt tcc tct gag gaa	1027
Gln Lys Val Glu Ser Ala Asp Trp Ala Lys Pro Arg Ser Ser Glu Glu	
295 300 305	
gat ttc cca gtc cgg tcc atg gtg att gac cgc atc gag gtc acc gga	1075
Asp Phe Pro Val Arg Ser Met Val Ile Asp Arg Ile Glu Val Thr Gly	
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tct ccc gca gta tct gaa gac acc ccc atg cca gat acc acc cag ctt	1123
Ser Pro Ala Val Ser Glu Asp Thr Pro Met Pro Asp Thr Thr Gln Leu	
330 335 340	
ttg acc caa gac act ctg gaa tac ctc ggt cgc atg cca gtg ctg gaa	1171
Leu Thr Gln Asp Thr Leu Glu Tyr Leu Gly Arg Met Pro Val Leu Glu	
345 350 355	
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Arg Tyr Glu Pro Ala Ser Ala Asp Phe Ala Asp Gly Arg Pro Ser	
360 365 370	
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Trp Asn Tyr Phe Asn Leu Lys Glu Ser Trp Gln Asn Pro Glu Leu Glu	
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Thr Arg Arg His Cys Leu Ala Thr Thr Asp Ile Ala Thr Pro Glu	
410 415 420	
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Asn Ala Gln Glu Glu Pro Cys Ala Pro Gly Glu Val Thr Arg Tyr Ser	
425 430 435	
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Thr Val Arg Ala Arg Ala Gln Ser Glu Glu Leu Val Asp Gly Val Arg	
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Pro Ala Ile Trp Met Gln Asn Asn Thr Asn Phe Cys Ala Asp Asn Asp	
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Gly Arg Pro Tyr Gly Glu Leu Asp Ile Thr Glu Phe Tyr Ser Ser Arg	
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gtg aac acc cag tac tcg gca gta cac ctt gga tgt gct ggc aac cgc	1651
Val Asn Thr Gln Tyr Ser Ala Val His Leu Gly Cys Ala Gly Asn Arg	
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cca gag atg aag ctt cgc caa atg gaa atg gaa gag tcc atg ttt ggg	1699
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585	590	595	
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gcg gtc gac aat aac gag gcg ttc cca gaa cac cgc ttc caa att gac			1987
Ala Val Asp Asn Asn Glu Ala Phe Pro Glu His Arg Phe Gln Ile Asp			
615	620	625	
cat gtg gca gta gat atc gag tct gac tct gtg gac aat gta tgg cct			2035
His Val Ala Val Asp Ile Glu Ser Asp Ser Val Asp Asn Val Trp Pro			
630	635	640	645
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Asp Ala Ala Asn Glu Ile Pro Asp Asn Val Gly Ile Glu Asp Ser Asp			
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gat ggc agc gac ctg gag gtt ggt tcg acc gga agc tct aca gct gag			2131
Asp Gly Ser Asp Leu Glu Val Gly Ser Thr Gly Ser Ser Thr Ala Glu			
665	670	675	
acc gtg agc tgg atc tcg ttg ttc acc gcg ttg agc tcg ctg gtc ttc			2179
Thr Val Ser Trp Ile Ser Leu Phe Thr Ala Leu Ser Ser Leu Val Phe			
680	685	690	
aca ctg gct ctc aat caa gaa gca ttg cag aat ttg att aat cag ttc			2227
Thr Leu Ala Leu Asn Gln Glu Ala Leu Gln Asn Leu Ile Asn Gln Phe			
695	700	705	
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710			

<210> 2310

<211> 714

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2310

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20										25					30				
Gln	Val	Ala	Asn	Pro	Ala	Pro	Asp	Leu	Ser	Ala	Pro	Tyr	Thr	Trp	Val				
		35					40					45							
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		50					55					60							
Gln	Pro	Asp	Tyr	Gly	Ser	Asp	Lys	Val	Leu	Tyr	Thr	Glu	Asp	Ala	Leu				
		65					70					75							
Ser	Ile	Glu	Asp	Gly	Lys	Leu	Thr	Ile	Thr	Thr	Gln	Arg	His	Cys	Val				
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Asp	Glu	Asp	Phe	Ala	Ile	Ser	Asp	Pro	Val	Asn	Arg	Gly	Lys	Leu	Asn				
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Asp	Ser	Thr	Ala	Gln	Val	Glu	Pro	Cys	Ala	Pro	Gly	Gln	Phe	Glu	Lys				
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Phe	Thr	Ser	Ala	Arg	Ile	Val	Thr	Pro	Lys	Ile	Ala	Arg	Gly	Glu	Phe				
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Asp	Leu	Ser	Val	Thr	Ala	Thr	Leu	Asn	Thr	Gly	Gly	Val	Glu	Gly	Val				
						145					150								
Arg	Ser	Ala	Ile	Trp	Met	Gln	Asn	Gly	Glu	Gln	Ala	Cys	Ser	Ser	Ala				
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Thr	Asn	Asn	Gly	Leu	Tyr	Gly	Glu	Leu	Asp	Leu	Val	Glu	His	Phe	Ser				
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Tyr	Asp	Leu	Arg	Ser	Pro	Trp	Ser	Pro	Ser	Asn	Thr	His	Leu	Gly	Cys				
						195					200								
Asp	Pro	Glu	Ser	Val	Asn	Gly	Thr	Asn	Arg	Ala	Pro	Arg	Glu	Leu	Lys				
						210					215								
Leu	Asp	Glu	Ser	Leu	Asp	Gly	Val	Glu	His	Thr	Trp	Thr	Val	Ser	Thr				
						225					230								
Thr	Arg	Asp	Gly	Val	Glu	Tyr	Phe	Ile	Asp	Asp	Glu	Ala	Ile	Asn	Arg				
						245					250								
Gln	Ser	Trp	Arg	Asn	Asp	Val	Thr	Leu	Gly	His	Ala	Glu	Ile	Asp	Asp				
						260					265								
Phe	Gly	Ile	Ser	Ala	Gln	Thr	Phe	Asp	Glu	Ile	Val	Asp	Arg	Glu	Trp				
						275					280								
Thr	Leu	Thr	Leu	Asn	Gln	Lys	Val	Glu	Ser	Ala	Asp	Trp	Ala	Lys	Pro				
						290					295								
Arg	Ser	Ser	Glu	Glu	Asp	Phe	Pro	Val	Arg	Ser	Met	Val	Ile	Asp	Arg				
						305					310								
Ile	Glu	Val	Thr	Gly	Ser	Pro	Ala	Val	Ser	Glu	Asp	Thr	Pro	Met	Pro				
						325					330								
Asp	Thr	Thr	Gln	Leu	Leu	Thr	Gln	Asp	Thr	Leu	Glu	Tyr	Leu	Gly	Arg				
						340					345								

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Met Pro Val Leu Glu Arg Tyr Glu Pro Ala Ser Ala Asp Phe Ala Asp
   355                               360                               365

Gly Arg Arg Pro Ser Trp Asn Tyr Phe Asn Leu Lys Glu Ser Trp Gln
   370                               375                               380

Asn Pro Glu Leu Glu Gln Arg Pro Glu Ala Val Glu Phe Val Asp Gly
   385                               390                               395                               400

Arg Met Asp Ile Val Thr Arg Arg His Cys Leu Ala Thr Thr Asp Asp
                   405                               410                               415

Ile Ala Thr Pro Glu Asn Ala Gln Glu Glu Pro Cys Ala Pro Gly Glu
   420                               425                               430

Val Thr Arg Tyr Ser Ser Ala Arg Val His Leu Pro Glu Ile Pro Ala
   435                               440                               445

Gly Asn Phe Arg Leu Thr Val Arg Ala Arg Ala Gln Ser Glu Glu Leu
   450                               455                               460

Val Asp Gly Val Arg Pro Ala Ile Trp Met Gln Asn Asn Thr Asn Phe
   465                               470                               475                               480

Cys Ala Asp Asn Asp Gly Arg Pro Tyr Gly Glu Leu Asp Ile Thr Glu
                   485                               490                               495

Phe Tyr Ser Ser Arg Val Asn Thr Gln Tyr Ser Ala Val His Leu Gly
                   500                               505                               510

Cys Ala Gly Asn Arg Pro Glu Met Lys Leu Arg Gln Met Glu Met Glu
   515                               520                               525

Glu Ser Met Phe Gly Asp Trp His Asp Trp Gly Val Glu Val Phe Asp
   530                               535                               540

Gly Gln Ile Val Phe Thr Ile Asp Gly Lys Ala Val Thr Ser Ser Gly
   545                               550                               555                               560

Lys Asp Val Phe Gly Asn Ser Val Thr Pro Ala Ala Ala Pro Leu Arg
                   565                               570                               575

Pro Ala His Phe Lys Leu Ser Glu Glu Glu Tyr Arg Glu Val Ile Gly
   580                               585                               590

Gln Pro Trp His Leu Ile Leu Asn Thr Met Val Glu Gln Ser Gly Lys
   595                               600                               605

Asp Ser Trp Ile Thr Ala Val Asp Asn Asn Glu Ala Phe Pro Glu His
   610                               615                               620

Arg Phe Gln Ile Asp His Val Ala Val Asp Ile Glu Ser Asp Ser Val
   625                               630                               635                               640

Asp Asn Val Trp Pro Asp Ala Ala Asn Glu Ile Pro Asp Asn Val Gly
                   645                               650                               655

Ile Glu Asp Ser Asp Asp Gly Ser Asp Leu Glu Val Gly Ser Thr Gly
   660                               665                               670

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Ser Ser Thr Ala Glu Thr Val Ser Trp Ile Ser Leu Phe Thr Ala Leu
675 680 685

Ser Ser Leu Val Phe Thr Leu Ala Leu Asn Gln Glu Ala Leu Gln Asn
690 695 700

Leu Ile Asn Gln Phe Met Arg Gln Phe Lys
705 710

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<211> 453
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(430)
<223> RXA01560

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tgcatcagta agcgatgcgt tttaggcaca tctgcgatcc gtg ggc gtg tcc tac 115
Val Gly Val Ser Tyr
1 5

atc atc gcc ggc gat gag cag ctg gat atg gca gaa gcc gtt cgc aaa 163
Ile Ile Ala Gly Asp Glu Gln Leu Asp Met Ala Glu Ala Val Arg Lys
10 15 20

att ggg gag acc ttt aaa act gag gaa att atc ctt ggt ggc gga gga 211
Ile Gly Glu Thr Phe Lys Thr Glu Glu Ile Ile Leu Gly Gly Gly Gly
25 30 35

acc ctg aac tgg tcc atg ctc cgc gac ggt ttg tgc gac gag gtt agc 259
Thr Leu Asn Trp Ser Met Leu Arg Asp Gly Leu Cys Asp Glu Val Ser
40 45 50

atc gtg atg atg cca atc gcc gat ggt gaa aag cac acc cac tct ttg 307
Ile Val Met Met Pro Ile Ala Asp Gly Glu Lys His Thr His Ser Leu
55 60 65

ttc gaa gcc gat gaa aaa tac tca gca ccg ttg ccg atc ggt ttt tca 355
Phe Glu Ala Asp Glu Lys Tyr Ser Ala Pro Leu Pro Ile Gly Phe Ser
70 75 80 85

ctc gcc agc gtt gaa cca cta gaa gat gga agc gtt tgg atg cgt tac 403
Leu Ala Ser Val Glu Pro Leu Glu Asp Gly Ser Val Trp Met Arg Tyr
90 95 100

ggg gtc aat ggc cca gtg gac gcg aac taggtagcaa atactcgctc 450
Gly Val Asn Gly Pro Val Asp Ala Asn
105 110

ttt 453

<210> 2312
<211> 110
<212> PRT

<213> Corynebacterium glutamicum

<400> 2312

Val Gly Val Ser Tyr Ile Ile Ala Gly Asp Glu Gln Leu Asp Met Ala
 1 5 10 15

Glu Ala Val Arg Lys Ile Gly Glu Thr Phe Lys Thr Glu Glu Ile Ile
 20 25 30

Leu Gly Gly Gly Gly Thr Leu Asn Trp Ser Met Leu Arg Asp Gly Leu
 35 40 45

Cys Asp Glu Val Ser Ile Val Met Met Pro Ile Ala Asp Gly Glu Lys
 50 55 60

His Thr His Ser Leu Phe Glu Ala Asp Glu Lys Tyr Ser Ala Pro Leu
 65 70 75 80

Pro Ile Gly Phe Ser Leu Ala Ser Val Glu Pro Leu Glu Asp Gly Ser
 85 90 95

Val Trp Met Arg Tyr Gly Val Asn Gly Pro Val Asp Ala Asn
 100 105 110

<210> 2313

<211> 1143

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1120)

<223> RXA01575

<400> 2313

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gttaggtgcc accgacccca gtgatgataa cttgattgtc atg aaa tcc att gat 115
 Met Lys Ser Ile Asp
 1 5

ctt gag cag ctg gcg ggc acg caa tcg cgc acg tat caa tcg cga aag 163
 Leu Glu Gln Leu Ala Gly Thr Gln Ser Arg Thr Tyr Gln Ser Arg Lys
 10 15 20

atc acc gat gag atg gtc gcc cgg ccg gtg cat gtg gcg atc gcg ctg 211
 Ile Thr Asp Glu Met Val Ala Arg Pro Val His Val Ala Ile Ala Leu
 25 30 35

tgg gaa gtg ccg tgg gag tcg gca aaa tcc ggc aag att gag ggt tgg 259
 Trp Glu Val Pro Trp Glu Ser Ala Lys Ser Gly Lys Ile Glu Gly Trp
 40 45 50

gtc att gcc gtg gat tcg ccg cgt ggg cgg ttt gtg cgc agc ggg cag 307
 Val Ile Ala Val Asp Ser Pro Arg Gly Arg Phe Val Arg Ser Gly Gln
 55 60 65

acc aaa aat ggc gac gcc gtc aac cgg act gtg tcg atg ctg aaa tca 355
 Thr Lys Asn Gly Asp Ala Val Asn Arg Thr Val Ser Met Leu Lys Ser
 70 75 80 85

gcg ttg aaa ggg gtc cgc ggg aag gcg tgg att gta act ggg cgt cga	403
Ala Leu Lys Gly Val Arg Gly Lys Ala Trp Ile Val Thr Gly Arg Arg	
90 95 100	
caa gca gct tta cgc gca gcc ctg gtg cgc gaa aac tac ctg gtc acc	451
Gln Ala Ala Leu Arg Ala Ala Leu Val Arg Glu Asn Tyr Leu Val Thr	
105 110 115	
gga agc ttc gcc gag caa aat agg gcc ggc gtg aag gcg tgg gcg atc	499
Gly Ser Phe Ala Glu Gln Asn Arg Ala Gly Val Lys Ala Ser Ala Ile	
120 125 130	
tcg cgc cgc gcc gaa caa tcc gcg ctc tac aag gcg aaa aaa atc ggc	547
Ser Arg Arg Ala Glu Gln Ser Ala Leu Tyr Lys Ala Lys Lys Ile Gly	
135 140 145	
gaa ttc gcc gag cgc gcc cca cgc gtc aaa gag cgg caa gag gca cat	595
Glu Phe Ala Glu Arg Ala Pro Arg Val Lys Glu Arg Gln Glu Ala His	
150 155 160 165	
tgg tgg cca cgg ttg tca cgc acg caa ggc acc gca ggc gtt tta cgc	643
Trp Trp Pro Arg Leu Ser Arg Thr Gln Gly Thr Ala Gly Val Leu Arg	
170 175 180	
tta gcg acg gac gcc tct acc gat ggg gtc ttc cgc ggc gcc atg tgc	691
Leu Ala Thr Asp Ala Ser Thr Asp Gly Val Phe Arg Gly Ala Met Cys	
185 190 195	
ttc gta gcc tca aac ggc gac tac ctc ctg gag acc caa gac acc acc	739
Phe Val Ala Ser Asn Gly Asp Tyr Leu Leu Glu Thr Gln Asp Thr Thr	
200 205 210	
gca agc tcc gac gaa tta gaa ctc gaa agc atc acc cac gcc ctg atc	787
Ala Ser Ser Asp Glu Leu Glu Leu Glu Ser Ile Thr His Ala Leu Ile	
215 220 225	
tac ctc aaa acc atc ggc gcg acc caa gcc atc atc gaa tcc gac agc	835
Tyr Leu Lys Thr Ile Gly Ala Thr Gln Ala Ile Ile Glu Ser Asp Ser	
230 235 240 245	
aaa gcc gca ctt gaa gcc atc gac ttc atc ctc aac aac cga ccg cgc	883
Lys Ala Ala Leu Glu Ala Ile Asp Phe Ile Leu Asn Asn Arg Pro Arg	
250 255 260	
cgg ggc agg tgg cgc ggc atc acc gca tgc gcc cgc aac cgg ttc cgg	931
Arg Gly Arg Trp Arg Gly Ile Thr Ala Cys Ala Arg Asn Arg Phe Arg	
265 270 275	
gat gcc tgg gaa gcg ctt atc gac gac tgc gtt gtg gaa tta tcc cgc	979
Asp Ala Trp Glu Ala Leu Ile Asp Asp Cys Val Val Glu Leu Ser Arg	
280 285 290	
gta cta ggg cac gcc ggg gat cca ctg aac caa gca gcc gac caa atc	1027
Val Leu Gly His Ala Gly Asp Pro Leu Asn Gln Ala Ala Asp Gln Ile	
295 300 305	
gca tac atg ggc atg cgc gcc gta att ttt gaa caa aaa tcc gca cac	1075
Ala Tyr Met Gly Met Arg Ala Val Ile Phe Glu Gln Lys Ser Ala His	
310 315 320 325	

ccc aca ttg ctc aaa gga att gac aag gcg ctt cgc aag gcc gag 1120
 Pro Thr Leu Leu Lys Gly Ile Asp Lys Ala Leu Arg Lys Ala Glu
 330 335 340

taagggtgggc aacgagtcgg tga 1143

<210> 2314

<211> 340

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2314

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Tyr Gln Ser Arg Lys Ile Thr Asp Glu Met Val Ala Arg Pro Val His
 20 25 30

Val Ala Ile Ala Leu Trp Glu Val Pro Trp Glu Ser Ala Lys Ser Gly
 35 40 45

Lys Ile Glu Gly Trp Val Ile Ala Val Asp Ser Pro Arg Gly Arg Phe
 50 55 60

Val Arg Ser Gly Gln Thr Lys Asn Gly Asp Ala Val Asn Arg Thr Val
 65 70 75 80

Ser Met Leu Lys Ser Ala Leu Lys Gly Val Arg Gly Lys Ala Trp Ile
 85 90 95

Val Thr Gly Arg Gln Ala Ala Leu Arg Ala Ala Leu Val Arg Glu
 100 105 110

Asn Tyr Leu Val Thr Gly Ser Phe Ala Glu Gln Asn Arg Ala Gly Val
 115 120 125

Lys Ala Ser Ala Ile Ser Arg Arg Ala Glu Gln Ser Ala Leu Tyr Lys
 130 135 140

Ala Lys Lys Ile Gly Glu Phe Ala Glu Arg Ala Pro Arg Val Lys Glu
 145 150 155 160

Arg Gln Glu Ala His Trp Trp Pro Arg Leu Ser Arg Thr Gln Gly Thr
 165 170 175

Ala Gly Val Leu Arg Leu Ala Thr Asp Ala Ser Thr Asp Gly Val Phe
 180 185 190

Arg Gly Ala Met Cys Phe Val Ala Ser Asn Gly Asp Tyr Leu Leu Glu
 195 200 205

Thr Gln Asp Thr Thr Ala Ser Ser Asp Glu Leu Glu Leu Glu Ser Ile
 210 215 220

Thr His Ala Leu Ile Tyr Leu Lys Thr Ile Gly Ala Thr Gln Ala Ile
 225 230 235 240

Ile Glu Ser Asp Ser Lys Ala Ala Leu Glu Ala Ile Asp Phe Ile Leu
 245 250 255

Asn Asn Arg Pro Arg Arg Gly Arg Trp Arg Gly Ile Thr Ala Cys Ala
 260 265 270
 Arg Asn Arg Phe Arg Asp Ala Trp Glu Ala Leu Ile Asp Asp Cys Val
 275 280 285
 Val Glu Leu Ser Arg Val Leu Gly His Ala Gly Asp Pro Leu Asn Gln
 290 295 300
 Ala Ala Asp Gln Ile Ala Tyr Met Gly Met Arg Ala Val Ile Phe Glu
 305 310 315
 Gln Lys Ser Ala His Pro Thr Leu Leu Lys Gly Ile Asp Lys Ala Leu
 325 330 335
 Arg Lys Ala Glu
 340

<210> 2315

<211> 498

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(475)

<223> RKA01577

<400> 2315

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taaacatcct ggccgacggc ttcctagcga ggagactccc atg acg cag acc acc 115
 Met Thr Gln Thr Thr
 1 5

acc caa atc atc atc cag ata ctg ctt ctc ctg gca acc gca gca ctg 163
 Thr Gln Ile Ile Ile Gln Ile Leu Leu Leu Leu Ala Thr Ala Ala Leu
 10 15 20

gca cta tat ttc ctc cga aac cgc cgc aaa gcc cgc gcc aaa gca tgg 211
 Ala Leu Tyr Phe Leu Arg Asn Arg Arg Lys Ala Arg Ala Lys Ala Trp
 25 30 35

gtg aaa atc ggc ttc gta gta ttc att ttc gcc gca gta tgg gca gtg 259
 Val Lys Ile Gly Phe Val Val Phe Ile Phe Ala Ala Val Trp Ala Val
 40 45 50

ctc cgc ccc gat gac ctc acc caa cta gcc aac ttt gtg ggc gtg gac 307
 Leu Arg Pro Asp Asp Leu Thr Gln Leu Ala Asn Phe Val Gly Val Asp
 55 60 65

cgc ggc acc gac cta atg ctt tac gcc ctg gtt gtg gca ttt atg ttc 355
 Arg Gly Thr Asp Leu Met Leu Tyr Ala Leu Val Val Ala Phe Met Phe
 70 75 80 85

acc acg ctg tcc agt tat gtg cgt ttc cgt gaa caa gag ctg cgt tat 403
 Thr Thr Leu Ser Ser Tyr Val Arg Phe Arg Glu Gln Glu Leu Arg Tyr
 90 95 100

tcc aag. ctg gcc cgc gct gtc gct ttg caa aat gtg gtg ctg ccg gag 451

Ser Lys Leu Ala Arg Ala Val Ala Leu Gln Asn Val Val Leu Pro Glu
 105 110 115
 gat tcc cag ggt tct gac ccc gct taggaaagcg cttggcctct gga 498
 Asp Ser Gln Gly Ser Asp Pro Ala
 120 125

<210> 2316
 <211> 125
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2316
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 1 5 10 15
 Ala Thr Ala Ala Leu Ala Leu Tyr Phe Leu Arg Asn Arg Arg Lys Ala
 20 25 30
 Arg Ala Lys Ala Trp Val Lys Ile Gly Phe Val Val Phe Ile Phe Ala
 35 40 45
 Ala Val Trp Ala Val Leu Arg Pro Asp Asp Leu Thr Gln Leu Ala Asn
 50 55 60
 Phe Val Gly Val Asp Arg Gly Thr Asp Leu Met Leu Tyr Ala Leu Val
 65 70 75 80
 Val Ala Phe Met Phe Thr Thr Leu Ser Ser Tyr Val Arg Phe Arg Glu
 85 90 95
 Gln Glu Leu Arg Tyr Ser Lys Leu Ala Arg Ala Val Ala Leu Gln Asn
 100 105 110
 Val Val Leu Pro Glu Asp Ser Gln Gly Ser Asp Pro Ala
 115 120 125

<210> 2317
 <211> 507
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(484)
 <223> RXA01579

<400> 2317
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 ttgtgagaag ggtgctcagc agcaatgccc aggtgcgtcg ttg acc gag gta ttc 115
 Leu Thr Glu Val Phe
 1 5
 aac act gac cag cgg gtg ctt aac gcg ctt ttc aat gtt gta gaa gaa 163
 Asn Thr Asp Gln Arg Val Leu Asn Ala Leu Phe Asn Val Val Glu Glu
 10 15 20
 gat gac tcc ggc gat acc gat gat gaa cag cac aac cac cag aat cca 211

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Asp Asp Ser Gly Asp Thr Asp Asp Glu Gln His Asn His Gln Asn Pro
      25                      30                      35
gtt cgc ggc acc gag ttt gcc ggc ctc gtt gaa agc cat gag caa aga 259
Val Arg Gly Thr Glu Phe Ala Gly Leu Val Glu Ser His Glu Gln Arg
      40                      45                      50

tcc aat gga cac cgc cag tgg cag cac acc aag cca gtc cat ctt egg 307
Ser Asn Gly His Arg Gln Trp Gln His Thr Lys Pro Val His Leu Arg
      55                      60                      65

ggt ttc ttc agc ggt gga ttc ctt cac gct gaa agg cag tgc gag ggc 355
Gly Phe Phe Ser Gly Gly Phe Leu His Ala Glu Arg Gln Cys Glu Gly
      70                      75                      80                      85

agc gac agc gca gaa agc agc cat gac cca gaa gat gga acg gaa acc 403
Ser Asp Ser Ala Glu Ser Ser His Asp Pro Glu Asp Gly Thr Glu Thr
      90                      95                      100

aag tgt ttc agc caa cca gcc acc agc aag cgc gtc cac gcc gcc gat 451
Lys Cys Phe Ser Gln Pro Ala Thr Ser Lys Arg Val His Ala Ala Asp
      105                      110                      115

acc acc gtt gac aga ggt aac aat tcc gag aag tagcgcatat tgcttttcat 504
Thr Thr Val Asp Arg Gly Asn Asn Ser Glu Lys
      120                      125

tgg
800 507

<210> 2318
<211> 128
<212> PRT
<213> Corynebacterium glutamicum

<400> 2318
Leu Thr Glu Val Phe Asn Thr Asp Gln Arg Val Leu Asn Ala Leu Phe
  1                      5                      10                      15

Asn Val Val Glu Glu Asp Asp Ser Gly Asp Thr Asp Asp Glu Gln His
      20                      25                      30

Asn His Gln Asn Pro Val Arg Gly Thr Glu Phe Ala Gly Leu Val Glu
      35                      40                      45

Ser His Glu Gln Arg Ser Asn Gly His Arg Gln Trp Gln His Thr Lys
      50                      55                      60

Pro Val His Leu Arg Gly Phe Phe Ser Gly Gly Phe Leu His Ala Glu
      65                      70                      75                      80

Arg Gln Cys Glu Gly Ser Asp Ser Ala Glu Ser Ser His Asp Pro Glu
      85                      90                      95

Asp Gly Thr Glu Thr Lys Cys Phe Ser Gln Pro Ala Thr Ser Lys Arg
      100                      105                      110

Val His Ala Ala Asp Thr Thr Val Asp Arg Gly Asn Asn Ser Glu Lys
      115                      120                      125

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<210> 2319
<211> 750
<212> DNA
<213> *Corynebacterium glutamicum*

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<221> CDS
<222> (101)..(727)
<223> RXA01585
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ctactgatga ggtgcagtcg caggaagctc tagaaaagta gtg gtt gag act ctt 115																						
																	Val	Val	Glu	Thr	Leu	5
tct	atc	acc	tca	ggt	gcg	gct	ggc	ctg	gln	cgc	ctt	gtt	gcg	cgt	gcg							163
Ser	Ile	Thr	Ser	10	Ala	Ala	Gly	Leu	15	Ala	Leu	Val	Ala	Arg	Ala							20
ggt	ggt	ttg	aat	gag	ttg	gcg	agc	gcg	cgt	ttc	cgc	cag	ctc	acg	cca							211
Val	Gly	Leu	Asn	25	Glu	Leu	Ala	Ser	30	Ala	Arg	Phe	Arg	Gln	Leu	Thr	Pro					35
gag	gtc	ggt	gat	ggt	ttt	gtc	acc	act	cgc	ttc	aac	gtg	acg	gcg	tcg							259
Glu	Val	Val	Asp	40	Val	Phe	Val	Thr	45	Thr	Pro	Phe	Asn	Val	Thr	Ala	Ser					50
cgc	cgg	gta	ttt	ggt	gtg	gcg	ggt	cgc	gat	ggc	gct	gca	ggt	ggc	gcg							307
Arg	Arg	Val	Phe	55	Gly	Val	Ala	Gly	60	Arg	Asp	Gly	Ala	Ala	Val	Gly	Ala					65
aag	gat	ttg	ctg	cag	gca	ctc	agc	gag	ggc	cgg	gaa	gac	gta	ggc	acc							355
Lys	Asp	Leu	Leu	75	Gln	Ala	Leu	Ser	80	Glu	Gly	Arg	Glu	Asp	Val	Gly	Thr					85
tcc	cgc	gac	gcc	agc	tgg	cgc	ggc	tca	ttg	cgc	cca	gcc	acg	ggc	ttt							403
Ser	Arg	Asp	Ala	90	Ser	Trp	Pro	Gly	Ser	95	Pro	Pro	Ala	Thr	Gly	Phe					100	
acg	ctt	gtc	gac	gaa	ctc	ccc	acc	cac	gtg	gtg	cgc	act	ttg	gct	gat							451
Thr	Thr	Val	Asp	105	Glu	Leu	Pro	Thr	110	Val	Val	Arg	Thr	Leu	Ala	Asp					115	
cag	ggt	cag	gca	ttg	gct	cgc	cag	ttc	tcc	ggc	cgc	ctt	ggc	cct	cgc							499
Gln	Gly	Gln	Ala	120	Leu	Ala	Arg	Gln	125	Phe	Ser	Gly	Pro	Gly	Pro					130		
gct	tcg	ttg	atg	gat	cag	gaa	gtt	att	tca	gca	gaa	ggc	aat	ggc	aag							547
Ala	Ser	Leu	Met	Asp	Gln	Glu	Val	Ile	Ser	Ala	Glu	Gly	Asn	Gly	Lys					145		
aag	gcc	gga	atc	cgc	atg	cgc	acg	gta	ttt	acc	tgc	act	tcg	ctt	ggt							595
Lys	Ala	Gly	Ile	Pro	Met	Arg	Thr	Val	Phe	Thr	Cys	Thr	Ser	Leu	Gly					165		
ttg	atc	cca	ggt	ttt	gag	gca	gcc	aat	gat	gtg	ccg	agg	cac	ctg	cgg							643

Leu Ile Pro Gly Phe Glu Ala Ala Asn Asp Val Pro Arg His Leu Arg
 170 175 180
 gta tcg gtg aat ggt cgt tgg acc cgc gtt gat gct ccc tat ggc agt 691
 Val Ser Val Asn Gly Arg Trp Thr Arg Val Asp Ala Pro Tyr Gly Ser
 185 190 195
 gtt tat cac tcg tca ggt ttg ggt ctg agc gtt ttc taaagcaaga 737
 Val Tyr His Ser Ser Gly Leu Gly Leu Ser Val Phe
 200 205
 cccagcctgc aag 750

<210> 2320

<211> 209

<212> PRT

<213> Corynebacterium glutamicum

<400> 2320

Val Val Glu Thr Leu Ser Ile Thr Ser Gly Ala Ala Gly Leu Gln Ala
 1 5 10 15
 Leu Val Ala Arg Ala Val Gly Leu Asn Glu Leu Ala Ser Ala Arg Phe
 20 25 30
 Arg Gln Leu Thr Pro Glu Val Val Asp Val Phe Val Thr Thr Pro Phe
 35 40 45
 Asn Val Thr Ala Ser Arg Arg Val Phe Gly Val Ala Gly Arg Asp Gly
 50 55 60
 Ala Ala Val Gly Ala Lys Asp Leu Leu Gln Ala Leu Ser Glu Gly Arg
 65 70 75 80
 Glu Asp Val Gly Thr Ser Arg Asp Ala Ser Trp Pro Gly Ser Leu Pro
 85 90 95
 Pro Ala Thr Gly Phe Thr Leu Val Asp Glu Leu Pro Thr His Val Val
 100 105 110
 Arg Thr Leu Ala Asp Gln Gly Gln Ala Leu Ala Arg Gln Phe Ser Gly
 115 120 125
 Pro Leu Gly Pro Pro Ala Ser Leu Met Asp Gln Glu Val Ile Ser Ala
 130 135 140
 Glu Gly Asn Gly Lys Lys Ala Gly Ile Pro Met Arg Thr Val Phe Thr
 145 150 155 160
 Cys Thr Ser Leu Gly Leu Ile Pro Gly Phe Glu Ala Ala Asn Asp Val
 165 170 175
 Pro Arg His Leu Arg Val Ser Val Asn Gly Arg Trp Thr Arg Val Asp
 180 185 190
 Ala Pro Tyr Gly Ser Val Tyr His Ser Ser Gly Leu Gly Leu Ser Val
 195 200 205

Phe

<210> 2321
 <211> 392
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (1)..(369)
 <223> RXA01586

<400> 2321
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 Asn Asn Ala Ala Phe Ile Glu Ile Ala Gln Glu Ala Arg Leu Ala Phe
 1 5 10 15
 gcg gag gat cag ttc cgt gag cgt ggc tat gag atc cct gct gtg ttt 96
 Ala Glu Asp Gln Phe Arg Glu Arg Gly Tyr Glu Ile Pro Ala Val Phe
 20 25 30
 gtg cgc cac ttg gaa gtt gat tat ttg cgt gcg atc ttg ccg gat acc 144
 Val Arg His Leu Glu Val Asp Tyr Leu Arg Ala Ile Leu Pro Asp Thr
 35 40 45
 acc cag gct gtc gtg gag aca cag gtg acc aag atc ggt aat act tcc 192
 Thr Gln Ala Val Val Glu Thr Gln Val Thr Lys Ile Gly Asn Thr Ser
 50 55 60
 ttc agc act cgt caa gag gtc aag gat cgt aac ggt cgt gtg tgc tgc 240
 Phe Ser Thr Arg Gln Glu Val Lys Asp Arg Asn Gly Arg Val Cys Cys
 65 70 75 80
 gtg gtt gag tgc gtg cag gtg gct gtc aat gtg cag act gct gcg ccc 288
 Val Val Glu Cys Val Gln Val Ala Val Asn Val Gln Thr Ala Ala Pro
 85 90 95
 cgt tcc atc agc aag gtg gag cgc aag gtg ctg acc gct gtc gct act 336
 Arg Ser Ile Ser Lys Val Glu Arg Lys Val Leu Thr Ala Val Ala Thr
 100 105 110
 gat gag gtg cag tgc cag gaa gct cta gaa aag tagtgggtga gactctttct 389
 Asp Glu Val Gln Ser Gln Glu Ala Leu Glu Lys
 115 120
 atc 392

<210> 2322
 <211> 123
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 2322
 Asn Asn Ala Ala Phe Ile Glu Ile Ala Gln Glu Ala Arg Leu Ala Phe
 1 5 10 15
 Ala Glu Asp Gln Phe Arg Glu Arg Gly Tyr Glu Ile Pro Ala Val Phe
 20 25 30
 Val Arg His Leu Glu Val Asp Tyr Leu Arg Ala Ile Leu Pro Asp Thr

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35              40              45

Thr  Gln  Ala  Val  Val  Glu  Thr  Gln  Val  Thr  Lys  Ile  Gly  Asn  Thr  Ser
50              55              60

Phe  Ser  Thr  Arg  Gln  Glu  Val  Lys  Asp  Arg  Asn  Gly  Arg  Val  Cys  Cys
65              70              75              80

Val  Val  Glu  Cys  Val  Gln  Val  Ala  Val  Asn  Val  Gln  Thr  Ala  Ala  Pro
85              90              95

Arg  Ser  Ile  Ser  Lys  Val  Glu  Arg  Lys  Val  Leu  Thr  Ala  Val  Ala  Thr
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Asp  Glu  Val  Gln  Ser  Gln  Glu  Ala  Leu  Glu  Lys
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<223> RXA01595

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Met Thr Ala Pro Thr
1 5

aac gct ggg gaa ctc agg cga gtt ttg ctg gtt cca cac acc ggg cgt 163
Asn Ala Gly Glu Leu Arg Val Leu Leu Val Pro His Thr Gly Arg
10 15 20

tct tcc aat att gaa tcc gcc atc ttg gca gcc aag ctg ctc gac gat 211
Ser Ser Asn Ile Glu Ser Ala Ile Leu Ala Ala Lys Leu Leu Asp Asp
25 30 35

gct gga atc gat gtg agg gtg ctg atc aat gat gca gat gat cca att 259
Ala Gly Ile Asp Val Arg Val Leu Ile Asn Asp Ala Asp Asp Pro Ile
40 45 50

gca gag cac tcc gtt tta ggc cgt ttc acc cat gtc agg cac gct gca 307
Ala Glu His Ser Val Leu Gly Arg Phe Thr His Val Arg His Ala Ala
55 60 65

gac gcc gct gac ggc gca gaa cta gtt ctg gtg ctg ggt gga gat ggc 355
Asp Ala Ala Asp Gly Ala Glu Leu Val Leu Val Leu Gly Gly Asp Gly
70 75 80 85

acc ttc ctc cgc gca gca gat atg gcc cac gct gtt gat ttg cct gtt 403
Thr Phe Leu Arg Ala Ala Asp Met Ala His Ala Val Asp Leu Pro Val
90 95 100

ctg ggc atc aac cta ggc cat gtg gga ttc ttg gct gaa tgg gag tct 451
Leu Gly Ile Asn Leu Gly His Val Gly Phe Leu Ala Glu Trp Glu Ser

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	att gaa gat cgc atg acc tta act gtc gtt gtc cta gac ggc ggt gga			547
	Ile Glu Asp Arg Met Thr Leu Thr Val Val Val Leu Asp Gly Gly Gly			
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	gaa gaa atc ggc cga ggc tgg gct ctc aat gag gtc agt att gaa aac			595
	Glu Glu Ile Gly Arg Gly Trp Ala Leu Asn Glu Val Ser Ile Glu Asn			
	150	155	160	165
	tta aac cgc agg gga gtg ctc gat gca acc ctc gag gta gat gca cga			643
	Leu Asn Arg Arg Gly Val Leu Asp Ala Thr Leu Glu Val Asp Ala Arg			
	170	175	180	
	cca gtt gct tcc ttt ggt tgc gat ggc gtg ctg att tcc acc cca acc			691
	Pro Val Ala Ser Phe Gly Cys Asp Gly Val Leu Ile Ser Thr Pro Thr			
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	ggc tcc acc gct tat gca ttt tcc gcc ggt ggt cct gta ctg tgg cca			739
	Gly Ser Thr Ala Tyr Ala Phe Ser Ala Gly Gly Pro Val Leu Trp Pro			
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	gaa ctc gat gcc atc ttg gtg gtt cct aat aac gcc cac gcg ctg ttt			787
	Glu Leu Asp Ala Ile Leu Val Val Pro Asn Asn Ala His Ala Leu Phe			
	215	220	225	
	acc aaa ccg ctg gtt gtg agc cca aaa tcc acc gta gct gtg gaa tcc			835
	Thr Lys Pro Leu Val Val Ser Pro Lys Ser Thr Val Ala Val Glu Ser			
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	aat tca gat act tca gca gcg atg gcc gtc atg gat ggt ttc cgt ccc			883
	Asn Ser Asp Thr Ser Ala Ala Met Ala Val Met Asp Gly Phe Arg Pro			
	250	255	260	
	att cct atg cct cca gga tcc cgt gtt gag gtc acc agg ggt gag cgt			931
	Ile Pro Met Pro Pro Gly Ser Arg Val Glu Val Thr Arg Gly Glu Arg			
	265	270	275	
	ccc gtg cgt tgg gtg agg ott gat tct tca ccg ttt acc gac cga ctt			979
	Pro Val Arg Trp Val Arg Leu Asp Ser Ser Pro Phe Thr Asp Arg Leu			
	280	285	290	
	gtg agc aaa tta agg ctc ccc gtt acc ggt tgg cgg ggt ccg caa aaa			1027
	Val Ser Lys Leu Arg Leu Pro Val Thr Gly Trp Arg Gly Pro Gln Lys			
	295	300	305	
	cag gcg gaa aat aaa gat ccc agg tca gcg ggg taattcgaaa accattcgaa			1080
	Gln Ala Glu Asn Lys Asp Pro Arg Ser Ala Gly			
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	caa			1083

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<212> PRT

<213> Corynebacterium glutamicum

<400> 2324

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Lys Leu Leu Asp Asp Ala Gly Ile Asp Val Arg Val Leu Ile Asn Asp
          35             40             45

Ala Asp Asp Pro Ile Ala Glu His Ser Val Leu Gly Arg Phe Thr His
          50             55             60

Val Arg His Ala Ala Asp Ala Ala Asp Gly Ala Glu Leu Val Leu Val
          65             70             75             80

Leu Gly Gly Asp Gly Thr Phe Leu Arg Ala Ala Asp Met Ala His Ala
          85             90             95

Val Asp Leu Pro Val Leu Gly Ile Asn Leu Gly His Val Gly Phe Leu
          100            105            110

Ala Glu Trp Glu Ser Asp Ser Leu Glu Glu Ala Leu Lys Arg Val Ile
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Asp Arg Asp Tyr Arg Ile Glu Asp Arg Met Thr Leu Thr Val Val Val
          130            135            140

Leu Asp Gly Gly Gly Glu Glu Ile Gly Arg Gly Trp Ala Leu Asn Glu
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Val Ser Ile Glu Asn Leu Asn Arg Arg Gly Val Leu Asp Ala Thr Leu
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Glu Val Asp Ala Arg Pro Val Ala Ser Phe Gly Cys Asp Gly Val Leu
          180            185            190

Ile Ser Thr Pro Thr Gly Ser Thr Ala Tyr Ala Phe Ser Ala Gly Gly
          195            200            205

Pro Val Leu Trp Pro Glu Leu Asp Ala Ile Leu Val Val Pro Asn Asn
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Ala His Ala Leu Phe Thr Lys Pro Leu Val Val Ser Pro Lys Ser Thr
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Val Ala Val Glu Ser Asn Ser Asp Thr Ser Ala Ala Met Ala Val Met
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Asp Gly Phe Arg Pro Ile Pro Met Pro Pro Gly Ser Arg Val Glu Val
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Thr Arg Gly Glu Arg Pro Val Arg Trp Val Arg Leu Asp Ser Ser Pro
          275            280            285

Phe Thr Asp Arg Leu Val Ser Lys Leu Arg Leu Pro Val Thr Gly Trp
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Arg Gly Pro Gln Lys Gln Ala Glu Asn Lys Asp Pro Arg Ser Ala Gly
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 <222> (101)..(769)
 <223> RXA01600

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tttgagctg cgtgtccacc cttagatcta caatgtgata atg gtt tcg aag atg 115
 Met Val Ser Lys Met
 1 5

cac att ccc ggt acc cat gag ttc acg gtg aca gat act gaa ctg ttg 163
 His Ile Pro Gly Thr His Glu Phe Thr Val Thr Asp Thr Glu Leu Leu
 10 15 20

tta gag tcc cca att ttg ggc gtt cgt cga gat tca ttg atc atg ccg 211
 Leu Glu Ser Pro Ile Leu Gly Val Arg Arg Asp Ser Leu Ile Met Pro
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ggg ggt tcc act gcc cgc cgt gaa gtg gtt gaa cac ttt ggg gcg gtc 259
 Gly Gly Ser Thr Ala Arg Arg Glu Val Val Glu His Phe Gly Ala Val
 40 45 50

gca gtg gtt gcc ttt gat ggt gaa aac att gcg atg gtc aag cag tac 307
 Ala Val Val Ala Phe Asp Gly Glu Asn Ile Ala Met Val Lys Gln Tyr
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cgt cgc agc gtg ggg gat tcc ttg tgg gag ctg cct gca ggt ttg ttg 355
 Arg Arg Ser Val Gly Asp Ser Leu Trp Glu Leu Pro Ala Gly Leu Leu
 70 75 80 85

gat att gct gat gag gat gaa ctc acg ggc gcg cag cgc gag ctc atg 403
 Asp Ile Ala Asp Glu Asp Glu Leu Thr Gly Ala Gln Arg Glu Leu Met
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gag gag gct ggt ttg gag gcc agt gag tgg tcc gtg ctc act gat ttg 451
 Glu Glu Ala Gly Leu Glu Ala Ser Glu Trp Ser Val Leu Thr Asp Leu
 105 110 115

att acc tcg cct ggt ttc tgc gat gaa gcg gtg cgt gtc ttt cta gcc 499
 Ile Thr Ser Pro Gly Phe Cys Asp Glu Ala Val Arg Val Phe Leu Ala
 120 125 130

cga ggc ctc aca aag gtt gag cgc ccg aag gtt atg ggc gat gaa gaa 547
 Arg Gly Leu Thr Lys Val Glu Arg Pro Lys Val Met Gly Asp Glu Glu
 135 140 145

gcg gac atg att aac cag tgg gtt ccg cta cat gag gca gtg gga atg 595
 Ala Asp Met Ile Asn Gln Trp Val Pro Leu His Glu Ala Val Gly Met
 150 155 160 165

gtg ttt agt ggc cag ttg gtt aac tcc att gcc att gcg ggt gtc atg 643
 Val Phe Ser Gly Gln Leu Val Asn Ser Ile Ala Ile Ala Gly Val Met
 170 175 180

gct gct gat gct gtg att gcg ggt cgt gcg tct gcg cgt gcc gtc acc 691
 Ala Ala Asp Ala Val Ile Ala Gly Arg Ala Ser Ala Arg Ala Val Thr
 185 190 195

gcg cag ttt acc tat cgc cct acg gcg ttg gcg cag cgt cga aaa gcg 739
 Ala Pro Phe Thr Tyr Arg Pro Thr Ala Leu Ala Gln Arg Arg Lys Ala
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cac gcc att gtt cct gac atg aaa aaa cta tgaaggctcg cggttttagcg 789
 His Gly Ile Val Pro Asp Met Lys Lys Leu
 215 220

aaa 792

<210> 2326

<211> 223

<212> PRT

<213> Corynebacterium glutamicum

<400> 2326

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 20 25 30

Ser Leu Ile Met Pro Gly Gly Ser Thr Ala Arg Arg Glu Val Val Glu
 35 40 45

His Phe Gly Ala Val Ala Val Val Ala Phe Asp Gly Glu Asn Ile Ala
 50 55 60

Met Val Lys Gln Tyr Arg Arg Ser Val Gly Asp Ser Leu Trp Glu Leu
 65 70 75 80

Pro Ala Gly Leu Leu Asp Ile Ala Asp Glu Asp Glu Leu Thr Gly Ala
 85 90 95

Gln Arg Glu Leu Met Glu Glu Ala Gly Leu Glu Ala Ser Glu Trp Ser
 100 105 110

Val Leu Thr Asp Leu Ile Thr Ser Pro Gly Phe Cys Asp Glu Ala Val
 115 120 125

Arg Val Phe Leu Ala Arg Gly Leu Thr Lys Val Glu Arg Pro Lys Val
 130 135 140

Met Gly Asp Glu Glu Ala Asp Met Ile Asn Gln Trp Val Pro Leu His
 145 150 155 160

Glu Ala Val Gly Met Val Phe Ser Gly Gln Leu Val Asn Ser Ile Ala
 165 170 175

Ile Ala Gly Val Met Ala Ala Asp Ala Val Ile Ala Gly Arg Ala Ser
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Ala Arg Ala Val Thr Ala Pro Phe Thr Tyr Arg Pro Thr Ala Leu Ala
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<210> 2327

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<212> DNA

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<220>

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<222> (101)..(1630)

<223> RXA01602

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tgcaggggcg actttctagc acttttaaag gaatttttta atg gct aaa acc cat 115
Met Ala Lys Thr His
1 5

att cgg tta cag gac ctt tcc ctg tca tac acc tca acc cgg tta att 163
Ile Arg Leu Gln Asp Leu Ser Leu Ser Tyr Thr Ser Thr Pro Leu Ile
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acg aag ctc aat atc act gtt tct tct gga cag tgc gca gtg att gtt 211
Thr Lys Leu Asn Ile Thr Val Ser Ser Gly Gln Cys Ala Val Ile Val
25 30 35

ggg gag aat ggt cga ggt aaa acc aca ctt ctg cga gca ctg gct cga 259
Gly Glu Asn Gly Arg Gly Lys Thr Thr Leu Leu Arg Ala Leu Ala Arg
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gea ttc cgg cca tct gca ggt gag att ctc act cat ggc acg gta gca 307
Glu Phe Pro Pro Ser Ala Gly Glu Ile Leu Thr His Gly Thr Val Ala
55 60 65

att gct cat caa cac atg cct gca ggt gat ctg tcc gtc gga gag atc 355
Ile Ala His Gln His Met Pro Ala Gly Asp Leu Ser Val Gly Glu Ile
70 75 80 85

tgt gat gag gca att cgt gat tca aag aat gct ctc gaa gag ctt gag 403
Cys Asp Glu Ala Ile Arg Asp Ser Lys Asn Ala Leu Glu Glu Leu Glu
90 95 100

aga gct gga gct cta ctt gag aca aac act gcg cac gca ctt gat gga 451
Arg Ala Gly Ala Leu Leu Glu Thr Asn Thr Ala His Ala Leu Asp Gly
105 110 115

tat caa caa gcc ctt gat gcc gct gaa gtg ctt gac gca tgg aac gct 499
Tyr Gln Gln Ala Leu Asp Ala Glu Val Leu Asp Ala Trp Asn Ala
120 125 130

gea cat cga tta gaa aaa gct ctg cgc agc ttt ggc gcg atc acc gat 547
Glu His Arg Leu Glu Lys Ala Leu Arg Ser Phe Gly Ala Ile Thr Asp
135 140 145

aga tcc cgt gca ctc agt gag cta tcg atc ggg caa agg tat cgg gta	595
Arg Ser Arg Ala Leu Ser Glu Leu Ser Ile Gly Gln Arg Tyr Arg Val	
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Arg Leu Ala Cys Leu Ile Gly Gly Asp Ala Asp Ile Leu Leu Leu Asp	
170 175 180	
gaa ccc acc aat cat ctt gac cgg ggc gcg ctt aac tat ctc acc gaa	691
Glu Pro Thr Asn His Leu Asp Arg Gly Ala Leu Asn Tyr Leu Thr Glu	
185 190 195	
gcc ata acc tcc cac aaa ggt gtg gta ctt gtt gtt tct cat gat caa	739
Ala Ile Thr Ser His Lys Gly Val Val Leu Val Val Ser His Asp Gln	
200 205 210	
gca ctg atc aaa gat gtc gcg gat ttc atc atc gat att gat tca acc	787
Ala Leu Ile Lys Asp Val Ala Asp Phe Ile Ile Asp Ile Asp Ser Thr	
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cca gac gcc cta cca cgg atc tat cat gag ggt ttt gat tct tat cga	835
Pro Asp Gly Leu Pro Arg Ile Tyr His Glu Gly Phe Asp Ser Tyr Arg	
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Arg Gln Arg Ser Ala Leu Leu Glu Thr Trp Arg Gln Asp Tyr Ala Ala	
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gca caa act gtg caa cag caa ttg cag gag gat cta gag cac gca cgc	931
Ala Gln Thr Val Gln Gln Gln Leu Gln Glu Asp Leu Glu His Ala Arg	
265 270 275	
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Gln Arg Val Asn Ser Ser Trp Lys Pro Pro Lys Gly Thr Gly Lys His	
280 285 290	
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Thr Arg Ala Ser Arg Ala Pro Gly Val Val Gln Ala Leu Lys Arg Ala	
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Gln Asp Ala Leu Asp Ser Lys Ala Leu Asp Val Pro Pro Ala Pro Ala	
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Pro Leu Leu Leu Pro Thr Leu Lys Val Arg Pro Asp Lys Pro Met Val	
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Asp Phe Ser Asp Leu Phe Val Pro His Arg Leu Arg Leu Pro Gly Ser	
345 350 355	
cat tca gtg gta tca ggt gac aaa ata gtg atc act ggt gac aac gcc	1219
His Ser Val Val Ser Gly Asp Lys Ile Val Ile Thr Gly Asp Asn Gly	
360 365 370	
gct ggc aaa tca acg ctc atc gaa gtc ttg tct ggg gtt ttg act ccg	1267
Ala Gly Lys Ser Thr Leu Ile Glu Val Leu Ser Gly Val Leu Thr Pro	
375 380 385	
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Ala Ser Gly Ser Val Ala Asn His Ala Arg Thr Gly Val Leu Gly Gln
390 395 400 405

gaa tca ctt gtc ggc gag gtg cca tca ata gca cga gat cac gca gtt 1363
Glu Ser Leu Val Gly Glu Val Pro Ser Ile Ala Arg Asp His Ala Val
410 415 420

aag tgg gga ctt tta agt gtt gag gag agc cga ttt gcc cta cag gaa 1411
Lys Trp Gly Leu Ser Val Glu Glu Ser Arg Phe Ala Leu Gln Glu
425 430 435

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Phe Ser Ile Gly Gln Arg Arg Leu Asp Leu Ala Met Ser Leu Ala
440 445 450

ggc aat cct gaa ctg ttg ctt ctc gat gaa cct tcg aac cat ctg tct 1507
Gly Asn Pro Glu Leu Leu Leu Asp Glu Pro Ser Asn His Leu Ser
455 460 465

atg cac ttg gtt tcc gca ctt aca gag tgg ctg gac acg acc gcg gct 1555
Met His Leu Val Ser Ala Leu Thr Glu Trp Leu Asp Thr Thr Ala Ala
470 475 480 485

gca gtg atc atg gta acg cat gat cga cag cta ctc cgc gat acg gct 1603
Ala Val Ile Met Val Thr His Asp Arg Gln Leu Leu Arg Asp Thr Ala
490 495 500

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His Trp Arg His Ile Glu Leu Lys Ser
505 510

cac 1653

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<212> PRT
<213> *Corynebacterium glutamicum*

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35 40 45
Arg Ala Leu Ala Arg Glu Phe Pro Pro Ser Ala Gly Glu Ile Leu Thr
50 55 60
His Gly Thr Val Ala Ile Ala His Gln His Met Pro Ala Gly Asp Leu
65 70 75 80
Ser Val Gly Glu Ile Cys Asp Glu Ala Ile Arg Asp Ser Lys Asn Ala
85 90 95
Leu Glu Glu Leu Glu Arg Ala Gly Ala Leu Leu Glu Thr Asn Thr Ala
100 105 110

His Ala Leu Asp Gly Tyr Gln Gln Ala Leu Asp Ala Ala Glu Val Leu
 115 120 125
 Asp Ala Trp Asn Ala Glu His Arg Leu Glu Lys Ala Leu Arg Ser Phe
 130 135 140
 Gly Ala Ile Thr Asp Arg Ser Arg Ala Leu Ser Glu Leu Ser Ile Gly
 145 150 155 160
 Gln Arg Tyr Arg Val Arg Leu Ala Cys Leu Ile Gly Gly Asp Ala Asp
 165 170 175
 Ile Leu Leu Leu Asp Glu Pro Thr Asn His Leu Asp Arg Gly Ala Leu
 180 185 190
 Asn Tyr Leu Thr Glu Ala Ile Thr Ser His Lys Gly Val Val Leu Val
 195 200 205
 Val Ser His Asp Gln Ala Leu Ile Lys Asp Val Ala Asp Phe Ile Ile
 210 215 220
 Asp Ile Asp Ser Thr Pro Asp Gly Leu Pro Arg Ile Tyr His Glu Gly
 225 230 235 240
 Phe Asp Ser Tyr Arg Arg Gln Arg Ser Ala Leu Leu Glu Thr Trp Arg
 245 250 255
 Gln Asp Tyr Ala Ala Ala Gln Thr Val Gln Gln Gln Leu Gln Glu Asp
 260 265 270
 Leu Glu His Ala Arg Gln Arg Val Asn Ser Ser Trp Lys Pro Pro Lys
 275 280 285
 Gly Thr Gly Lys His Thr Arg Ala Ser Arg Ala Pro Gly Val Val Gln
 290 295 300
 Ala Leu Lys Arg Ala Gln Asp Ala Leu Asp Ser Lys Ala Leu Asp Val
 305 310 315 320
 Pro Pro Ala Pro Ala Pro Leu Leu Leu Pro Thr Leu Lys Val Arg Pro
 325 330 335
 Asp Lys Pro Met Val Asp Phe Ser Asp Leu Phe Val Pro His Arg Leu
 340 345 350
 Arg Leu Pro Gly Ser His Ser Val Val Ser Gly Asp Lys Ile Val Ile
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 Thr Gly Asp Asn Gly Ala Gly Lys Ser Thr Leu Ile Glu Val Leu Ser
 370 375 380
 Gly Val Leu Thr Pro Ala Ser Gly Ser Val Ala Asn His Ala Arg Thr
 385 390 395 400
 Gly Val Leu Gly Gln Glu Ser Leu Val Gly Glu Val Pro Ser Ile Ala
 405 410 415
 Arg Asp His Ala Val Lys Trp Gly Leu Leu Ser Val Glu Glu Ser Arg
 420 425 430
 Phe Ala Leu Gln Glu Phe Ser Ile Gly Gln Arg Arg Arg Leu Asp Leu

435 440 445

Ala Met Ser Leu Ala Gly Asn Pro Glu Leu Leu Leu Leu Asp Glu Pro
 450 455 460

Ser Asn His Leu Ser Met His Leu Val Ser Ala Leu Thr Glu Trp Leu
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 <223> RXA01605

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 Val Thr Ser Asp Ser
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ccc gcg cca gca acc gtc aac gcg gta ttc aac aac agc aac ggc ttc 163
 Pro Ala Pro Ala Thr Val Asn Ala Val Phe Asn Asn Ser Asn Gly Phe
 10 15 20

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 Met Asp Thr Glu Phe Gly Val Arg Ile Val Asp Asn Met Leu Val Gly
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ttc tcc acc ttg ggc gac ggc atg aac caa gcc gcc gaa ggt gcc act 307
 Phe Ser Thr Leu Gly Asp Gly Met Asn Gln Ala Ala Glu Gly Ala Thr
 55 60 65

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 Thr Leu Ser Asp Gly Val Gly Ser Ala Asn Asp Gly Ala Val Gln Leu
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gcc gac ggc gcg gtc acc ctg cgc gac ggc atc gca agt gcc aat gag 403
 Ala Asp Gly Ala Val Thr Leu Arg Asp Gly Ile Ala Ser Ala Asn Glu
 90 95 100

ggt gcg caa tcg ctt gcc gac ggc gcc agc cag ctc gac acc ggc ctc 451
 Gly Ala Gln Ser Leu Ala Asp Gly Ala Ser Gln Leu Asp Thr Gly Leu
 105 110 115

ggc tcc gcg gct aca ggc agc caa acg ctc gcc gac ggt cta tcc agc 499

Gly	Ser	Ala	Ala	Thr	Gly	Ser	Gln	Thr	Leu	Ala	Asp	Gly	Leu	Ser	Ser	
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Leu	Ser	Ala	Gly	Thr	Ala	Gln	Leu	Gly	Gln	Gly	Ala	Thr	Gln	Val	Ser	
		135				140					145					
gat	ggc	gtg	ggc	caa	ctt	gtc	gac	caa	gta	gca	cca	ctg	acc	gcc	tat	595
Asp	Gly	Val	Gly	Gln	Leu	Val	Asp	Gln	Val	Ala	Pro	Leu	Thr	Ala	Tyr	
		150				155					160				165	
gtt	cca	gac	atc	aac	tct	cag	ttg	atc	acc	ctg	cgc	gac	ggc	gca	gcc	643
Val	Pro	Asp	Ile	Asn	Ser	Gln	Leu	Ile	Thr	Leu	Arg	Asp	Gly	Ala	Ala	
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acc	att	gcc	tct	gaa	cta	tct	gat	ccc	tcc	agc	acc	tac	cgc	tcc	ggc	691
Thr	Ile	Ala	Ser	Glu	Leu	Ser	Asp	Pro	Ser	Ser	Thr	Tyr	Arg	Ser	Gly	
				185					190					195		
gtg	gac	tcc	gct	gtg	agc	gca	tcc	cag	caa	cta	gca	gcc	ggc	ctg	caa	739
Val	Asp	Ser	Ala	Val	Ser	Ala	Ser	Gln	Gln	Leu	Ala	Ala	Gly	Leu	Gln	
		200					205					210				
acc	ctg	aaa	gac	gga	tcc	agc	caa	ctc	agc	atc	ggc	gca	cgc	acc	ctc	787
Thr	Leu	Lys	Asp	Gly	Ser	Ser	Gln	Leu	Ser	Ile	Gly	Ala	Arg	Thr	Leu	
		215				220					225					
gct	gat	ggc	acc	agc	caa	ttg	gcc	gca	ggc	tcc	gaa	cag	cta	gtt	gtt	835
Ala	Asp	Gly	Thr	Ser	Gln	Leu	Ala	Ala	Gly	Ser	Glu	Gln	Leu	Val	Val	
		230				235					240				245	
ggc	gca	caa	gca	ctg	cgc	gac	ggc	acc	gtc	cag	ctt	gat	gaa	ggc	tcc	883
Gly	Ala	Gln	Ala	Leu	Arg	Asp	Gly	Thr	Val	Gln	Leu	Asp	Glu	Gly	Ser	
				250					255					260		
agc	gaa	ctc	gcc	ctc	aaa	ctc	acc	gac	ggc	gca	agc	caa	gta	cca	acc	931
Ser	Glu	Leu	Ala	Leu	Lys	Leu	Thr	Asp	Gly	Ala	Ser	Gln	Val	Pro	Thr	
			265					270						275		
ttc	gct	gac	ggc	gca	gac	acc	acc	atc	gca	acc	cca	gtt	gaa	aca	gaa	979
Phe	Ala	Asp	Gly	Ala	Asp	Thr	Thr	Ile	Ala	Thr	Pro	Val	Glu	Thr	Glu	
			280				285						290			
caa	gca	gga	gac	acc	aca	ccg	ctc	ttc	ggc	att	ggc	ctc	gca	cca	ttc	1027
Gln	Ala	Gly	Asp	Thr	Thr	Pro	Leu	Phe	Gly	Ile	Gly	Leu	Ala	Pro	Phe	
		295				300					305					
ttc	atg	gct	gtc	ggc	ctg	ttc	atg	gga	gca	acc	gtt	gcc	tgg	atg	atc	1075
Phe	Met	Ala	Val	Gly	Leu	Phe	Met	Gly	Ala	Thr	Val	Ala	Trp	Met	Ile	
		310				315					320				325	
ctg	cac	cca	atc	agt	cgc	cgc	gca	ctc	gac	tcc	cgc	atg	gga	ggc	ttc	1123
Leu	His	Pro	Ile	Ser	Arg	Arg	Ala	Leu	Asp	Ser	Arg	Met	Gly	Gly	Phe	
				330					335					340		
cga	ggc	acc	ctg	gca	agc	tac	ctt	cca	tca	aca	gtc	tta	ggc	ott	ggc	1171
Arg	Gly	Thr	Leu	Ala	Ser	Tyr	Leu	Pro	Ser	Thr	Val	Leu	Gly	Leu	Gly	
			345					350					355			
caa	gca	acc	atc	atg	tgg	gca	gta	ctg	tac	ttc	ctg	ctc	gac	ctc	aat	1219
Gln	Ala	Thr	Ile	Met	Trp	Ala	Val	Leu	Tyr	Phe	Leu	Leu	Asp	Leu	Asn	

360	365	370	
cca gct cac cca gct gga ctg tgg atg gcg atg gtc gcc atc tca tgg			1267
Pro Ala His Pro Ala Gly Leu Trp Met Ala Met		Val Ala Ile Ser Trp	
375	380	385	
gta ttc atc tcc att acc cat atg ttc aac aac gtg gca gga ccc tcc			1315
Val Phe Ile Ser Ile Thr His Met Phe Asn		Val Ala Gly Pro Ser	
390	395	400	405
gca ggc cgt gtg ctg tcc atc gtg atg atg tcc ttc cag cta gtc tcc			1363
Ala Gly Arg Val Leu Ser Ile Val Met Ser		Phe Gln Leu Val Ser	
410	415	420	
tcc ggt ggc cta tac cca cca gaa acc cag cca gca ttc ttc cac tgg			1411
Ser Gly Gly Leu Tyr Pro Pro Glu Thr Gln Pro		Ala Phe Phe His Trp	
425	430	435	
ttc cac acc tac gac ccg atc acc tac gca gtc aac ctc gtg cgc caa			1459
Phe His Thr Tyr Asp Pro Ile Thr Tyr Ala Val		Asn Leu Val Arg Gln	
440	445	450	
atg atc ttc aac gaa acc cca tcc aac gac cca cgc ttc ata caa gca			1507
Met Ile Phe Asn Glu Thr Pro Ser Asn Asp Pro		Arg Phe Ile Gln Ala	
455	460	465	
atc tgg gta ctg ctc ttc atc tgg gca ctg atg ctc gcc atc tcc acc			1555
Ile Trp Val Leu Leu Phe Ile Trp Ala Leu Met		Leu Ala Ile Ser Thr	
470	475	480	485
ctg gcg aat aga aca aac aag gtt ctt cgc atg aag gac tac cac cca			1603
Leu Ala Asn Arg Thr Asn Lys Val Leu Arg Met		Lys Asp Tyr His Pro	
490	495	500	
gaa ctg aag gtc taaaagcttt tcccgcgcgg ttc			1638
Glu Leu Lys Val			
505			

<210> 2330

<211> 505

<212> PRT

<213> Corynebacterium glutamicum

<400> 2330

Val Thr Ser Asp Ser Pro Ala Pro Ala Thr Val Asn Ala Val Phe Asn
1 5 10 15

Asn Ser Asn Gly Phe Ile Ala Ser Met Leu Gly Asn Gln Val Val Asn
20 25 30

Thr Val Val Glu Thr Met Asp Thr Glu Phe Gly Val Arg Ile Val Asp
35 40 45

Asn Met Leu Val Gly Phe Ser Thr Leu Gly Asp Gly Met Asn Gln Ala
50 55 60

Ala Glu Gly Ala Thr Thr Leu Ser Asp Gly Val Gly Ser Ala Asn Asp
65 70 75 80

Gly Ala Val Gln Leu Ala Asp Gly Ala Val Thr Leu Arg Asp Gly Ile

85										90					95				
Ala	Ser	Ala	Asn	Glu	Gly	Ala	Gln	Ser	Leu	Ala	Asp	Gly	Ala	Ser	Gln				
			100					105						110					
Leu	Asp	Thr	Gly	Leu	Gly	Ser	Ala	Ala	Thr	Gly	Ser	Gln	Thr	Leu	Ala				
		115					120					125							
Asp	Gly	Leu	Ser	Ser	Leu	Ser	Ala	Gly	Thr	Ala	Gln	Leu	Gly	Gln	Gly				
		130				135					140								
Ala	Thr	Gln	Val	Ser	Asp	Gly	Val	Gly	Gln	Leu	Val	Asp	Gln	Val	Ala				
					150					155					160				
Pro	Leu	Thr	Ala	Tyr	Val	Pro	Asp	Ile	Asn	Ser	Gln	Leu	Ile	Thr	Leu				
				165					170					175					
Arg	Asp	Gly	Ala	Ala	Thr	Ile	Ala	Ser	Glu	Leu	Ser	Asp	Pro	Ser	Ser				
			180					185					190						
Thr	Tyr	Arg	Ser	Gly	Val	Asp	Ser	Ala	Val	Ser	Ala	Ser	Gln	Gln	Leu				
		195				200						205							
Ala	Ala	Gly	Leu	Gln	Thr	Leu	Lys	Asp	Gly	Ser	Ser	Gln	Leu	Ser	Ile				
						215					220								
Gly	Ala	Arg	Thr	Leu	Ala	Asp	Gly	Thr	Ser	Gln	Leu	Ala	Ala	Gly	Ser				
					230					235				240					
Glu	Gln	Leu	Val	Val	Gly	Ala	Gln	Ala	Leu	Arg	Asp	Gly	Thr	Val	Gln				
				245					250					255					
Leu	Asp	Glu	Gly	Ser	Ser	Glu	Leu	Ala	Leu	Lys	Leu	Thr	Asp	Gly	Ala				
			260					265					270						
Ser	Gln	Val	Pro	Thr	Phe	Ala	Asp	Gly	Ala	Asp	Thr	Thr	Ile	Ala	Thr				
			275				280					285							
Pro	Val	Glu	Thr	Glu	Gln	Ala	Gly	Asp	Thr	Thr	Pro	Leu	Phe	Gly	Ile				
						295					300								
Gly	Leu	Ala	Pro	Phe	Phe	Met	Ala	Val	Gly	Leu	Phe	Met	Gly	Ala	Thr				
					310					315					320				
Val	Ala	Trp	Met	Ile	Leu	His	Pro	Ile	Ser	Arg	Arg	Ala	Leu	Asp	Ser				
				325					330					335					
Arg	Met	Gly	Gly	Phe	Arg	Gly	Thr	Leu	Ala	Ser	Tyr	Leu	Pro	Ser	Thr				
			340					345					350						
Val	Leu	Gly	Leu	Gly	Gln	Ala	Thr	Ile	Met	Trp	Ala	Val	Leu	Tyr	Phe				
			355				360					365							
Leu	Leu	Asp	Leu	Asn	Pro	Ala	His	Pro	Ala	Gly	Leu	Trp	Met	Ala	Met				
			370			375					380								
Val	Ala	Ile	Ser	Trp	Val	Phe	Ile	Ser	Ile	Thr	His	Met	Phe	Asn	Asn				
					390					395					400				
Val	Ala	Gly	Pro	Ser	Ala	Gly	Arg	Val	Leu	Ser	Ile	Val	Met	Met	Ser				
				405					410					415					

Phe Gln Leu Val Ser Ser Gly Gly Leu Tyr Pro Pro Glu Thr Gln Pro
420 425 430

Ala Phe Phe His Trp Phe His Thr Tyr Asp Pro Ile Thr Tyr Ala Val
435 440 445

Asn Leu Val Arg Gln Met Ile Phe Asn Glu Thr Pro Ser Asn Asp Pro
450 455 460

Arg Phe Ile Gln Ala Ile Trp Val Leu Leu Phe Ile Trp Ala Leu Met
465 470 475 480

Leu Ala Ile Ser Thr Leu Ala Asn Arg Thr Asn Lys Val Leu Arg Met
485 490 495

Lys Asp Tyr His Pro Glu Leu Lys Val
500 505

<210> 2331

<211> 852

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(829)

<223> RXA01610

<400> 2331

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tccatatctt tagtttgca aagcgatcaa cttaaaacac gtg tcc ggt ttt ctt 115
Val Ser Gly Phe Leu
1 5

act ccc cca gct aca ccc cat att cgg acg gca act gcc agt att gct 163
Thr Pro Pro Ala Thr Pro His Ile Arg Thr Ala Thr Ala Ser Ile Ala
10 15 20

acc gca gtt gcc gta gca ctg tca gtg ttc gct gct gca ctc att cca 211
Thr Ala Val Ala Val Ala Leu Ser Val Phe Ala Ala Ala Leu Ile Pro
25 30 35

gga agc gct ctg tat tct gtg ctg acc gct gga ggg gtg gca ctt gga 259
Gly Ser Ala Leu Tyr Ser Val Leu Thr Ala Gly Gly Val Ala Leu Gly
40 45 50

gca gca tca ggc gtt gcc gcg tta cgc cat cgc gga ggg ctt cgc att 307
Ala Ala Ser Gly Val Ala Ala Leu Arg His Arg Gly Gly Leu Arg Ile
55 60 65

ttt caa tgg ctg tct gcg ctt ggt gga atc gtc att ttg ctg atc ggt 355
Phe Gln Trp Leu Ser Ala Leu Gly Gly Ile Val Ile Leu Leu Ile Gly
70 75 80 85

atc gta gtg gca gtt gca aag ttt ggg gcc tcg gca aaa ctt gcc acg 403
Ile Val Val Ala Val Ala Lys Phe Gly Ala Ser Ala Lys Leu Ala Thr
90 95 100

tta ggc ctg gtg acc tcg tat tat ctc atg ccg tct gcg gca ttg gcc 451
 Leu Gly Leu Val Thr Ser Tyr Tyr Leu Met Pro Ser Ala Ala Leu Ala
 105 110 115
 tgt tat atc gga ggg ctt ggc cag cta cca gcc aaa tgg att gcg cca 499
 Cys Tyr Ile Gly Gly Leu Gly Gln Leu Pro Ala Lys Trp Ile Ala Pro
 120 125 130
 gcg ttt atg gct acg gct ggt gca ggt gct gcg gga tgg ttt tca ttg 547
 Ala Phe Met Ala Thr Ala Gly Ala Gly Ala Ala Gly Trp Phe Ser Leu
 135 140 145
 ggg gca ggc acc ggt ttt gaa cgg ttc ctc att gct gtt gca gcg gtg 595
 Gly Ala Gly Thr Gly Phe Glu Arg Phe Leu Ile Ala Val Ala Ala Val
 150 155 160 165
 ttt tca ctg atg gga tgt gta tac cca gtg tgg gga tgc gtc gta aag 643
 Phe Ser Leu Met Gly Cys Val Tyr Pro Val Trp Gly Cys Val Val Lys
 170 175 180
 cgt cca cgt caa gtg gct gca tgg ctg gtc gcg ctg gcg gcc ctg gtg 691
 Arg Pro Arg Gln Val Ala Ala Trp Leu Val Ala Leu Ala Leu Val
 185 190 195
 ctt ggg gcg ctc atg ctt ttt atg gtg agc atg gtg gtg gcg ccg ggt 739
 Leu Gly Ala Leu Met Leu Phe Met Val Ser Met Val Val Ala Pro Gly
 200 205 210
 ttg ctg tgg ctg cag ccc acg acg gtc gca tgg ggt ttt atg att gcc 787
 Leu Leu Trp Leu Gln Pro Thr Thr Val Ala Trp Gly Phe Met Ile Ala
 215 220 225
 ggg gtt ctt gcg acg gtc gca ggc ttg tgg cct agg cgt ttt 829
 Gly Val Leu Ala Thr Val Ala Gly Leu Trp Pro Arg Arg Phe
 230 235 240
 tagacggaat cgtctgggag ggt 852

<210> 2332

<211> 243

<212> PRT

<213> Corynebacterium glutamicum

<400> 2332

Val Ser Gly Phe Leu Thr Pro Pro Ala Thr Pro His Ile Arg Thr Ala
1 5 10 15

Thr Ala Ser Ile Ala Thr Ala Val Ala Val Ala Leu Ser Val Phe Ala
20 25 30

Ala Ala Leu Ile Pro Gly Ser Ala Leu Tyr Ser Val Leu Thr Ala Gly
35 40 45

Gly Val Ala Leu Gly Ala Ala Ser Gly Val Ala Ala Leu Arg His Arg
50 55 60

Gly Gly Leu Arg Ile Phe Gln Trp Leu Ser Ala Leu Gly Gly Ile Val
65 70 75 80

Ile Leu Leu Ile Gly Ile Val Val Ala Val Ala Lys Phe Gly Ala Ser

85 90 95

Ala Lys Leu Ala Thr Leu Gly Leu Val Thr Ser Tyr Tyr Leu Met Pro
100 105 110

Ser Ala Ala Leu Ala Cys Tyr Ile Gly Gly Leu Gly Gln Leu Pro Ala
115 120 125

Lys Trp Ile Ala Pro Ala Phe Met Ala Thr Ala Gly Ala Gly Ala Ala
130 135 140

Gly Trp Phe Ser Leu Gly Ala Gly Thr Gly Phe Glu Arg Phe Leu Ile
145 150 155 160

Ala Val Ala Ala Val Phe Ser Leu Met Gly Cys Val Tyr Pro Val Trp
165 170 175

Gly Cys Val Val Lys Arg Pro Arg Gln Val Ala Ala Trp Leu Val Ala
180 185 190

Leu Ala Ala Leu Val Leu Gly Ala Leu Met Leu Phe Met Val Ser Met
195 200 205

Val Val Ala Pro Gly Leu Leu Trp Leu Gln Pro Thr Thr Val Ala Trp
210 215 220

Gly Phe Met Ile Ala Gly Val Leu Ala Thr Val Ala Gly Leu Trp Pro
225 230 235 240

Arg Arg Phe

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<210> 2333
<211> 480
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (101)..(457)
<223> RXA01611

<400> 2333
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tcttcatcta tagcttagct ttaactgaaag gcttttcata atg cgt aaa ttc cgc 115
Met Arg Lys Phe Arg
1 5

aac act gca att gca cta gtt tct gca gct gca atc acc ttg ggt ggc 163
Asn Thr Ala Ile Ala Leu Val Ser Ala Ala Ala Ile Thr Leu Gly Gly
10 15 20

gtt acc gct gct acc gct cag gaa gac gaa act cct cct gca gca gag 211
Val Thr Ala Ala Thr Ala Gln Glu Asp Glu Thr Pro Pro Ala Ala Glu
25 30 35

acc gag acc act tct cct tcc ggt tcc tca ggc tct tcc tgg aac gac 259
Thr Glu Thr Thr Ser Pro Ser Gly Ser Ser Gly Ser Trp Asn Asp
40 45 50

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tac aac gaa gag tac gaa ggc gac caa gag ggc tac gga atc gac ggc 307
Tyr Asn Glu Glu Tyr Glu Gly Asp Gln Glu Gly Tyr Gly Ile Asp Gly
    55          60          65

ttt ggt tct tcc cgc gat gac tcc gga gaa gaa gtt cca cgt tgg ttg 355
Phe Gly Ser Ser Arg Asp Asp Ser Gly Glu Glu Val Pro Arg Trp Leu
    70          75          80          85

gag acc tgg ggc aag gta ttt gac gct ttg acc att acc tcc gtt ctt 403
Glu Thr Trp Gly Lys Val Phe Asp Ala Leu Thr Ile Thr Ser Val Leu
    90          95          100

ggt ctt gtt gtc ttc cct gtt gtt aac ttc ctg aag tac aac ggc ctc 451
Gly Leu Val Val Phe Pro Val Val Asn Phe Leu Lys Tyr Asn Gly Leu
    105          110          115

att aag taatctgcaa tttcctgtca aat 480
Ile Lys

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<210> 2334
<211> 119
<212> PRT
<213> Corynebacterium glutamicum

<400> 2334
Met Arg Lys Phe Arg Asn Thr Ala Ile Ala Leu Val Ser Ala Ala Ala
  1          5          10          15

Ile Thr Leu Gly Gly Val Thr Ala Ala Thr Ala Gln Glu Asp Glu Thr
  20          25          30

Pro Pro Ala Ala Glu Thr Glu Thr Thr Ser Pro Ser Gly Ser Ser Gly
  35          40          45

Ser Ser Trp Asn Asp Tyr Asn Glu Glu Tyr Glu Gly Asp Gln Glu Gly
  50          55          60

Tyr Gly Ile Asp Gly Phe Gly Ser Ser Arg Asp Ser Ser Gly Glu Glu
  65          70          75          80

Val Pro Arg Trp Leu Glu Thr Trp Gly Lys Val Phe Asp Ala Leu Thr
  85          90          95

Ile Thr Ser Val Leu Gly Leu Val Val Phe Pro Val Val Asn Phe Leu
  100          105          110

Lys Tyr Asn Gly Leu Ile Lys
  115

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<210> 2335
<211> 468
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(445)

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<223> RXA01612

<400> 2335

gaaaaaacga cggttggttcg tagtcgctgg aaatttaata attcctccgt ccccttcaac 60

taggggggtgg aaaccgcgact atttccgaag gactattctc atg cgt tct ttc cgt 115
 Met Arg Ser Phe Arg
 1 5

acc gcg gca gtt gca ggc ctt act gca gtt gca ctt tcc gta ggt tcc 163
 Thr Ala Ala Val Ala Gly Leu Thr Ala Val Ala Leu Ser Val Gly Ser
 10 15 20

gcc acc gtg gca act gcg gaa gaa tct gat caa aac ctc tca tcc ggc 211
 Ala Thr Val Ala Thr Ala Glu Glu Ser Asp Gln Asn Leu Ser Ser Gly
 25 30 35

ttc tca gca ctt tct tcc ggt ggc gca gcg gcc gta ggt gag gac tgg 259
 Phe Ser Ala Leu Ser Ser Gly Gly Ala Ala Ala Val Gly Glu Asp Trp
 40 45 50

gat gca gac cag ccc gtc aca ggt gaa gac atc ttt ggt gaa gag cac 307
 Asp Ala Asp Gln Pro Val Thr Gly Glu Asp Ile Phe Gly Glu Glu His
 55 60 65

gag cgc gat aac gaa aac acc cca gcg tgg gct aag aac atg tac gat 355
 Glu Arg Asp Asn Glu Asn Thr Pro Ala Trp Ala Lys Asn Met Tyr Asp
 70 75 80 85

cta acc gtc ttg ggt ggc att gct tcc ctt ctc ggt gtc atc gta ttc 403
 Leu Thr Val Leu Gly Gly Ile Ala Ser Leu Leu Gly Val Ile Val Phe
 90 95 100

ccc gct tac aac tac ttg gtt tac acc ggt gtt atc aag ggc 445
 Pro Ala Tyr Asn Tyr Leu Val Tyr Thr Gly Val Ile Lys Gly
 105 110 115

taaatcgctt aacctctatc ttc 468

<210> 2336

<211> 115

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2336

Met Arg Ser Phe Arg Thr Ala Ala Val Ala Gly Leu Thr Ala Val Ala
 1 5 10 15

Leu Ser Val Gly Ser Ala Thr Val Ala Thr Ala Glu Glu Ser Asp Gln
 20 25 30

Asn Leu Ser Ser Gly Phe Ser Ala Leu Ser Ser Gly Gly Ala Ala Ala
 35 40 45

Val Gly Glu Asp Trp Asp Ala Asp Gln Pro Val Thr Gly Glu Asp Ile
 50 55 60

Phe Gly Glu Glu His Glu Arg Asp Asn Glu Asn Thr Pro Ala Trp Ala
 65 70 75 80

ttc ctg gat atg aaa cca ggg gag tgg ctg atc caa aac tcc gca aac 547
Phe Leu Asp Met Lys Pro Gly Glu Trp Leu Ile Gln Asn Ser Ala Asn

135	140	145	
ggt gcc gtc ggc cgc atg ctc gca cag ctg gca gaa tcc cgc ggc atc Gly Ala Val Gly Arg Met Leu Ala Gln Leu Ala Glu Ser Arg Gly Ile 150 155 160 165			595
cat gtc gtt ggt ctc gtc cgc cgt gac gcc ggt gtc caa gaa ctc gct His Val Val Gly Leu Val Arg Arg Asp Ala Gly Val Gln Glu Leu Ala 170 175 180			643
gct caa aac atc agc ggc gtc gtt tcc act gag acc cca ggc tgg gaa Ala Gln Asn Ile Ser Gly Val Val Ser Thr Glu Thr Pro Gly Trp Glu 185 190 195			691
aag cag gtc gaa gac atc acc ggt ggc gca agc atc gcc gtc gca ctt Lys Gln Val Glu Asp Ile Thr Gly Gly Ala Ser Ile Ala Val Ala Leu 200 205 210			739
gat tcc gtc ggt gga tcc tcc gca gct gac ctg gtg aaa ctg ctt ggc Asp Ser Val Gly Gly Ser Ser Ala Ala Asp Leu Val Lys Leu Leu Gly 215 220 225			787
gaa ggc ggc acc ctc gtc tcc ttc ggc gcc atg ggc aac cca atc atg Glu Gly Gly Thr Leu Val Ser Phe Gly Ala Met Gly Asn Pro Ile Met 230 235 240 245			835
gaa atc cca tcc ggc ccc gtc atc ttc aag cac atc acc gtc aag ggc Glu Ile Pro Ser Gly Pro Val Ile Phe Lys His Ile Thr Val Lys Gly 250 255 260			883
ttc tgg gga agc aaa gtc agc cgc gaa atg cca gca gag aag aaa acc Phe Trp Gly Ser Lys Val Ser Arg Glu Met Pro Ala Glu Lys Lys Thr 265 270 275			931
cag ttg ttc ggc gag ctc att gcg cgc ata ctt gat gga aca ttg acc Gln Leu Phe Gly Glu Leu Ile Ala Arg Ile Leu Asp Gly Thr Leu Thr 280 285 290			979
ctt cca gtt gat tcc acc ttt gat gcc gct gac atc gtc tgc gcc gtg Leu Pro Val Asp Ser Thr Phe Asp Ala Ala Asp Ile Val Ser Ala Val 295 300 305			1027
cgc gcc tcc agc gag cct ggc cgt gcc gga aaa gtg ctc att cgt ttc Arg Ala Ser Ser Glu Pro Gly Arg Ala Gly Lys Val Leu Ile Arg Phe 310 315 320 325			1075
taaactgttta aggccattta gac			1098
<210> 2338			
<211> 325			
<212> PRT			
<213> <i>Corynebacterium glutamicum</i>			
<400> 2338			
Met Arg Ala Ile Thr His Asn Thr Phe Gly Asp Pro Ala Asp Val Leu 1 5 10 15			
Gln Ile Thr Glu Lys Glu Ile Pro Thr Pro Gly Pro Gly Gln Val Arg 20 25 30			

Ile Gln Val Thr Leu Ala Thr Ile His Asn His Asp Leu Trp Thr Val
 35 40 45
 Lys Gly Ser Tyr Gly Phe Val Pro Asp Leu Pro Ala Ala Ala Gly Thr
 50 55 60
 Glu Ala Val Gly Ile Val Asp Ala Leu Gly Glu Gly Val Glu Gly Leu
 65 70 75 80
 Gln Val Gly Gln Arg Val Ala Ser Gly Thr Ser Phe Gly Ile Trp Ala
 85 90 95
 Glu Tyr Ala Leu Val Asp Ala Ser Gly Leu Ile Pro Val Pro Glu Gln
 100 105 110
 Leu Ser Asp Glu Ser Ala Ala Gln Leu Val Ala Met Pro Phe Ser Ala
 115 120 125
 Ile Ser Leu Leu Asp Phe Leu Asp Met Lys Pro Gly Glu Trp Leu Ile
 130 135 140
 Gln Asn Ser Ala Asn Gly Ala Val Gly Arg Met Leu Ala Gln Leu Ala
 145 150 155 160
 Glu Ser Arg Gly Ile His Val Val Gly Leu Val Arg Arg Asp Ala Gly
 165 170 175
 Val Gln Glu Leu Ala Ala Gln Asn Ile Ser Gly Val Val Ser Thr Glu
 180 185 190
 Thr Pro Gly Trp Glu Lys Gln Val Glu Asp Ile Thr Gly Gly Ala Ser
 195 200 205
 Ile Ala Val Ala Leu Asp Ser Val Gly Gly Ser Ser Ala Ala Asp Leu
 210 215 220
 Val Lys Leu Leu Gly Glu Gly Gly Thr Leu Val Ser Phe Gly Ala Met
 225 230 235 240
 Gly Asn Pro Ile Met Glu Ile Pro Ser Gly Pro Val Ile Phe Lys His
 245 250 255
 Ile Thr Val Lys Gly Phe Trp Gly Ser Lys Val Ser Arg Glu Met Pro
 260 265 270
 Ala Glu Lys Lys Thr Gln Leu Phe Gly Glu Leu Ile Ala Arg Ile Leu
 275 280 285
 Asp Gly Thr Leu Thr Leu Pro Val Asp Ser Thr Phe Asp Ala Ala Asp
 290 295 300
 Ile Val Ser Ala Val Arg Ala Ser Ser Glu Pro Gly Arg Ala Gly Lys
 305 310 315 320
 Val Leu Ile Arg Phe
 325

<210> 2339

<211> 726

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> {101}..(703)

<223> RXA01622

<400> 2339

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gccatcgag agctgaagag ctggtgggaa ggagaaaaca atg agt gat ttt tat 115
 Met Ser Asp Phe Tyr
 1 5

gcc gac agg ttg ttt aac gcg atg gag cgc aat gag gta gct cca ggc 163
 Ala Asp Arg Leu Phe Asn Ala Met Glu Arg Asn Glu Val Ala Pro Gly
 10 15 20

atg ttg ttg gtg gct gcg ccc gat atg gcg tcg gag gat ttt gag cgc 211
 Met Leu Leu Val Ala Ala Pro Asp Met Ala Ser Glu Asp Phe Glu Arg
 25 30 35

agc atc gtg ttg atc atc gag cat tct cct gcc acc act ttt ggt gtg 259
 Ser Ile Val Leu Ile Ile Glu His Ser Pro Ala Thr Thr Phe Gly Val
 40 45 50

aac att tct tca cgt tcc gat gtt gct gtg gcc aat gtg ttg ccc gag 307
 Asn Ile Ser Ser Arg Ser Asp Val Ala Val Ala Asn Val Leu Pro Glu
 55 60 65

tgg gtg gac ctc acc tcg aag cca cag gca ctg tac atc ggt ggg ccg 355
 Trp Val Asp Leu Thr Ser Lys Pro Gln Ala Leu Tyr Ile Gly Gly Pro
 70 75 80 85

ttg agc cag cag gct gtg gtt ggt ttg ggc gtg acc aag ccg ggc gtg 403
 Leu Ser Gln Gln Ala Val Val Gly Leu Gly Val Thr Lys Pro Gly Val
 90 95 100

gat att gaa aat tcc acc agc ttc aac aag ctc gcc aac cgc ctg gtg 451
 Asp Ile Glu Asn Ser Thr Ser Phe Asn Lys Leu Ala Asn Arg Leu Val
 105 110 115

cac gtg gat ctg cgt tct gca cct gaa gat gtg gct gat gat ctt gag 499
 His Val Asp Leu Arg Ser Ala Pro Glu Asp Val Ala Asp Asp Leu Glu
 120 125 130

ggc atg cgc ttt ttt gcg ggc tac gcg gag tgg gct ccg ggc cag ctc 547
 Gly Met Arg Phe Phe Ala Gly Tyr Ala Glu Trp Ala Pro Gly Gln Leu
 135 140 145

aac gag gaa att gag cag ggt gat tgg ttc gtc aca cct gcg ttg ccg 595
 Asn Glu Glu Ile Glu Gln Gly Asp Trp Phe Val Thr Pro Ala Leu Pro
 150 155 160 165

tcg gac att atc gcg ccg ggc cgc gtc gat att tgg ggc gac gtg atg 643
 Ser Asp Ile Ile Ala Pro Gly Arg Val Asp Ile Trp Gly Asp Val Met
 170 175 180

cgt cga caa gca atg cct ttg ccg ttg tat tcc acg ttt ccg tcg gac 691
 Arg Arg Gln Ala Met Pro Leu Pro Leu Tyr Ser Thr Phe Pro Ser Asp
 185 190 195

cct tca gat aat tagatgagtt ccgaaaatttt aaa
 Pro Ser Asp Asn
 200

726

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 <211> 201
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2340
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 Glu Val Ala Pro Gly Met Leu Leu Val Ala Ala Pro Asp Met Ala Ser
 20 25 30
 Glu Asp Phe Glu Arg Ser Ile Val Leu Ile Ile Glu His Ser Pro Ala
 35 40 45
 Thr Thr Phe Gly Val Asn Ile Ser Ser Arg Ser Asp Val Ala Val Ala
 50 55 60
 Asn Val Leu Pro Glu Trp Val Asp Leu Thr Ser Lys Pro Gln Ala Leu
 65 70 75 80
 Tyr Ile Gly Gly Pro Leu Ser Gln Gln Ala Val Val Gly Leu Gly Val
 85 90 95
 Thr Lys Pro Gly Val Asp Ile Glu Asn Ser Thr Ser Phe Asn Lys Leu
 100 105 110
 Ala Asn Arg Leu Val His Val Asp Leu Arg Ser Ala Pro Glu Asp Val
 115 120 125
 Ala Asp Asp Leu Glu Gly Met Arg Phe Phe Ala Gly Tyr Ala Glu Trp
 130 135 140
 Ala Pro Gly Gln Leu Asn Glu Glu Ile Glu Gln Gly Asp Trp Phe Val
 145 150 155 160
 Thr Pro Ala Leu Pro Ser Asp Ile Ile Ala Pro Gly Arg Val Asp Ile
 165 170 175
 Trp Gly Asp Val Met Arg Arg Gln Ala Met Pro Leu Pro Leu Tyr Ser
 180 185 190
 Thr Phe Pro Ser Asp Pro Ser Asp Asn
 195 200

<210> 2341
 <211> 834
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(811)
 <223> RXA01623

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gttgattatcc acgtttccgt cggacccttc agataattag atg agt tcc gaa aat 115
Met Ser Ser Glu Asn
1 5

tta aaa gaa att cgc ggc gga atc ggt gag act tta acg gtc ggt ttg 163
Leu Lys Glu Ile Arg Gly Gly Ile Gly Glu Thr Leu Thr Val Gly Leu
10 15 20

ggg ctg att ccg ctg ggt ttg gcc ttt ggg ctg ttg atg gtc cag aca 211
Gly Leu Ile Pro Leu Gly Leu Ala Phe Gly Leu Leu Met Val Gln Thr
25 30 35

ggg ttc gcc tgg tgg tgg acg ccg att ttc tcc ttc gtg atc tat gcc 259
Gly Phe Ala Trp Trp Trp Thr Pro Ile Phe Ser Phe Val Ile Tyr Ala
40 45 50

ggg tgc atg gaa ttt ctg gca atc ggc atg gtc acc gca ggt atc gcc 307
Gly Ser Met Glu Phe Leu Ala Ile Gly Met Val Thr Ala Gly Ile Gly
55 60 65

ccg ttt tgc gcg gcg gtc gct ggt ttc atg gtg aat ttc cgc cac att 355
Pro Phe Ser Ala Ala Val Ala Gly Phe Met Val Asn Phe Arg His Ile
70 75 80 85

ttc tac ggt ctc acc ttc cca cgc cac cgc atc aag tcc gcc gcc gcc 403
Phe Tyr Gly Leu Thr Phe Pro Arg His Arg Ile Lys Ser Gly Ala Gly
90 95 100

cgc gcc tat tcc acc tac gcg ctt acc gac gag tcc tac gcc atc gtg 451
Arg Ala Tyr Ser Thr Tyr Ala Leu Thr Asp Glu Ser Tyr Ala Ile Val
105 110 115

tca gcc cgc cca cct ggc gat atc agt ggc acg ccg gtg ctt acc gtt 499
Ser Ala Arg Pro Pro Gly Asp Ile Ser Gly Thr Arg Val Leu Thr Val
120 125 130

caa att ttg tgc caa gct ctg tgg gtt atc cca gga att att gcc gcc 547
Gln Ile Leu Cys Gln Ala Leu Trp Val Ile Pro Gly Ile Ile Gly Ala
135 140 145

ttg gtt ggt caa gtg ctg ccc gat gat cta aaa ggc atg gat ttt gcc 595
Leu Val Gly Gln Val Leu Pro Asp Asp Leu Lys Gly Met Asp Phe Ala
150 155 160 165

ctg acc gcg ctg ttt gtg gtg ctg gcg tgg gag gca ttc aaa aat aac 643
Leu Thr Ala Leu Phe Val Val Leu Ala Trp Glu Ala Phe Lys Asn Asn
170 175 180

aag gat tat tgc ctg cca tta ttc gcg gtg gta ttg gct ctg gtt tcc 691
Lys Asp Tyr Ser Leu Pro Leu Phe Ala Val Val Leu Ala Leu Val Ser
185 190 195

ggg ttt gtg gcg ccc gag cag atg ctg gtt atc gct ttg acc acg tac 739
Gly Phe Val Ala Pro Glu Gln Met Leu Val Ile Ala Leu Thr Thr Tyr
200 205 210

ttt ttg atc ctt ctt ctc cgc gtc cgc ttc ccc aac ctg gac aag aaa 787

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Phe Leu Ile Leu Leu Leu Arg Val Arg Phe Pro Asn Leu Asp Lys Lys
 215 220 225

ctg gag atc agg act tcc cat gag tgagtttggc ctgccagaag ggc 834
 Leu Glu Ile Arg Thr Ser His Glu
 230 235

<210> 2342

<211> 237

<212> PRT

<213> Corynebacterium glutamicum

<400> 2342

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Leu Thr Val Gly Leu Gly Leu Ile Pro Leu Gly Leu Ala Phe Gly Leu
 20 25 30

Leu Met Val Gln Thr Gly Phe Ala Trp Trp Trp Thr Pro Ile Phe Ser
 35 40 45

Phe Val Ile Tyr Ala Gly Ser Met Glu Phe Leu Ala Ile Gly Met Val
 50 55 60

Thr Ala Gly Ile Gly Pro Phe Ser Ala Ala Val Ala Gly Phe Met Val
 65 70 75 80

Asn Phe Arg His Ile Phe Tyr Gly Leu Thr Phe Pro Arg His Arg Ile
 85 90 95

Lys Ser Gly Ala Gly Arg Ala Tyr Ser Thr Tyr Ala Leu Thr Asp Glu
 100 105 110

Ser Tyr Ala Ile Val Ser Ala Arg Pro Pro Gly Asp Ile Ser Gly Thr
 115 120 125

Arg Val Leu Thr Val Gln Ile Leu Cys Gln Ala Leu Trp Val Ile Pro
 130 135 140

Gly Ile Ile Gly Ala Leu Val Gly Gln Val Leu Pro Asp Asp Leu Lys
 145 150 155 160

Gly Met Asp Phe Ala Leu Thr Ala Leu Phe Val Val Leu Ala Trp Glu
 165 170 175

Ala Phe Lys Asn Asn Lys Asp Tyr Ser Leu Pro Leu Phe Ala Val Val
 180 185 190

Leu Ala Leu Val Ser Gly Phe Val Ala Pro Glu Gln Met Leu Val Ile
 195 200 205

Ala Leu Thr Thr Tyr Phe Leu Ile Leu Leu Leu Arg Val Arg Phe Pro
 210 215 220

Asn Leu Asp Lys Lys Leu Glu Ile Arg Thr Ser His Glu
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<210> 2343

<211> 468
 <212> DNA
 <213> *Corynebacterium glutamicum*

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 <222> (101)..(445)
 <223> RXA01624

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ttcccccaacc tggacaagaa actggagatc aggacttccc atg agt gag ttt ggc 115
 Met Ser Glu Phe Gly
 1 5

ctg cca gaa ggc gtc acg ctg ctc aac gtc gcc gtc gtg ttg atc ccc 163
 Leu Pro Glu Gly Val Thr Leu Leu Asn Val Ala Ala Val Leu Ile Pro
 10 15 20

atc gcg atc atc acc ttg ctg ctg cgc atc ttc ccc ttc gcc gcg atg 211
 Ile Ala Ile Ile Thr Leu Leu Leu Arg Ile Phe Pro Phe Ala Ala Met
 25 30 35

aaa cgc gtc aac agc aac caa ctc atg gga gtt ttg ggg cgc aca atg 259
 Lys Arg Val Asn Ser Asn Gln Leu Met Gly Val Leu Gly Arg Thr Met
 40 45 50

cca gtc gga gtg atg gtc gta ttg gtc att tac acg ctc ttt ggc cag 307
 Pro Val Gly Val Met Val Val Leu Val Ile Tyr Thr Leu Phe Gly Gln
 55 60 65

gtc agt gcg cca ggt ggt gtg ggt gct tca ctg atc gcg gtg gca ttc 355
 Val Ser Ala Pro Gly Gly Val Gly Ala Ser Leu Ile Ala Val Ala Phe
 70 75 80 85

acc gcg ctg ctg cac tgg ttg aaa ggc tcc gcc ggg ctg tcc atc gtc 403
 Thr Ala Leu Leu His Trp Leu Lys Gly Ser Ala Gly Leu Ser Ile Val
 90 95 100

ggc ggc acc ttg gcc tac atg ttt ctg gtc aac gtc gtt ttt 445
 Gly Gly Thr Leu Ala Tyr Met Phe Leu Val Asn Val Val Phe
 105 110 115

taaaagatgc ttctcgacgc aaa 468

<210> 2344
 <211> 115
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 2344
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 20 25 30
 Pro Phe Ala Ala Met Lys Arg Val Asn Ser Asn Gln Leu Met Gly Val
 35 40 45

Leu Gly Arg Thr Met Pro Val Gly Val Met Val Val Leu Val Ile Tyr
 50 55 60
 Thr Leu Phe Gly Gln Val Ser Ala Pro Gly Gly Val Gly Ala Ser Leu
 65 70 75 80
 Ile Ala Val Ala Phe Thr Ala Leu Leu His Trp Leu Lys Gly Ser Ala
 85 90 95
 Gly Leu Ser Ile Val Gly Gly Thr Leu Ala Tyr Met Phe Leu Val Asn
 100 105 110
 Val Val Phe
 115

<210> 2345
 <211> 1137
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1114)
 <223> RXA01628
 <400> 2345
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 ttctctaagg aagctccgac ccatcacatg tagccttttc ttg gtt ctc gta ggg 115
 Leu Val Leu Val Gly
 1 5
 tgc agc aac acg gca gag tcc acg acc acc gat acg gca ggc tcc act 163
 Cys Ser Asn Thr Ala Glu Ser Thr Thr Thr Asp Thr Ala Gly Ser Thr
 10 15 20
 gaa act tca tca cag att tca ccc acc act cca gtc agc acc acc gaa 211
 Glu Thr Ser Ser Gln Ile Ser Pro Thr Thr Pro Val Ser Thr Thr Glu
 25 30 35
 gca gcg ccg cct gaa gat cca agc gca aac gct ttg gaa gag tat gct 259
 Ala Ala Pro Pro Glu Asp Pro Ser Ala Asn Ala Leu Glu Glu Tyr Ala
 40 45 50
 cag atc ctt gcc aat cca agc atc tac ccc tta acc gaa att tca caa 307
 Gln Ile Leu Ala Asn Pro Ser Ile Tyr Pro Leu Thr Glu Ile Ser Gln
 55 60 65
 ttc gtc ccc aca ggc aca tat gcc tac aca ctt gtt gaa gca act tcc 355
 Phe Val Pro Thr Gly Thr Tyr Ala Tyr Thr Leu Val Glu Ala Thr Ser
 70 75 80 85
 gat tcc atc cca gaa cta cta ctc cgc gcc gat agt cac gaa ttc gcg 403
 Asp Ser Ile Pro Glu Leu Leu Leu Arg Ala Asp Ser His Glu Phe Ala
 90 95 100
 cca att ttg gtt ttc acc tat gac gaa aac aca caa tcc gca acc caa 451
 Pro Ile Leu Val Phe Thr Tyr Asp Glu Asn Thr Gln Ser Ala Thr Gln
 105 110 115

gct gga gga gtc cta att gac ggt gtc gcc agc gcc ggc ggt tca cga	499
Ala Gly Gly Val Leu Ile Asp Gly Val Ala Ser Ala Gly Gly Ser Arg	
120 125 130	
gtc aag gtc aga gct tca aat tca gga gca gga atc tac caa ttg aat	547
Val Lys Val Arg Ala Ser Asn Ser Gly Ala Gly Ile Tyr Gln Leu Asn	
135 140 145	
tgg tac tcg ata caa cca gtt ggc gaa agc tct ttg tac gga atc caa	595
Trp Tyr Ser Ile Gln Pro Val Gly Glu Ser Ser Leu Tyr Gly Ile Gln	
150 155 160 165	
gga aac tcc ctg aca caa atc gca gac ccc gag gat ttc atg gtc cgt	643
Gly Asn Ser Leu Thr Gln Ile Ala Asp Pro Glu Asp Phe Met Val Arg	
170 175 180	
gaa cta tta cct gac cac cac gaa att acc tgg gtt gat tcc aac gac	691
Glu Leu Leu Pro Asp His His Glu Ile Thr Trp Val Asp Ser Asn Asp	
185 190 195	
ccc tcc ggc cta tca acc gtt cag act ggt gga gcc aac att caa caa	739
Pro Ser Gly Leu Ser Thr Val Gln Thr Gly Gly Ala Asn Ile Gln Gln	
200 205 210	
gca gcc cca act ccc gtt caa cag cct gcg tca aac ctg cac tac ttc	787
Ala Ala Pro Thr Pro Val Gln Gln Pro Ala Ser Asn Leu His Tyr Phe	
215 220 225	
tct ggt gta gta acg atg cag acc gcc ggc gaa ctc atg cga ggt gaa	835
Ser Gly Val Val Thr Met Gln Thr Ala Gly Glu Leu Met Arg Gly Glu	
230 235 240 245	
cga act ccc aat ggt gag cct gcc act gat ctc tat ctc gta ctg gtc	883
Arg Thr Pro Asn Gly Glu Pro Ala Thr Asp Leu Tyr Leu Val Leu Val	
250 255 260	
ctt gat tcc cca att gaa atc aca gca cga aac gca gct aca gac cct	931
Leu Asp Ser Pro Ile Glu Ile Thr Ala Arg Asn Ala Ala Thr Asp Pro	
265 270 275	
cag act cgt acc att tcc gaa gtc agc ctc ggc cga tac atc ccc gct	979
Gln Thr Arg Thr Ile Ser Glu Val Ser Leu Gly Arg Tyr Ile Pro Ala	
280 285 290	
gat ggt gac aat gat tgg ata ggc tac ctc gac acc cac gtg gaa atc	1027
Asp Gly Asp Asn Asp Trp Ile Gly Tyr Leu Asp Thr His Val Glu Ile	
295 300 305	
act gca aca acg gat cag gtc tgg ttc cca acc gac acc ggt cta cct	1075
Thr Ala Thr Thr Asp Gln Val Trp Phe Pro Thr Asp Thr Gly Leu Pro	
310 315 320 325	
ctt gga atg ctt cgt cta gcg gac tac aaa agc atc tca taaaccgacg	1124
Leu Gly Met Leu Arg Leu Ala Asp Tyr Lys Ser Ile Ser	
330 335	
cagcactcgt cga	1137

<210> 2346

<211> 338

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2346

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Thr Ala Gly Ser Thr Glu Thr Ser Ser Gln Ile Ser Pro Thr Thr Thr Pro
 20 25 30

Val Ser Thr Thr Glu Ala Ala Pro Pro Glu Asp Pro Ser Ala Asn Ala
 35 40 45

Leu Glu Glu Tyr Ala Gln Ile Leu Ala Asn Pro Ser Ile Tyr Pro Leu
 50 55 60

Thr Glu Ile Ser Gln Phe Val Pro Thr Gly Thr Tyr Ala Tyr Thr Leu
 65 70 75 80

Val Glu Ala Thr Ser Asp Ser Ile Pro Glu Leu Leu Leu Arg Ala Asp
 85 90 95

Ser His Glu Phe Ala Pro Ile Leu Val Phe Thr Tyr Asp Glu Asn Thr
 100 105 110

Gln Ser Ala Thr Gln Ala Gly Gly Val Leu Ile Asp Gly Val Ala Ser
 115 120 125

Ala Gly Gly Ser Arg Val Lys Val Arg Ala Ser Asn Ser Gly Ala Gly
 130 135 140

Ile Tyr Gln Leu Asn Trp Tyr Ser Ile Gln Pro Val Gly Glu Ser Ser
 145 150 155 160

Leu Tyr Gly Ile Gln Gly Asn Ser Leu Thr Gln Ile Ala Asp Pro Glu
 165 170 175

Asp Phe Met Val Arg Glu Leu Leu Pro Asp His His Glu Ile Thr Trp
 180 185 190

Val Asp Ser Asn Asp Pro Ser Gly Leu Ser Thr Val Gln Thr Gly Gly
 195 200 205

Ala Asn Ile Gln Gln Ala Ala Pro Thr Pro Val Gln Gln Pro Ala Ser
 210 215 220

Asn Leu His Tyr Phe Ser Gly Val Val Thr Met Gln Thr Ala Gly Glu
 225 230 235 240

Leu Met Arg Gly Glu Arg Thr Pro Asn Gly Glu Pro Ala Thr Asp Leu
 245 250 255

Tyr Leu Val Leu Val Leu Asp Ser Pro Ile Glu Ile Thr Ala Arg Asn
 260 265 270

Ala Ala Thr Asp Pro Gln Thr Arg Thr Ile Ser Glu Val Ser Leu Gly
 275 280 285

Arg Tyr Ile Pro Ala Asp Gly Asp Asn Asp Trp Ile Gly Tyr Leu Asp
 290 295 300

Thr His Val Glu Ile Thr Ala Thr Thr Asp Gln Val Trp Phe Pro Thr
305 310 315 320

Asp Thr Gly Leu Pro Leu Gly Met Leu Arg Leu Ala Asp Tyr Lys Ser
325 330 335

Ile Ser

<210> 2347

<211> 1200

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1177)

<223> RXA01630

<400> 2347

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ccagataaaa acctgcgggt tgcgttttag gagaattccc atg agt gat caa aaa 115
Met Ser Asp Gln Lys
1 5

att gtt gtt ggc ctg cta ggc atc acc cac cgg cat gcg tcg gcg cgg 163
Ile Val Val Gly Leu Leu Gly Ile Thr His Pro His Ala Ser Ala Arg
10 15 20

gtg cgt gcc ctg cgt gaa att gat ggg gta gag gtc gtc gcc gcc gcg 211
Val Arg Ala Leu Arg Glu Ile Asp Gly Val Glu Val Val Ala Ala Ala
25 30 35

gat act gat tcc cgc ctg cag tac ttc acc gac aaa tat gat gtt gaa 259
Asp Thr Asp Ser Arg Leu Gln Tyr Phe Thr Asp Lys Tyr Asp Val Glu
40 45 50

ccc cgc gag atc gat gac gtc ttg aac gac gat cgc atc aac gcc atc 307
Pro Arg Glu Ile Asp Asp Val Leu Asn Asp Asp Arg Ile Asn Ala Ile
55 60 65

atg gtt cac tcc aag agc aag gac atg gtc cct cac gcc aag cgc gcg 355
Met Val His Ser Lys Ser Lys Asp Met Val Pro His Ala Lys Arg Ala
70 75 80 85

ctc gcg gcc gga aaa tcc gtc gtc gtg gag aag ccc gcc ggg gga aca 403
Leu Ala Ala Gly Lys Ser Val Val Val Glu Lys Pro Gly Gly Gly Thr
90 95 100

gtg gcg gat ctt gag gag ctg ctg gcc ctc aaa gaa gct gcc gat cct 451
Val Ala Asp Leu Glu Glu Leu Leu Ala Leu Lys Glu Ala Ala Asp Pro
105 110 115

cag cga atc gtg cag gtc ggg tac aac gtc cgc ctg tct gaa tcg gtt 499
Gln Arg Ile Val Gln Val Gly Tyr Asn Val Arg Leu Ser Glu Ser Val
120 125 130

cag aga tta aaa gag ctt ctg gac gcc gcc ctc atc gcc gaa gtc gtc 547

Gln Arg Leu Lys Glu Leu Leu Asp Ala Gly Leu Ile Gly Glu Val Val	
135 140 145	
agc gtg caa gca cgc gcc gcc gca aaa gta ggt gag cat atc acc gag	595
Ser Val Gln Ala Arg Gly Ala Ala Lys Val Gly Glu His Ile Thr Glu	
150 155 160 165	
cac ctc aac caa ccc gca gac atg gcc ggt gtg ttg tgg att ctt gcc	643
His Leu Asn Gln Pro Ala Asp Met Gly Gly Val Leu Trp Ile Leu Gly	
170 175 180	
tgc cac atg ctc gat gca ttg gtg gaa gtc ttc gga gct cca gaa tcc	691
Cys His Met Leu Asp Ala Leu Val Glu Val Phe Gly Ala Pro Glu Ser	
185 190 195	
gtg aac gcc cga gtg cat aag acc gca aaa ctc tct gac gac acc agc	739
Val Asn Ala Arg Val His Lys Thr Ala Lys Leu Ser Asp Asp Thr Ser	
200 205 210	
cgc gaa gac tca gcc tcc gca ctg ctg tac tac cca gat ttc tcc gtc	787
Arg Glu Asp Ser Ala Ser Ala Leu Leu Tyr Tyr Pro Asp Phe Ser Val	
215 220 225	
agc ttc agc ttc gac gcc cac gat gat ctg gaa tgg ttc gaa agc tcc	835
Ser Phe Ser Phe Asp Gly His Asp Asp Leu Glu Trp Phe Glu Ser Ser	
230 235 240 245	
cga ctc acg gtc tat gga acc aag gcc atg atc gaa gcc gga atc ctc	883
Arg Leu Thr Val Tyr Gly Thr Lys Gly Met Ile Glu Ala Gly Ile Leu	
250 255 260	
cct cag aca ctg cgc gta tac ctc aat gag tca cgc cag gcc tgg cca	931
Pro Gln Thr Leu Arg Val Tyr Leu Asn Glu Ser Arg Gln Gly Trp Pro	
265 270 275	
cag ggt tgg acc gag tgg acc cag agc tac ttc acc cca cgg ttt gct	979
Gln Gly Trp Thr Glu Trp Thr Gln Ser Tyr Phe Thr Pro Phe Ala	
280 285 290	
cgc aca gaa tcc aac aaa ttc tca gag ctt cca gag cta gaa aac atc	1027
Arg Thr Glu Ser Asn Lys Phe Ser Glu Leu Pro Glu Leu Glu Asn Ile	
295 300 305	
agc aac ttc cgc aca gaa atg cag ggg tgg gtg aat tcc att cgc act	1075
Ser Asn Phe Arg Thr Glu Met Gln Gly Trp Val Asn Ser Ile Arg Thr	
310 315 320 325	
gga tcc cgc aat gtg gcg cca gtt gag gat got ctc aca gtc gct cgc	1123
Gly Ser Arg Asn Val Ala Pro Val Glu Asp Ala Leu Thr Val Ala Arg	
330 335 340	
att gtc agt gca tgc tac gaa tcc gac aac aac cag gcc att tcc gta	1171
Ile Val Ser Ala Cys Tyr Glu Ser Asp Asn Asn Gln Gly Ile Ser Val	
345 350 355	
aac atc taagaggagc actccatgaa acc	1200
Asn Ile	

<211> 359

<212> PRT

<213> Corynebacterium glutamicum

<400> 2348

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His Ala Ser Ala Arg Val Arg Ala Leu Arg Glu Ile Asp Gly Val Glu
 20 25 30

Val Val Ala Ala Ala Asp Thr Asp Ser Arg Leu Gln Tyr Phe Thr Asp
 35 40 45

Lys Tyr Asp Val Glu Pro Arg Glu Ile Asp Asp Val Leu Asn Asp Asp
 50 55 60

Arg Ile Asn Ala Ile Met Val His Ser Lys Ser Lys Asp Met Val Pro
 65 70 75 80

His Ala Lys Arg Ala Leu Ala Ala Gly Lys Ser Val Val Val Glu Lys
 85 90 95

Pro Gly Gly Gly Thr Val Ala Asp Leu Glu Glu Leu Leu Ala Leu Lys
 100 105 110

Glu Ala Ala Asp Pro Gln Arg Ile Val Gln Val Gly Tyr Asn Val Arg
 115 120 125

Leu Ser Glu Ser Val Gln Arg Leu Lys Glu Leu Leu Asp Ala Gly Leu
 130 135 140

Ile Gly Glu Val Val Ser Val Gln Ala Arg Gly Ala Ala Lys Val Gly
 145 150 155 160

Glu His Ile Thr Glu His Leu Asn Gln Pro Ala Asp Met Gly Gly Val
 165 170 175

Leu Trp Ile Leu Gly Cys His Met Leu Asp Ala Leu Val Glu Val Phe
 180 185 190

Gly Ala Pro Glu Ser Val Asn Ala Arg Val His Lys Thr Ala Lys Leu
 195 200 205

Ser Asp Asp Thr Ser Arg Glu Asp Ser Ala Ser Ala Leu Leu Tyr Tyr
 210 215 220

Pro Asp Phe Ser Val Ser Phe Ser Phe Asp Gly His Asp Asp Leu Glu
 225 230 235 240

Trp Phe Glu Ser Ser Arg Leu Thr Val Tyr Gly Thr Lys Gly Met Ile
 245 250 255

Glu Ala Gly Ile Leu Pro Gln Thr Leu Arg Val Tyr Leu Asn Glu Ser
 260 265 270

Arg Gln Gly Trp Pro Gln Gly Trp Thr Glu Trp Thr Gln Ser Tyr Phe
 275 280 285

Thr Pro Pro Phe Ala Arg Thr Glu Ser Asn Lys Phe Ser Glu Leu Pro
 290 295 300

Glu Leu Glu Asn Ile Ser Asn Phe Arg Thr Glu Met Gln Gly Trp Val
305 310 315 320

Asn Ser Ile Arg Thr Gly Ser Arg Asn Val Ala Pro Val Glu Asp Ala
325 330 335

Leu Thr Val Ala Arg Ile Val Ser Ala Cys Tyr Glu Ser Asp Asn Asn
340 345 350

Gln Gly Ile Ser Val Asn Ile
355

<210> 2349

<211> 1494

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1471)

<223> RXA01641

<400> 2349

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Leu Ala Ile Asp Asn
1 5

gcg ctg cgc gtg agc atc cgc ata gat ctc acc gtt gcc gat gcg ccc 163
Ala Leu Arg Val Ser Ile Arg Ile Asp Leu Thr Val Gly Asp Ala Pro
10 15 20

gct gct gtg gct gat gtg gcg cta cct gca ggt tcg agt ctg gcg gac 211
Ala Ala Val Ala Asp Val Ala Leu Pro Ala Gly Ser Ser Leu Ala Asp
25 30 35

att ttg gat gaa att tta gaa ctc acc gat gca ccc cgg att tcc agg 259
Ile Leu Asp Glu Ile Leu Glu Leu Thr Asp Ala Pro Arg Ile Ser Arg
40 45 50

cgg tgg gtg gct cac act gct gcg gga agt ccc att gat tgc ggg att 307
Pro Trp Val Ala His Thr Ala Ala Gly Ser Pro Ile Asp Cys Gly Ile
55 60 65

cgg ctt gca gaa aca caa gtg gaa caa gcc agc gtg gtg gtc ctt tca 355
Pro Leu Ala Glu Thr Gln Val Glu Gln Gly Ser Val Val Val Leu Ser
70 75 80 85

ccc gaa agg gac ttg gaa gcc ccc gtg ttg cgt gat gtc gcc gaa gcg 403
Pro Glu Arg Asp Leu Glu Ala Pro Val Leu Arg Asp Val Ala Glu Ala
90 95 100

ttg gtg gag ttt tct tcc acg aac cgc gcc ggg cac ctc gtg gaa ttg 451
Leu Val Glu Phe Ser Ser Thr Asn Arg Ala Gly His Leu Val Glu Leu
105 110 115

atg act ttc gcg ggg ctc atc ggg gct gcc gtg tta atg aca agt cct 499
Met Thr Phe Ala Gly Leu Ile Gly Ala Ala Val Leu Met Thr Ser Pro

120	125	130	
gct gcc tcc gga att att gtg ccc ggc cgc atg gga atc ttc gtc gca Ala Ala Ser Gly Ile Ile Val Pro Gly Arg Met Gly Ile Phe Val Ala 135 140 145			547
atc tgc gct cta ctg ctt ctg tgg ctc cca ccc gcg cac acc ccg atc Ile Cys Ala Leu Leu Leu Trp Leu Pro Ala His Thr Pro Ile 150 155 160 165			595
ctt cga aac gtc ctg ccg att acc ctg atc ttg ggc gca ggc gga gcg Leu Arg Asn Val Leu Pro Ile Thr Leu Ile Leu Gly Ala Gly Gly Ala 170 175 180			643
gta tca gtg ctg gtt gca ggc act tct ggg act tct ccc ggc gcg ctt Val Ser Val Leu Val Ala Gly Thr Ser Gly Thr Ser Pro Gly Ala Leu 185 190 195			691
acc tgg acg att ttc gct ggc gcg tgc act att ctt gcc agt tgc ctg Thr Trp Thr Ile Phe Ala Gly Ala Cys Thr Ile Leu Ala Ser Ser Leu 200 205 210			739
ctg gtt cat gtg gtg tat cgt cca gca att ctt ctg gtg gca aca ctg Leu Val His Val Val Tyr Arg Pro Ala Ile Leu Leu Val Ala Thr Leu 215 220 225			787
tcc aca ttg ggg ctc ggt ctc tta gtc ctt gca gca acc acc act ctg Ser Thr Leu Gly Leu Gly Leu Leu Val Leu Ala Ala Thr Thr Thr Leu 230 235 240 245			835
tgg aag ctc aaa gct acc gaa gat ttc agc ggt cca gca gcg atc acg Trp Lys Leu Lys Ala Thr Glu Asp Phe Ser Gly Pro Ala Ala Ile Thr 250 255 260			883
gtc acc gct tcc acc atc acc atg tgc ttc gcc ccg aaa atc gca gca Val Thr Ala Ser Thr Ile Thr Met Cys Phe Ala Pro Lys Ile Ala Ala 265 270 275			931
tcg cta gca ggc ctg cgc gtc cca tgc ctt ccc acc gcc ggc gaa gat Ser Leu Ala Gly Leu Arg Val Pro Ser Leu Pro Thr Ala Gly Glu Asp 280 285 290			979
ctc tcc gtc agc gac ctc acc atg act gat ccc gag aaa aga ata aaa Leu Ser Val Ser Asp Leu Thr Met Thr Asp Pro Glu Lys Arg Ile Lys 295 300 305			1027
aca aca aag acg ctt ttc gac gcc cag atc ctt ggc ctt ggc gtt ttg Thr Thr Lys Thr Leu Phe Asp Ala Gln Ile Leu Gly Leu Gly Val Leu 310 315 320 325			1075
agc ggg cct ttg gcg ttg ttg tgc gtt acc ccg ggc acc tgg aca acc Ser Gly Pro Leu Ala Leu Leu Ser Val Thr Pro Gly Thr Trp Thr Thr 330 335 340			1123
acc gtt ttt agt tta tgc atc gcg gtg gct tgc ctg ctt cac gct aat Thr Val Phe Ser Leu Cys Ile Ala Val Ala Ser Leu Leu His Ala Asn 345 350 355			1171
cgt cat caa gca cca att ccc acg tgg aca ttg atg ggg tta tct gcc Arg His Gln Ala Pro Ile Pro Thr Trp Thr Leu Met Gly Leu Ser Ala 360 365 370			1219

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ctt ggt ttc att tcc atg gcg tta tcc gca agc cga tca ggt tca cta 1267
Leu Gly Phe Ile Ser Met Ala Leu Ser Ala Ser Arg Ser Gly Ser Leu
375 380 385

att gca ctg atc ggt tct gtg gtt atc atc gct gtg ctg gtc agc gtg 1315
Ile Ala Leu Ile Gly Ser Val Val Ile Ile Ala Val Leu Val Ser Val
390 395 400 405

gca ttg tgg atc agt aca gtc ccc acg ctg gaa ccc acc acc att gtg 1363
Ala Leu Trp Ile Ser Thr Val Pro Thr Leu Glu Pro Thr Thr Ile Val
410 415 420

tgg ctt gaa agg ttg gaa tca ctg tgt ctt gca gct agt ctg cca ctc 1411
Trp Leu Glu Arg Leu Glu Ser Leu Cys Leu Ala Ala Ser Leu Pro Leu
425 430 435

gca ctg cat ttg ctg gat gta ttt gga atg ctg cgc ggt ctt gat att 1459
Ala Leu His Leu Leu Asp Val Phe Gly Met Leu Arg Gly Leu Asp Ile
440 445 450

gga ttc ggt gga taagatgcgc agactcatcg cg 1494
Gly Phe Gly Gly
455

<210> 2350
<211> 457
<212> PRT
<213> Corynebacterium glutamicum

<400> 2350
Leu Ala Ile Asp Asn Ala Leu Arg Val Ser Ile Arg Ile Asp Leu Thr
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Val Gly Asp Ala Pro Ala Ala Val Ala Asp Val Ala Leu Pro Ala Gly
20 25 30
Ser Ser Leu Ala Asp Ile Leu Asp Glu Ile Leu Glu Leu Thr Asp Ala
35 40 45
Pro Arg Ile Ser Arg Pro Trp Val Ala His Thr Ala Ala Gly Ser Pro
50 55 60
Ile Asp Cys Gly Ile Pro Leu Ala Glu Thr Gln Val Glu Gln Gly Ser
65 70 75 80
Val Val Val Leu Ser Pro Glu Arg Asp Leu Glu Ala Pro Val Leu Arg
85 90 95
Asp Val Ala Glu Ala Leu Val Glu Phe Ser Ser Thr Asn Arg Ala Gly
100 105 110
His Leu Val Glu Leu Met Thr Phe Ala Gly Leu Ile Gly Ala Ala Val
115 120 125
Leu Met Thr Ser Pro Ala Ala Ser Gly Ile Ile Val Pro Gly Arg Met
130 135 140
Gly Ile Phe Val Ala Ile Cys Ala Leu Leu Leu Trp Leu Pro Pro
145 150 155 160

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<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1342)

<223> RXA01642

<400> 2351

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ggaatgctgc gcggtcttga tattggattc ggtggataag atg cgc aga ctc atc 115
 Met Arg Arg Leu Ile
 1 5

gcg gtt agc ttg gcc gct ctg ttt atg ttg gct tcc act cca gcg acg 163
 Ala Val Ser Leu Ala Ala Leu Phe Met Leu Ala Ser Thr Pro Ala Thr
 10 15 20

agg gca cag gaa gta gaa gct ctc gct tgc ccc gag gta gcg atc gcc 211
 Arg Ala Gln Glu Val Glu Ala Leu Ala Cys Pro Glu Val Ala Ile Ala
 25 30 35

gat cct tcc tcc gca gtt tta gat gaa cac ctt tcg cag tca tta tcc 259
 Asp Pro Ser Ser Ala Val Leu Asp Glu His Leu Ser Gln Ser Leu Ser
 40 45 50

caa gct cac caa cta gca act ggc gcc ggt gtg atg gtg gca gtc atc 307
 Gln Ala His Gln Leu Ala Thr Gly Ala Gly Val Met Val Ala Val Ile
 55 60 65

gac acc gga gta tcc ctg cat cca cgt ctg ccc cac tta att ccc ggc 355
 Asp Thr Gly Val Ser Leu His Pro Arg Leu Pro His Leu Ile Pro Gly
 70 75 80 85

ggt gat ttc gtg ggc gcc cac caa agc ccc gat gtg cca ggt gaa ctt 403
 Gly Asp Phe Val Gly Ala His Gln Ser Pro Asp Val Pro Gly Glu Leu
 90 95 100

atc gat tgc gac ggc cac ggc acc atc gtc gcc gga atc atc gcc tcc 451
 Ile Asp Cys Asp Gly His Gly Thr Ile Val Ala Gly Ile Ile Ala Ser
 105 110 115

caa gga aac ccc ggc acc ggc tgg cca tat gac ggc agc tcc gat cct 499
 Gln Gly Asn Pro Gly Thr Gly Trp Pro Tyr Asp Gly Ser Ser Asp Pro
 120 125 130

tat atc ggt gtc gcc cca gat tcc gga atc atc tcc att aaa caa acc 547
 Tyr Ile Gly Val Ala Pro Asp Ser Gly Ile Ile Ser Ile Lys Gln Thr
 135 140 145

agc tca tat gtg cgt act cgt gaa gat tcc aac gtc gga acg ctg agc 595
 Ser Ser Tyr Val Arg Thr Arg Glu Asp Ser Asn Val Gly Thr Leu Ser
 150 155 160 165

acc ctg gcg gaa tcc atc cac cga gct ctc gat tcc ggt gcc cac gtg 643
 Thr Leu Ala Glu Ser Ile His Arg Ala Leu Asp Ser Gly Ala His Val
 170 175 180

atc aat att tcc gtg gtg tcc tgt ttg ccc caa tca ccc gac gag gcc 691
 Ile Asn Ile Ser Val Val Ser Cys Leu Pro Gln Ser Pro Asp Glu Ala

185	190	195	
gca tgc ttc cag cct ctg acg gat gct ctt aac aga gca gaa ctt caa Ala Ser Phe Gln Pro Leu Thr Asp Ala Leu Asn Arg Ala Glu Leu Gln 200 205 210			739
ggg gtg ata gtg gtg gca gca gca gga aac ctc ggg cag gat tgt cca Gly Val Ile Val Val Ala Ala Gly Asn Leu Gly Gln Asp Cys Pro 215 220 225			787
gtt gga tct acc gtt tat cct gca cat tca gac act gtg ctc tct gtg Val Gly Ser Thr Val Tyr Pro Ala His Ser Asp Thr Val Leu Ser Val 230 235 240 245			835
tcg gca cgt ttt gat tct cac acg ctt gca gaa tat tcc atg cct ggc Ser Ala Arg Phe Asp Ser His Thr Leu Ala Glu Tyr Ser Met Pro Gly 250 255 260			883
aac caa caa atc ctc tct gca cca agc cac att cag gct ggt cta tca Asn Gln Gln Ile Leu Ser Ala Pro Ser His Ile Gln Ala Gly Leu Ser 265 270 275			931
ccg cgt ggc gac ggc ttc gcc agc cac atg atc acc acc gct ggc gaa Pro Arg Gly Asp Gly Phe Ala Ser His Met Ile Thr Thr Ala Gly Glu 280 285 290			979
agc ccc ttc gag ggc acc agt ttt gcc gct cca gtt gtc agc gcc aca Ser Pro Phe Glu Gly Thr Ser Phe Ala Ala Pro Val Val Ser Ala Thr 295 300 305			1027
gct gca ctg ctt cgc cag cat ttt ccc ttt gcc aca ccc tat gaa att Ala Ala Leu Leu Arg Gln His Phe Pro Phe Ala Thr Pro Tyr Glu Ile 310 315 320 325			1075
cgt gca cga atc ttc aac agc atc gac cct gca aga ggc gct att gat Arg Ala Arg Ile Phe Asn Ser Ile Asp Pro Ala Arg Gly Ala Ile Asp 330 335 340			1123
ccc tac ctg gca ctt act caa gaa atc tat ccc acc act ccc ctg gtt Pro Tyr Leu Ala Leu Thr Gln Glu Ile Tyr Pro Thr Thr Pro Leu Val 345 350 355			1171
cat gag atc gca cta agt gtt ccc acg ccg ccg gat gat tct cca cgg His Glu Ile Ala Leu Ser Val Pro Thr Pro Pro Asp Asp Ser Pro Arg 360 365 370			1219
gag cgg ggc atc cta gtt acc gca atc att gtt ggg ttg ctc gca gtg Glu Arg Gly Ile Leu Val Thr Ala Ile Ile Val Gly Leu Leu Ala Val 375 380 385			1267
tta gct gtg ctg atg gga cta cgc cga att cat cat cac tcg gcc ttt Leu Ala Val Leu Met Gly Leu Arg Arg Ile His His His Ser Ala Phe 390 395 400 405			1315
caa aaa gct agc tca agt gtt atc act taatctatga ggcaccgttc Gln Lys Ala Ser Ser Val Ile Thr 410			1362
aga			1365

<210> 2352

<211> 414

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2352

Met Arg Arg Leu Ile Ala Val Ser Leu Ala Ala Leu Phe Met Leu Ala
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Ser Thr Pro Ala Thr Arg Ala Gln Glu Val Glu Ala Leu Ala Cys Pro
 20 25 30

Glu Val Ala Ile Ala Asp Pro Ser Ser Ala Val Leu Asp Glu His Leu
 35 40 45

Ser Gln Ser Leu Ser Gln Ala His Gln Leu Ala Thr Gly Ala Gly Val
 50 55 60

Met Val Ala Val Ile Asp Thr Gly Val Ser Leu His Pro Arg Leu Pro
 65 70 75 80

His Leu Ile Pro Gly Gly Asp Phe Val Gly Ala His Gln Ser Pro Asp
 85 90 95

Val Pro Gly Glu Leu Ile Asp Cys Asp Gly His Gly Thr Ile Val Ala
 100 105 110

Gly Ile Ile Ala Ser Gln Gly Asn Pro Gly Thr Gly Trp Pro Tyr Asp
 115 120 125

Gly Ser Ser Asp Pro Tyr Ile Gly Val Ala Pro Asp Ser Gly Ile Ile
 130 135 140

Ser Ile Lys Gln Thr Ser Ser Tyr Val Arg Thr Arg Glu Asp Ser Asn
 145 150 155 160

Val Gly Thr Leu Ser Thr Leu Ala Glu Ser Ile His Arg Ala Leu Asp
 165 170 175

Ser Gly Ala His Val Ile Asn Ile Ser Val Val Ser Cys Leu Pro Gln
 180 185 190

Ser Pro Asp Glu Ala Ala Ser Phe Gln Pro Leu Thr Asp Ala Leu Asn
 195 200 205

Arg Ala Glu Leu Gln Gly Val Ile Val Val Ala Ala Ala Gly Asn Leu
 210 215 220

Gly Gln Asp Cys Pro Val Gly Ser Thr Val Tyr Pro Ala His Ser Asp
 225 230 235 240

Thr Val Leu Ser Val Ser Ala Arg Phe Asp Ser His Thr Leu Ala Glu
 245 250 255

Tyr Ser Met Pro Gly Asn Gln Gln Ile Leu Ser Ala Pro Ser His Ile
 260 265 270

Gln Ala Gly Leu Ser Pro Arg Gly Asp Gly Phe Ala Ser His Met Ile
 275 280 285

Thr Thr Ala Gly Glu Ser Pro Phe Glu Gly Thr Ser Phe Ala Ala Pro

290 295 300

Val Val Ser Ala Thr Ala Ala Leu Leu Arg Gln His Phe Pro Phe Ala
305 310 315 320

Thr Pro Tyr Glu Ile Arg Ala Arg Ile Phe Asn Ser Ile Asp Pro Ala
325 330 335

Arg Gly Ala Ile Asp Pro Tyr Leu Ala Leu Thr Gln Glu Ile Tyr Pro
340 345 350

Thr Thr Pro Leu Val His Glu Ile Ala Leu Ser Val Pro Thr Pro Pro
355 360 365

Asp Asp Ser Pro Arg Glu Arg Gly Ile Leu Val Thr Ala Ile Ile Val
370 375 380

Gly Leu Leu Ala Val Leu Ala Val Leu Met Gly Leu Arg Arg Ile His
385 390 395 400

His His Ser Ala Phe Gln Lys Ala Ser Ser Val Ile Thr
405 410

<210> 2353
<211> 549
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(526)
<223> RXA01643

<400> 2353
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cgatgtctcc ttcccaccgc cgagagacctg tagttaaccc atg ggc acg atg cga 115
Met Gly Thr Met Arg
1 5

gaa atg gtc agt gac cgc att gac cga cta caa gaa gca cac gcg cga 163
Glu Met Val Ser Asp Arg Ile Asp Arg Leu Gln Glu Ala His Ala Arg
10 15 20

tca aag cag aag aag ttc ggc ttc tta gtt cgg cca ggc acc ctg atc 211
Ser Lys Gln Lys Lys Phe Gly Phe Leu Val Arg Pro Gly Thr Leu Ile
25 30 35

ctt gga tgg ttg gtc acg atc atc ggt ctg atc acc att cca ctt ccc 259
Leu Gly Trp Leu Val Thr Ile Ile Gly Leu Ile Thr Ile Pro Leu Pro
40 45 50

ggc caa ggc tgg ctg acc acc ttc att ggt gtg ggc att ttg tct ctg 307
Gly Gln Gly Trp Leu Thr Thr Phe Ile Gly Val Gly Ile Leu Ser Leu
55 60 65

gag ctt aaa tgg gcg aag aac ctc ctg gcc tgg gga gtg cat cag tat 355
Glu Leu Lys Trp Ala Lys Asn Leu Leu Ala Trp Gly Val His Gln Tyr
70 75 80 85

$\langle 222 \rangle \quad (101) \dots (706)$

<223> RXA01645

<400> 2355

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ctgtgtcttg tggttcacgc cattcggcac ccaaaacccc gtg gtg cgc aaa ctc 115
 Val Val Arg Lys Leu
 1 5

tgg ccc agg gat ctg ctg cgc tcg agt ttc tat tgg aag atc atc ggc 163
 Trp Pro Arg Asp Leu Leu Arg Ser Ser Phe Tyr Trp Lys Ile Ile Gly
 10 15 20

tgg gat cga aaa tac tcc atc gct gat cgc ctg gaa gag cgc aaa ggc 211
 Trp Asp Arg Lys Tyr Ser Ile Ala Asp Arg Leu Glu Glu Arg Lys Gly
 25 30 35

cgc ccg gct agg gaa cgg gtg gtc caa gac gtg gaa gtt acg att gat 259
 Arg Pro Ala Arg Glu Arg Val Val Gln Asp Val Glu Val Thr Ile Asp
 40 45 50

aaa ctg cca gaa ttt ttg aaa tgg ttc ttt gaa agc agc gac atc gag 307
 Lys Leu Pro Glu Phe Leu Lys Trp Phe Phe Glu Ser Ser Asp Ile Glu
 55 60 65

ccg ctg tgg ctg tgc ccg atc aag ctt cgg gag gta cca ggt agt tcg 355
 Pro Leu Trp Leu Cys Pro Ile Lys Leu Arg Glu Val Pro Gly Ser Ser
 70 75 80 85

gtt ggt gct gga gaa att ttg agc tcc gct gaa gca atc gac tcc ggt 403
 Val Gly Ala Gly Glu Ile Leu Ser Ser Ala Glu Ala Ile Asp Ser Gly
 90 95 100

gct gct gaa cac cct tgg ccg ctg tat ccc ttg aag aag gac gtg ctg 451
 Ala Ala Glu His Pro Trp Pro Leu Tyr Pro Leu Lys Lys Asp Val Leu
 105 110 115

tgg gtc aac atc gga ttc tgg tcc tca gtg ccg gtt gat ctg atg ggc 499
 Trp Val Asn Ile Gly Phe Trp Ser Ser Val Pro Val Asp Leu Met Gly
 120 125 130

tcc gat gca cca gag gga gca ttt aac aga gaa atc gaa cgc gtc atg 547
 Ser Asp Ala Pro Glu Gly Ala Phe Asn Arg Glu Ile Glu Arg Val Met
 135 140 145

gca gag cta ggc gga cat aaa tcg ctg tac tcc gaa cgc ttc tac acc 595
 Ala Glu Leu Gly Gly His Lys Ser Leu Tyr Ser Glu Ala Phe Tyr Thr
 150 155 160 165

agg gaa gac ttt gaa aaa ctt tat ggc gga acc atc ccg cgc ctg cta 643
 Arg Glu Asp Phe Glu Lys Leu Tyr Gly Gly Thr Ile Pro Ala Leu Leu
 170 175 180

aaa aag cag tgg gat ccc cac agc cga ttc ccc ggt ttg tat gaa aag 691
 Lys Lys Gln Trp Asp Pro His Ser Arg Phe Pro Gly Leu Tyr Glu Lys
 185 190 195

aca gta aaa ggc gcc taggatcgct cactgtaggt aga 729
 Thr Val Lys Gly Ala
 200

<210> 2356
 <211> 202
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 2356
 Val Val Arg Lys Leu Trp Pro Arg Asp Leu Leu Arg Ser Ser Phe Tyr
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 Trp Lys Ile Ile Gly Trp Asp Arg Lys Tyr Ser Ile Ala Asp Arg Leu
 20 25 30
 Glu Glu Arg Lys Gly Arg Pro Ala Arg Glu Arg Val Val Gln Asp Val
 35 40 45
 Glu Val Thr Ile Asp Lys Leu Pro Glu Phe Leu Lys Trp Phe Phe Glu
 50 55 60
 Ser Ser Asp Ile Glu Pro Leu Trp Leu Cys Pro Ile Lys Leu Arg Glu
 65 70 75 80
 Val Pro Gly Ser Ser Val Gly Ala Gly Glu Ile Leu Ser Ser Ala Glu
 85 90 95
 Ala Ile Asp Ser Gly Ala Ala Glu His Pro Trp Pro Leu Tyr Pro Leu
 100 105 110
 Lys Lys Asp Val Leu Trp Val Asn Ile Gly Phe Trp Ser Ser Val Pro
 115 120 125
 Val Asp Leu Met Gly Ser Asp Ala Pro Glu Gly Ala Phe Asn Arg Glu
 130 135 140
 Ile Glu Arg Val Met Ala Glu Leu Gly Gly His Lys Ser Leu Tyr Ser
 145 150 155 160
 Glu Ala Phe Tyr Thr Arg Glu Asp Phe Glu Lys Leu Tyr Gly Gly Thr
 165 170 175
 Ile Pro Ala Leu Leu Lys Lys Gln Trp Asp Pro His Ser Arg Phe Pro
 180 185 190
 Gly Leu Tyr Glu Lys Thr Val Lys Gly Ala
 195 200

<210> 2357
 <211> 942
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(919)
 <223> RXA01646

<400> 2357
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 agcgctgcgcg cccacctatt aaggagtatg gtggccttac atg agc gga tta gtt 115

															Met 1	Ser 2	Gly 3	Leu 4	Val 5	
gac Asp	ccg Pro	gat Asp	agt Ser	act Thr 10	ttt Phe	tta Leu	aag Lys	acc Thr	atc Ile 15	gga Gly	aaa Lys	ctg Leu	agc Ser	aac Asn 20	agc Ser	163				
ttg Leu	tcc Ser	att Ile	ggt Gly 25	cgt Arg	gga Gly	gta Val	gat Asp	caa Gln 30	aaa Lys	gag Glu	gta Val	atc Ile	ccc Pro 35	aaa Pro Lys	ggc Gly	211				
tgg Trp	aac Asn	gcc Ala 40	cat His	tgg Trp	gag Glu	gca Ala	att Ile 45	aca Thr	aag Lys	ctt Leu	aag Lys	aga Arg 50	agc Ser	ttt Phe	gac Asp	259				
gcg Ala	att Ile 55	cct Pro	gct Ala	ggg Gly	gag Glu	cgg Arg 60	gtg Val	cgt Arg	tta Leu	gct Ala	aag Lys 65	aaa Lys	acc Thr	tcc Ser	aac Asn	307				
ctg Leu 70	ttc Phe	cgt Arg	gga Gly	cgc Arg	tcc Ser 75	gat Asp	gca Ala	ggt Gly	cac His 80	ggc Gly	cta Leu	gat Asp	gtg Val	gca Ala 85	gcg Ala	355				
ctt Leu	ggg Gly	gga Gly	gtg Val	att Ile 90	gcc Ala	att Ile	gat Asp	ccg Pro	gtc Val 95	aat Val Asn	gcc Ala	acc Thr	gcc Ala	gat Asp 100	gta Val	403				
cag Gln	ggc Gly	atg Met	tgc Cys 105	acg Thr	tat Tyr	gaa Glu	gac Asp	ctg Leu 110	gta Val	gat Asp	gcc Ala	act Thr	tta Leu 115	agt Ser	tat Tyr	451				
ggt Gly	ctg Leu	atg Met 120	ccg Pro	ttg Leu	gtt Val	gtg Val	cct Pro 125	caa Gln	ctg Leu	aaa Lys	acc Thr	atc Ile 130	acg Thr	ctt Leu	ggt Gly	499				
ggc Gly 135	gca Ala	gtg Val	acc Thr	gga Gly	atg Met	ggc Gly 140	gtg Val	gaa Glu	tcc Ser	aca Thr	tcc Ser	ttc Phe	cgc Arg	aac Asn	ggt Gly	547				
ttg Leu 150	cca Pro	cac His	gaa Glu	tca Ser 155	gtg Val	ctg Leu	gag Glu	atg Met	gat Asp	att Ile 160	ttt Phe	acc Thr	ggc Gly	act Thr 165	ggt Gly	595				
gag Glu	atc Ile	gtg Val	act Thr	tgc Cys 170	tcg Ser	ccc Pro	aca Thr	gaa Glu	aat Asn 175	gtc Val	gac Asp	ctt Leu	tac Tyr	aga Arg 180	ggc Gly	643				
ttt Phe	ccc Pro	aac Asn	tct Ser 185	tat Ser	ggt Gly	tcg Ser	ctg Leu	gga Gly 190	tac Tyr	gcg Ala	gtg Val	cgg Arg	cta Leu 195	aaa Lys	att Ile	691				
gag Glu	ctg Leu	gaa Glu 200	cca Pro	gtg Val	caa Gln	gat Asp	tac Tyr 205	gtc Val	cag Gln	ctg Leu	cgc Arg	cac His 210	gtg Val	cgc Arg	ttc Phe	739				
aac Asn 215	gat Leu	tta Leu	gag Glu	tct Ser	ttg Leu	acc Thr 220	aaa Lys	gcg Ala	att Ile	gag Glu 225	gaa Glu	gtc Val	alc Ala	tct Ser	tct Ser	787				
ctg Leu Glu	gag Phe	ttt Asp	gat Asn	aac Gln	ccc Gln	gct Pro	gat Val	tac Asp Tyr	ctt Leu	gac Leu	ggc Gly	gtg Val	gtg Val	ttt Phe		835				

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<210> 2358
<211> 273
<212> PRT
<213> Corynebacterium glutamicum
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400> 2358																
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Lys	Leu	Ser	Asn	Ser	Leu	Ser	Ile	Gly	Arg	Gly	Val	Asp	Gln	Lys	Glu	
			20					25					30			
Val	Ile	Pro	Lys	Gly	Trp	Asn	Ala	His	Trp	Glu	Ala	Ile	Thr	Lys	Leu	
		35					40					45				
Lys	Arg	Ser	Phe	Asp	Ala	Ile	Pro	Ala	Gly	Glu	Arg	Val	Arg	Leu	Ala	
	50					55					60					
Lys	Lys	Thr	Ser	Asn	Leu	Phe	Arg	Gly	Arg	Ser	Asp	Ala	Gly	His	Gly	
	65				70					75				80		
Leu	Asp	Val	Ala	Ala	Leu	Gly	Gly	Val	Ile	Ala	Ile	Asp	Pro	Val	Asn	
				85				90						95		
Ala	Thr	Ala	Asp	Val	Gln	Gly	Met	Cys	Thr	Tyr	Glu	Asp	Leu	Val	Asp	
		100						105					110			
Ala	Thr	Leu	Ser	Tyr	Gly	Leu	Met	Pro	Leu	Val	Val	Pro	Gln	Leu	Lys	
		115					120					125				
Thr	Ile	Thr	Leu	Gly	Gly	Ala	Val	Thr	Gly	Met	Gly	Val	Glu	Ser	Thr	
	130					135					140					
Ser	Phe	Arg	Asn	Gly	Leu	Pro	His	Glu	Ser	Val	Leu	Glu	Met	Asp	Ile	
	145				150					155				160		
Phe	Thr	Gly	Thr	Gly	Glu	Ile	Val	Thr	Cys	Ser	Pro	Thr	Glu	Asn	Val	
				165					170					175		
Asp	Leu	Tyr	Arg	Gly	Phe	Pro	Asn	Ser	Tyr	Gly	Ser	Leu	Gly	Tyr	Ala	
		180						185					190			
Val	Arg	Leu	Lys	Ile	Glu	Leu	Glu	Pro	Val	Gln	Asp	Tyr	Val	Gln	Leu	
		195					200					205				
Arg	His	Val	Arg	Phe	Asn	Asp	Leu	Glu	Ser	Leu	Thr	Lys	Ala	Ile	Glu	
	210					215					220					

Glu Val Ala Ser Ser Leu Glu Phe Asp Asn Gln Pro Val Asp Tyr Leu
 225 230 235 240
 Asp Gly Val Val Phe Ser Pro Thr Glu Ala Tyr Leu Val Leu Gly Thr
 245 250 255
 Gln Thr Ser Gln Pro Gly Pro Thr Ser Asp Tyr Thr Arg Asp Leu Ser
 260 265 270

Tyr

<210> 2359
 <211> 1020
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(997)
 <223> RXA01656

<400> 2359
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 atctaccgct agtccacttt gtggcggttg atcatctgtc atg acc gaa act caa 115
 Met Thr Glu Thr Gln
 1 5
 gaa act tac caa gca acc act cgt gtg aag cgc ggc ctt gcc gac atg 163
 Glu Thr Tyr Gln Ala Thr Thr Arg Val Lys Arg Gly Leu Ala Asp Met
 10 15 20
 ctc aag ggt ggt gtg atc atg gat gtg gtc acc cct gaa caa gcg cgc 211
 Leu Lys Gly Gly Val Ile Met Asp Val Val Thr Pro Glu Gln Ala Arg
 25 30 35
 atc gcc gaa gat gca ggt gcc agc gca gtt atg gca ctc gag cgc gtt 259
 Ile Ala Glu Asp Ala Gly Ala Ser Ala Val Met Ala Leu Glu Arg Val
 40 45 50
 ccc gcc gat atc cgt tct cag ggc ggc gtt gct cgc atg agt gat cct 307
 Pro Ala Asp Ile Arg Ser Gln Gly Gly Val Ala Arg Met Ser Asp Pro
 55 60 65
 gac ctg atc gaa gga atc gtc aat gcg gtc tcc atc ccg gtc atg gcg 355
 Asp Leu Ile Glu Gly Ile Val Asn Ala Val Ser Ile Pro Val Met Ala
 70 75 80 85
 aaa gct cgc atc ggt cac ttc gtg gaa gct cag gtt ctg gaa gct ctc 403
 Lys Ala Arg Ile Gly His Phe Val Glu Ala Gln Val Leu Glu Ala Leu
 90 95 100
 ggt gtt gat ttc atc gac gag tcc gaa gtt ctc agc cct gcc gac tac 451
 Gly Val Asp Phe Ile Asp Glu Ser Glu Val Leu Ser Pro Ala Asp Tyr
 105 110 115
 acg cac cac atc aac aag tgg aag ttc gac gtt cct ttc gtc tgt ggc 499
 Thr His His Ile Asn Lys Trp Lys Phe Asp Val Pro Phe Val Cys Gly
 120 125 130

gcg acc aac ctc ggc gaa gct ttg cga cgc atc acc gaa ggc gct gca 547
Ala Thr Asn Leu Gly Glu Ala Leu Arg Arg Ile Thr Glu Gly Ala Ala
135 140 145

atg atc cgt tcc aag ggc gaa gcc ggc acc ggc gat gtc tct gaa gct 595
Met Ile Arg Ser Lys Gly Glu Ala Gly Thr Gly Asp Val Ser Glu Ala
150 155 160 165

gtc cgt cac ctg cgc acc atc cgc ggc gac atc aat cgc ctg cgc tcc 643
Val Arg His Leu Arg Thr Ile Arg Gly Asp Ile Asn Arg Leu Arg Ser
170 175 180

ctg gat gag gat gaa ctc ttc gtc gcc gcc aag gaa ttc cag gca cca 691
Leu Asp Glu Asp Glu Leu Phe Val Ala Ala Lys Glu Phe Gln Ala Pro
185 190 195

tac gac ctg gtc cgc gaa gtc gcc tcc acc ggc aag ctc cct gtg gtc 739
Tyr Asp Leu Val Arg Glu Val Ala Ser Thr Gly Lys Leu Pro Val Val
200 205 210

acc ttc gtt gca ggt ggc gtc gca acc cca gcc gac gct gca ctc gtg 787
Thr Phe Val Ala Gly Gly Val Ala Thr Pro Ala Asp Ala Ala Leu Val
215 220 225

cgc caa atg ggc gcc gaa ggc gtc ttt gtc ggc tcc ggc atc ttc aaa 835
Arg Gln Met Gly Ala Glu Gly Val Phe Val Gly Ser Gly Ile Phe Lys
230 235 240 245

tcc ggc aat cca gcc gcc cgc gcc gca gcg atc gtc aag gct gca acg 883
Ser Gly Asn Pro Ala Ala Arg Ala Ala Ala Ile Val Lys Ala Ala Thr
250 255 260

ctt ttc gac gac ccc tcc gtc att gcc gac gta tcc cgc ggc ctg ggt 931
Leu Phe Asp Asp Pro Ser Val Ile Ala Asp Val Ser Arg Gly Leu Gly
265 270 275

gaa gcc atg gtg ggc atc aac gta tcc gac gtt cca gca cca cac cga 979
Glu Ala Met Val Gly Ile Asn Val Ser Asp Val Pro Ala Pro His Arg
280 285 290

ctc gcc gag cgc ggc tgg tgatcgttg agtttttagct ctc 1020
Leu Ala Glu Arg Gly Trp
295

<210> 2360

<211> 299

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2360

Met Thr Glu Thr Gln Glu Thr Tyr Gln Ala Thr Thr Arg Val Lys Arg
1 5 10 15

Gly Leu Ala Asp Met Leu Lys Gly Gly Val Ile Met Asp Val Val Thr
20 25 30

Pro Glu Gln Ala Arg Ile Ala Glu Asp Ala Gly Ala Ser Ala Val Met
35 40 45

Ala Leu Glu Arg Val Pro Ala Asp Ile Arg Ser Gln Gly Gly Val Ala
50 55 60

Arg Met Ser Asp Pro Asp Leu Ile Glu Gly Ile Val Asn Ala Val Ser
65 70 75 80

Ile Pro Val Met Ala Lys Ala Arg Ile Gly His Phe Val Glu Ala Gln
85 90 95

Val Leu Glu Ala Leu Gly Val Asp Phe Ile Asp Glu Ser Glu Val Leu
100 105 110

Ser Pro Ala Asp Tyr Thr His His Ile Asn Lys Trp Lys Phe Asp Val
115 120 125

Pro Phe Val Cys Gly Ala Thr Asn Leu Gly Glu Ala Leu Arg Arg Ile
130 135 140

Thr Glu Gly Ala Ala Met Ile Arg Ser Lys Gly Glu Ala Gly Thr Gly
145 150 155 160

Asp Val Ser Glu Ala Val Arg His Leu Arg Thr Ile Arg Gly Asp Ile
165 170 175

Asn Arg Leu Arg Ser Leu Asp Glu Asp Glu Leu Phe Val Ala Ala Lys
180 185 190

Glu Phe Gln Ala Pro Tyr Asp Leu Val Arg Glu Val Ala Ser Thr Gly
195 200 205

Lys Leu Pro Val Val Thr Phe Val Ala Gly Gly Val Ala Thr Pro Ala
210 215 220

Asp Ala Ala Leu Val Arg Gln Met Gly Ala Glu Gly Val Phe Val Gly
225 230 235 240

Ser Gly Ile Phe Lys Ser Gly Asn Pro Ala Ala Arg Ala Ala Ala Ile
245 250 255

Val Lys Ala Ala Thr Leu Phe Asp Asp Pro Ser Val Ile Ala Asp Val
260 265 270

Ser Arg Gly Leu Gly Glu Ala Met Val Gly Ile Asn Val Ser Asp Val
275 280 285

Pro Ala Pro His Arg Leu Ala Glu Arg Gly Trp
290 295

<210> 2361

<211> 843

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(820)

<223> RXA01665

<400> 2361

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gtgcttgagc	gaaaaccgct	gatgattagc	atggtttgtt	gtg	aag	atc	gat	gaa	115
				Val	Lys	Ile	Asp	Glu	
				1				5	
ttg att gct ctc gcc gcg gag caa ccc act cgc atc tcc agg cgt tcc	163								
Leu Ile Ala Leu Ala Ala Glu Gln Pro Thr Arg Ile Ser Arg Arg Ser									
	10								
	15								
	20								
ggt gtc tcg cgc tcg acc ctg aag cgg gtc ggc gat ggc acc agc gag	211								
Gly Val Ser Arg Ser Thr Leu Lys Arg Val Gly Asp Gly Thr Ser Ser Glu									
	25								
	30								
	35								
ccc acc ctg tcg acg ctg cgt gag gtc gcg ttg gcg ctc ggg ctt gat	259								
Pro Thr Leu Ser Thr Leu Arg Glu Val Ala Leu Ala Leu Gly Leu Asp									
	40								
	45								
	50								
att aag gtc gcc gcg cac cac gcc tgc gat ccc ttt gcg gcc gct gca	307								
Ile Lys Val Ala Ala His His Ala Cys Asp Pro Phe Ala Ala Ala Ala									
	55								
	60								
gcg cgc acg ctt atc gac gcc tcc gtc ccc gaa aat ccc cac aac cag	355								
Ala Arg Thr Leu Ile Asp Ala Ser Val Pro Glu Asn Pro His Asn Gln									
	70								
	75								
	80								
	85								
gaa att ctc gct tgg ttg cac cgt ttt gag cgg tgg aat atc aac gat	403								
Glu Ile Leu Ala Trp Leu His Arg Phe Glu Arg Trp Asn Ile Asn Asp									
	90								
	95								
	100								
ccg ctc acc ctt gtc tct gaa gcc gga acg ctt cag ggc atc aca cat	451								
Pro Leu Thr Leu Val Ser Glu Ala Gly Thr Leu Gln Gly Ile Thr His									
	105								
	110								
	115								
cgc cag gat gcg cag ttt gtg aaa ctc aat cca cgc ggc atc gct gag	499								
Arg Gln Asp Ala Gln Phe Val Lys Leu Asn Pro Arg Gly Ile Ala Glu									
	120								
	125								
	130								
cta ccg gag ctt ttc caa cag cac aaa acc aaa tgg gcg ctg tcg ggc	547								
Leu Pro Glu Leu Phe Gln Gln His Lys Thr Lys Trp Ala Leu Ser Gly									
	135								
	140								
	145								
gct gcg gct gcc acg gtg atc atg gga caa att gtg ctg ggg aat tcg	595								
Ala Ala Ala Ala Thr Val Ile Met Gly Gln Ile Val Leu Gly Asn Ser									
	150								
	155								
	160								
	165								
att gtg tgg cac gaa cct gcc cac gat ctc gat gtc tca gcg ctg ggc	643								
Ile Val Trp His Glu Pro Ala His Asp Leu Asp Val Ser Ala Leu Gly									
	170								
	175								
	180								
acc att gtt gat gtg gca gaa gac gcc gat cta att ctc ctg ccc gca	691								
Thr Ile Val Asp Val Ala Glu Asp Ala Asp Leu Ile Leu Leu Pro Ala									
	185								
	190								
	195								
acg gtc acg gaa ctg gtg gga agt tac acc cag gac agg cta aat ttt	739								
Thr Val Thr Glu Leu Val Gly Ser Tyr Thr Gln Asp Arg Leu Asn Phe									
	200								
	205								
	210								
gtg gca cct gtg caa tta gtt att gat cta cac agc ctc cac atg ttc	787								
Val Ala Pro Val Gln Leu Val Ile Asp Leu His Ser Leu His Met Phe									
	215								
	220								
	225								

gag gaa gcc gat tac ctc acg agc ggt tgg cgc taaaatactt agcgtacgca 840
 Glu Glu Ala Asp Tyr Leu Thr Ser Gly Trp Arg
 230 235 240

ccc

843

<210> 2362

<211> 240

<212> PRF

<213> *Corynebacterium glutamicum*

<400> 2362

Val Lys Ile Asp Glu Leu Ile Ala Leu Ala Ala Glu Gln Pro Thr Arg
 1 5 10 15

Ile Ser Arg Arg Ser Gly Val Ser Arg Ser Thr Leu Lys Arg Val Gly
 20 25 30

Asp Gly Thr Ser Glu Pro Thr Leu Ser Thr Leu Arg Glu Val Ala Leu
 35 40 45

Ala Leu Gly Leu Asp Ile Lys Val Ala Ala His His Ala Cys Asp Pro
 50 55 60

Phe Ala Ala Ala Ala Arg Thr Leu Ile Asp Ala Ser Val Pro Glu
 65 70 75 80

Asn Pro His Asn Gln Glu Ile Leu Ala Trp Leu His Arg Phe Glu Arg
 85 90 95

Trp Asn Ile Asn Asp Pro Leu Thr Leu Val Ser Glu Ala Gly Thr Leu
 100 105 110

Gln Gly Ile Thr His Arg Gln Asp Ala Gln Phe Val Lys Leu Asn Pro
 115 120 125

Arg Gly Ile Ala Glu Leu Pro Glu Leu Phe Gln Gln His Lys Thr Lys
 130 135 140

Trp Ala Leu Ser Gly Ala Ala Ala Thr Val Ile Met Gly Gln Ile
 145 150 155 160

Val Leu Gly Asn Ser Ile Val Trp His Glu Pro Ala His Asp Leu Asp
 165 170 175

Val Ser Ala Leu Gly Thr Ile Val Asp Val Ala Glu Asp Ala Asp Leu
 180 185 190

Ile Leu Leu Pro Ala Thr Val Thr Glu Leu Val Gly Ser Tyr Thr Gln
 195 200 205

Asp Arg Leu Asn Phe Val Ala Pro Val Gln Leu Val Ile Asp Leu His
 210 215 220

Ser Leu His Met Phe Glu Glu Ala Asp Tyr Leu Thr Ser Gly Trp Arg
 225 230 235 240

<210> 2363
 <211> 738
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(715)
 <223> RXA01671

<400> 2363
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ttttgtacc cgaatttga cccgaattta aggaatcgct atg aat cat gtt gtt 115
 Met Asn His Val Val
 1 5

aat ttt gct tca cat ttg gaa gac gca gcc ctg aag caa gcc gaa gct 163
 Asn Phe Ala Ser His Leu Glu Asp Ala Ala Leu Lys Gln Ala Glu Ala
 10 15 20

act gcc acc atg ccg ttt att tac ccg cat gtg gcg ttg atg cct gat 211
 Thr Ala Thr Met Pro Phe Ile Tyr Pro His Val Ala Leu Met Pro Asp
 25 30 35

gct cac ttt ggg ctg ggt tgc tgc gtg gga acg gtg ttc gcc acc aag 259
 Ala His Phe Gly Leu Gly Ser Ser Val Gly Thr Val Phe Gly Thr Lys
 40 45 50

ggg gcg atc att ccg gcg gct gtg ggt gtg gat ata ggt tgc gga atg 307
 Gly Ala Ile Ile Pro Ala Ala Val Gly Val Asp Ile Gly Cys Gly Met
 55 60 65

ata gga gtg tgt acc aat tac acg gcc tct gac ctg gag gga cgt gat 355
 Ile Gly Val Cys Thr Asn Tyr Thr Ala Ser Asp Leu Glu Gly Arg Asp
 70 75 80 85

ttg gtg acg ctt ccg gat tac atc gag ccg gtg att ccg ttg tct cct 403
 Leu Val Thr Leu Arg Asp Tyr Ile Glu Arg Val Ile Pro Leu Ser Pro
 90 95 100

gga aat tac aat tcc acc acc ttg aag gaa acc gcg aag gtg aag gtc 451
 Gly Asn Tyr Asn Ser Thr Thr Leu Lys Glu Thr Ala Lys Val Lys Val
 105 110 115

gcg gag ttg gag gaa ctc gcg gag cgc gat ggt gta gat ttg tgc cac 499
 Ala Glu Leu Glu Glu Leu Ala Glu Arg Asp Gly Val Asp Leu Ser His
 120 125 130

tct ccg acg tgg aag cgc cag ttg ggt tgc ctt ggt gga ggt aat cac 547
 Ser Pro Thr Trp Lys Arg Gln Leu Gly Ser Leu Gly Gly Asn His
 135 140 145

ttc att gag ttg tgt ctt gat gag ttg gat ccg gtg tgg atg ttt ttg 595
 Phe Ile Glu Leu Cys Leu Asp Glu Leu Asp Arg Val Trp Met Phe Leu
 150 155 160 165

cac tct ggt tcc cgc ggt gtg ggt aac aag att gcc cat aag cac atc 643
 His Ser Gly Ser Arg Gly Val Gly Asn Lys Ile Ala His Lys His Ile
 170 175 180

aag aac gcg cag gcc cag tgt aag aat gag gag ctt ccc gat aag gat 691
 Lys Asn Ala Gln Ala Gln Cys Lys Asn Glu Glu Leu Pro Asp Lys Asp
 185 190 195

ctt gcg tac ctt gac cga ggg gac tgaggagttt gaggcttaca tca 738
 Leu Ala Tyr Leu Asp Arg Gly Asp
 200 205

<210> 2364

<211> 205

<212> PRT

<213> Corynebacterium glutamicum

<400> 2364

Met Asn His Val Val Asn Phe Ala Ser His Leu Glu Asp Ala Ala Leu
 1 5 10 15

Lys Gln Ala Glu Ala Thr Ala Thr Met Pro Phe Ile Tyr Pro His Val
 20 25 30

Ala Leu Met Pro Asp Ala His Phe Gly Leu Gly Ser Ser Val Gly Thr
 35 40 45

Val Phe Gly Thr Lys Gly Ala Ile Ile Pro Ala Ala Val Gly Val Asp
 50 55 60

Ile Gly Cys Gly Met Ile Gly Val Cys Thr Asn Tyr Thr Ala Ser Asp
 65 70 75 80

Leu Glu Gly Arg Asp Leu Val Thr Leu Arg Asp Tyr Ile Glu Arg Val
 85 90 95

Ile Pro Leu Ser Pro Gly Asn Tyr Asn Ser Thr Thr Leu Lys Glu Thr
 100 105 110

Ala Lys Val Lys Val Ala Glu Leu Glu Glu Leu Ala Glu Arg Asp Gly
 115 120 125

Val Asp Leu Ser His Ser Pro Thr Trp Lys Arg Gln Leu Gly Ser Leu
 130 135 140

Gly Gly Gly Asn His Phe Ile Glu Leu Cys Leu Asp Glu Leu Asp Arg
 145 150 155 160

Val Trp Met Phe Leu His Ser Gly Ser Arg Gly Val Gly Asn Lys Ile
 165 170 175

Ala His Lys His Ile Lys Asn Ala Gln Ala Gln Cys Lys Asn Glu Glu
 180 185 190

Leu Pro Asp Lys Asp Leu Ala Tyr Leu Asp Arg Gly Asp
 195 200 205

<210> 2365

<211> 1158

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1135)

<223> RXA01673

<400> 2365

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cogtctacgg cgttcttttc aattagcgca accttgaagc atg tct aca aac ctt 115
 Met Ser Thr Asn Leu
 1 5

ctg gaa tcg acg ccg ccc ttt acc caa ctt cgc acc gga gtc ctc cag 163
 Leu Glu Ser Thr Pro Pro Phe Thr Gln Leu Arg Thr Gly Val Leu Gln
 10 15 20

aag tac acc ccg ggc ctg ctc tta tgc tcc att gcg gta ctc atc gct 211
 Lys Tyr Thr Pro Gly Leu Leu Leu Cys Ser Ile Ala Val Leu Ile Ala
 25 30 35

atg atc gtg aat cac ttt ttc tct ggt gtg agt ccg ctt atc gtc gcg 259
 Met Ile Val Asn His Phe Phe Ser Gly Val Ser Pro Leu Ile Val Ala
 40 45 50

atc att ctt ggc atc atc ctg acc aac ctg att cag ctc cca gca tcg 307
 Ile Ile Leu Gly Ile Ile Leu Thr Asn Leu Ile Gln Leu Pro Ala Ser
 55 60 65

acc tca ccc ggc atc acg ttg gcg tcg aaa aag ctt ttg cgg ctg gga 355
 Thr Ser Pro Gly Ile Thr Leu Ala Ser Lys Lys Leu Leu Arg Leu Gly
 70 75 80 85

atc gtc ttc ctt ggt ctg cag tta gtt ttc tca gat att ttg tca ctt 403
 Ile Val Phe Leu Gly Leu Gln Leu Val Phe Ser Asp Ile Leu Ser Leu
 90 95 100

ggt ttc ccc atg ctg gcg gtg att gtg tgc atc gtt gcc ggt ggt att 451
 Gly Phe Pro Met Leu Ala Val Ile Val Cys Ile Val Ala Gly Gly Ile
 105 110 115

ttt ggg acc atc ctc atg gga cac ctg ctc aga atg aaa cca acc caa 499
 Phe Gly Thr Ile Leu Met Gly His Leu Leu Arg Met Lys Pro Thr Gln
 120 125 130

gtt ctg ttg att gct tgt ggc ttt tct att tgt ggc gct gcg gcc gtg 547
 Val Leu Leu Ile Ala Cys Gly Phe Ser Ile Cys Gly Ala Ala Ala Val
 135 140 145

gca ggt gtt gaa gga gta act gat tcc gaa gaa gaa gag gtc gtt act 595
 Ala Gly Val Glu Gly Val Thr Asp Ser Glu Glu Glu Val Val Thr
 150 155 160 165

gcg gtt gca ctt gtt gtt att ttc gga acg ctg atg att cct ttt atc 643
 Ala Val Ala Leu Val Val Ile Phe Gly Thr Leu Met Ile Pro Phe Ile
 170 175 180

cca ttc gca acc aaa gtc ttg ggg tta tcc cct gaa atc ggt ggg atg 691
 Pro Phe Ala Thr Lys Val Leu Gly Leu Ser Pro Glu Ile Gly Gly Met
 185 190 195

tgg gca ggc gga tcc atc cat gaa atc gcc caa gta gta gca gct gga 739

Trp Ala Gly Gly Ser Ile His Glu Ile Ala Gln Val Val Ala Ala Gly
 200 205 210
 gga gtc att ggt ggt gga gca tta ggt gtt gca gtt gtg gtg aaa ctc 787
 Gly Val Ile Gly Gly Gly Ala Leu Gly Val Ala Val Val Val Lys Leu
 215 220 225
 gcc cga gta ctc cta ctt gca ccc att gct gcc att tta agt ttt cgc 835
 Ala Arg Val Leu Leu Leu Ala Pro Ile Ala Ala Ile Leu Ser Phe Arg
 230 235 240 245
 cag cgc cgc cag ggt tac acg tcc ccc gat gga aag aga cca ccg gtc 883
 Gln Arg Arg Gln Gly Tyr Thr Ser Pro Asp Gly Lys Arg Pro Pro Val
 250 255 260
 gtt ccc cta ttt atc ctt gga ttc ttg gcg atg gta gtt ttg cgc tcc 931
 Val Pro Leu Phe Ile Leu Gly Phe Leu Ala Met Val Val Leu Arg Ser
 265 270 275
 act gtt gcg ctc cca gac gag gta att gcg gct gga ggt ttc cta cag 979
 Thr Val Ala Leu Pro Asp Glu Val Ile Ala Ala Gly Gly Phe Leu Gln
 280 285 290
 aca gcc ttg ctc tct gca gca atg ttt ggt ctc ggg tgt gcc gta aaa 1027
 Thr Ala Leu Leu Ser Ala Ala Met Phe Gly Leu Gly Cys Gly Val Lys
 295 300 305
 atc cag aac ctg atc cat gtt ggg gtc aag cct ttc att ctg gct ttc 1075
 Ile Gln Asn Leu Ile His Val Gly Val Lys Pro Phe Ile Leu Ala Phe
 310 315 320 325
 gga tcc acg aca ctt gtc acc agt atc gca ctt gca gcc acc cta ctc 1123
 Gly Ser Thr Thr Leu Val Thr Ser Ile Ala Leu Ala Gly Thr Leu Leu
 330 335 340
 acc cac ctc gga tagaaccgaa gacccagttg tac 1158
 Thr His Leu Gly
 345
 <210> 2366
 <211> 345
 <212> PRT
 <213> *Corynebacterium glutamicum*
 <400> 2366
 Met Ser Thr Asn Leu Leu Glu Ser Thr Pro Pro Phe Thr Gln Leu Arg
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 Thr Gly Val Leu Gln Lys Tyr Thr Pro Gly Leu Leu Leu Cys Ser Ile
 20 25 30
 Ala Val Leu Ile Ala Met Ile Val Asn His Phe Phe Ser Gly Val Ser
 35 40 45
 Pro Leu Ile Val Ala Ile Ile Leu Gly Ile Ile Leu Thr Asn Leu Ile
 50 55 60
 Gln Leu Pro Ala Ser Thr Ser Pro Gly Ile Thr Leu Ala Ser Lys Lys
 65 70 75 80

Leu Leu Arg Leu Gly Ile Val Phe Leu Gly Leu Gln Leu Val Phe Ser
 85 90 95
 Asp Ile Leu Ser Leu Gly Phe Pro Met Leu Ala Val Ile Val Cys Ile
 100 105 110
 Val Ala Gly Gly Ile Phe Gly Thr Ile Leu Met Gly His Leu Leu Arg
 115 120 125
 Met Lys Pro Thr Gln Val Leu Leu Ile Ala Cys Gly Phe Ser Ile Cys
 130 135 140
 Gly Ala Ala Ala Val Ala Gly Val Glu Gly Val Thr Asp Ser Glu Glu
 145 150 155 160
 Glu Glu Val Val Thr Ala Val Ala Leu Val Val Ile Phe Gly Thr Leu
 165 170 175
 Met Ile Pro Phe Ile Pro Phe Ala Thr Lys Val Leu Gly Leu Ser Pro
 180 185 190
 Glu Ile Gly Gly Met Trp Ala Gly Gly Ser Ile His Glu Ile Ala Gln
 195 200 205
 Val Val Ala Ala Gly Gly Val Ile Gly Gly Gly Ala Leu Gly Val Ala
 210 215 220
 Val Val Val Lys Leu Ala Arg Val Leu Leu Leu Ala Pro Ile Ala Ala
 225 230 235 240
 Ile Leu Ser Phe Arg Gln Arg Arg Gln Gly Tyr Thr Ser Pro Asp Gly
 245 250 255
 Lys Arg Pro Pro Val Val Pro Leu Phe Ile Leu Gly Phe Leu Ala Met
 260 265 270
 Val Val Leu Arg Ser Thr Val Ala Leu Pro Asp Glu Val Ile Ala Ala
 275 280 285
 Gly Gly Phe Leu Gln Thr Ala Leu Leu Ser Ala Ala Met Phe Gly Leu
 290 295 300
 Gly Cys Gly Val Lys Ile Gln Asn Leu Ile His Val Gly Val Lys Pro
 305 310 315 320
 Phe Ile Leu Ala Phe Gly Ser Thr Thr Leu Val Thr Ser Ile Ala Leu
 325 330 335
 Ala Gly Thr Leu Leu Thr His Leu Gly
 340 345

<210> 2367

<211> 534

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(511)

<223> RXA01675

<400> 2367

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ctggctaacg gattgttttt gacagattgg aatgacaata atg aac gag att cca 115
 Met Asn Glu Ile Pro 5

gaa tgg ttg act ctt gta tct gtt gaa gca gga aag aga ctt ggg cgg 163
 Glu Trp Leu Thr Leu Val Ser Val Glu Ala Gly Lys Arg Leu Gly Arg 20

cct ggg cca ttg gtg ttt ccg ccg gag ttg gtc act ttg gca gtt gaa 211
 Pro Gly Pro Leu Val Phe Pro Pro Glu Leu Val Thr Leu Ala Val Glu 35

ggg att gag ctt att gaa ctt gag cct tca tgg act tct gat ttg cct 259
 Gly Ile Glu Leu Ile Glu Leu Glu Pro Ser Trp Thr Ser Asp Leu Pro 40 45 50

ctg ccg gaa ttc ggg ttc cta gct gcg gat atg gtt gat ttc tat gat 307
 Leu Pro Glu Phe Gly Phe Leu Ala Ala Asp Met Asp Phe Tyr Asp 55 60 65

gat tat gag ttt agt gaa tgg att ccg ggt gcg tgg cct ctt gct tta 355
 Asp Tyr Glu Phe Ser Glu Trp Ile Pro Gly Ala Trp Pro Leu Ala Leu 70 75 80 85

gat ggt gga gga ggt ttc ttt tgc ctt gat ctc cgt gct gcc aac gct 403
 Asp Gly Gly Gly Gly Phe Phe Cys Leu Asp Leu Arg Ala Ala Asn Ala 90 95 100

gat gga gag att cct gtt gtg tgg gtg cat gcc agc aac ttg ggt tgg 451
 Asp Gly Glu Ile Pro Val Val Trp Val His Ala Ser Asn Leu Gly Trp 105 110 115

ggt gat gat gag gca gta cgc gta gct gcc tcg ttg gca gat ttg ttg 499
 Gly Asp Asp Glu Ala Val Arg Val Ala Ala Ser Leu Ala Asp Leu Leu 120 125 130

agt ccg tcg aaa tagaagaatt agcatttacc gga 534
 Ser Pro Ser Lys 135

<210> 2368

<211> 137

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2368

Met Asn Glu Ile Pro Glu Trp Leu Thr Leu Val Ser Val Glu Ala Gly
 1 5 10 15

Lys Arg Leu Gly Arg Pro Gly Pro Leu Val Phe Pro Pro Glu Leu Val
 20 25 30

Thr Leu Ala Val Glu Gly Ile Glu Leu Ile Glu Leu Glu Pro Ser Trp
 35 40 45

Thr Ser Asp Leu Pro Leu Pro Glu Phe Gly Phe Leu Ala Ala Asp Met

50 55 60
 Val Asp Phe Tyr Asp Tyr Glu Phe Ser Glu Trp Ile Pro Gly Ala
 65 70 75 80
 Trp Pro Leu Ala Leu Asp Gly Gly Gly Gly Phe Phe Cys Leu Asp Leu
 85 90 95
 Arg Ala Ala Asn Ala Asp Gly Glu Ile Pro Val Val Trp Val His Ala
 100 105 110
 Ser Asn Leu Gly Trp Gly Asp Asp Glu Ala Val Arg Val Ala Ala Ser
 115 120 125
 Leu Ala Asp Leu Leu Ser Pro Ser Lys
 130 135

 <210> 2369
 <211> 879
 <212> DNA
 <213> *Corynebacterium glutamicum*

 <220>
 <221> CDS
 <222> (101)..(856)
 <223> RXA01676

 <400> 2369
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 accagcattt ttgcatocct cagtggtgagc tggcccgagc atg atc ctt cac ggt 115
 Met Ile Leu His Gly
 1 5

 gtt gtg ttc tac gca gga ctt cta gta ctt ctc gtg cca ctt ggc ctt 163
 Val Val Phe Tyr Ala Gly Leu Leu Val Leu Leu Val Pro Leu Gly Leu
 10 15 20

 ggt gcg gga atc ctc ggc gag ctg ttt atc acc caa cgc cag acc atc 211
 Gly Ala Gly Ile Leu Gly Glu Leu Phe Ile Thr Gln Arg Gln Thr Ile
 25 30 35

 atc gtg gtt tca tcg atc gtg ctg att atc cta ggt ttt gtc cag atc 259
 Ile Val Val Ser Ser Ile Val Leu Ile Ile Leu Gly Phe Val Gln Ile
 40 45 50

 ttc ggc ggc gga ttc gac ttc gga aaa gca ctc cca gga tta gat cgt 307
 Phe Gly Gly Gly Phe Asp Phe Gly Lys Ala Leu Pro Gly Leu Asp Arg
 55 60 65

 ctg caa tct aag gcc act gtg acc tca ggt cta gga aag agc ttt tta 355
 Leu Gln Ser Lys Ala Thr Val Thr Ser Gly Leu Gly Lys Ser Phe Leu
 70 75 80 85

 cta gga atg acc agt agt att gcc ggt ttt tgt tcc gga cca atc ctc 403
 Leu Gly Met Thr Ser Ser Ile Ala Gly Phe Cys Ser Gly Pro Ile Leu
 90 95 100

 gcc gcc gtt ctt act ttg gct gcc acc agt gga aac tcc atc acc tca 451
 Gly Ala Val Leu Thr Leu Ala Ala Thr Ser Gly Asn Ser Ile Thr Ser

105	110	115	
gca ctc att ttg agt gct tat ggt gcg gga atg gtg ctg ccc ctg atg			499
Ala Leu Ile Leu Ser Ala Tyr Gly Ala Gly Met Val Leu Pro Leu Met			
120	125	130	
gct att gca gcg ctc tgg gcc aaa ctc gga cag cgt gga cag cag atg			547
Ala Ile Ala Ala Leu Trp Ala Lys Leu Gly Gln Arg Gly Gln Gln Met			
135	140	145	
ctc cgc ggc cgg gaa ttc acc ttc ttg ggc agg cag tgg cac att gtt			595
Leu Arg Gly Arg Glu Phe Thr Phe Leu Gly Arg Gln Trp His Ile Val			
150	155	160	165
tct gtc att agc ggt gcc ctg atc atc gct gtc gga atc ctc ttt tgg			643
Ser Val Ile Ser Gly Ala Leu Ile Ile Ala Val Gly Ile Leu Phe Trp			
170	175	180	
tcc acg aac ggc ctt gtc agc atg ccg gag ctc gtt cca atg gac acc			691
Ser Thr Asn Gly Leu Val Ser Met Pro Glu Leu Val Pro Met Asp Thr			
185	190	195	
cag atc tgg cta cag gaa gcc aca ttc tca ctc ggg tca cca ctc ttt			739
Gln Ile Trp Leu Gln Glu Ala Thr Phe Ser Leu Gly Ser Pro Leu Phe			
200	205	210	
gac atc gca ttg atc att gtc gcc gct ggc ttg ttc ttg tac ttc tgg			787
Asp Ile Ala Leu Ile Ile Val Ala Ala Gly Leu Phe Leu Tyr Phe Trp			
215	220	225	
aac aaa cga caa aag cga aaa gaa gaa gct cag cga ccc aaa gaa agt			835
Asn Lys Arg Gln Lys Arg Lys Glu Glu Ala Gln Arg Pro Lys Glu Ser			
230	235	240	245
gga tgg gtt att aac cct cgc taattattag ttttggagcg agg			879
Gly Trp Val Ile Asn Pro Arg			
250			
<210> 2370			
<211> 252			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 2370			
Met Ile Leu His Gly Val Val Phe Tyr Ala Gly Leu Leu Val Leu Leu			
1	5	10	15
Val Pro Leu Gly Leu Gly Ala Gly Ile Leu Gly Glu Leu Phe Ile Thr			
20	25	30	
Gln Arg Gln Thr Ile Ile Val Val Ser Ser Ile Val Leu Ile Ile Leu			
35	40	45	
Gly Phe Val Gln Ile Phe Gly Gly Gly Phe Asp Phe Gly Lys Ala Leu			
50	55	60	
Pro Gly Leu Asp Arg Leu Gln Ser Lys Ala Thr Val Thr Ser Gly Leu			
65	70	75	80
Gly Lys Ser Phe Leu Leu Gly Met Thr Ser Ser Ile Ala Gly Phe Cys			

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      85              90              95
Ser Gly Pro Ile Leu Gly Ala Val Leu Thr Leu Ala Ala Thr Ser Gly
      100              105              110
Asn Ser Ile Thr Ser Ala Leu Ile Leu Ser Ala Tyr Gly Ala Gly Met
      115              120              125
Val Leu Pro Leu Met Ala Ile Ala Ala Leu Trp Ala Lys Leu Gly Gln
      130              135              140
Arg Gly Gln Gln Met Leu Arg Gly Arg Glu Phe Thr Phe Leu Gly Arg
      145              150              155              160
Gln Trp His Ile Val Ser Val Ile Ser Gly Ala Leu Ile Ile Ala Val
      165              170              175
Gly Ile Leu Phe Trp Ser Thr Asn Gly Leu Val Ser Met Pro Glu Leu
      180              185              190
Val Pro Met Asp Thr Gln Ile Trp Leu Gln Glu Ala Thr Phe Ser Leu
      195              200              205
Gly Ser Pro Leu Phe Asp Ile Ala Leu Ile Ile Val Ala Ala Gly Leu
      210              215              220
Phe Leu Tyr Phe Trp Asn Lys Arg Gln Lys Arg Lys Glu Glu Ala Gln
      225              230              235              240
Arg Pro Lys Glu Ser Gly Trp Val Ile Asn Pro Arg
      245              250

<210> 2371
<211> 867
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(844)
<223> RXA01677

<400> 2371
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agttgagggc ttcccagcag ggatggttaa ggagaattca gtg aac caa cag agt 115
Val Asn Gln Gln Ser
1 5
aaa aag tgg ctc gta ccg aca ctg gtc gtc atc att gca gtg ctc ctc 163
Lys Lys Trp Leu Val Pro Thr Leu Val Val Ile Ile Ala Val Leu Leu
10 15 20
atc gca gtt gtt ctg ttg atg tac cga gga aat gcg agt gat acg gcc 211
Ile Ala Val Val Leu Leu Met Tyr Arg Gly Asn Ala Ser Asp Thr Ala
25 30 35
gag ggc gtt tca gcc gct gcg act tcg gac tcg gct gct gct tcg act 259
Glu Gly Val Ser Ala Ala Ala Thr Ser Asp Ser Ala Ala Ala Ser Thr
40 45 50

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gct gct tcg ggt tcc gct tct ggt gct gcg gac tcc gat ctg acc agc 307
Ala Ala Ser Gly Ser Ala Ser Gly Ala Ala Asp Ser Asp Leu Thr Ser
55 60 65

gtg gaa gca cgc gac cct tcc gac cct gtt gcg gtg gga gac gtt gat 355
Val Glu Ala Arg Asp Pro Ser Asp Pro Val Ala Val Gly Asp Val Asp
70 75 80 85

gca cct gtt ggg tta gtg gtg ttt tcc gac tac caa tgc ccg ttc tgt 403
Ala Pro Val Gly Leu Val Val Phe Ser Asp Tyr Gln Cys Pro Phe Cys
90 95 100

gca aag tgg agc gat gaa acc ctg cca cag atg atg aag cat gtg gaa 451
Ala Lys Trp Ser Asp Glu Thr Leu Pro Gln Met Met Lys His Val Glu
105 110 115

gat gga aac ctc cgc att gaa tgg cgt gaa gtg aac atc ttt gga gaa 499
Asp Gly Asn Leu Arg Ile Glu Trp Arg Glu Val Asn Ile Phe Gly Glu
120 125 130

cca tct gag cgt gga gct cgc gcg gca tac gct gcg ggt ttg cag gac 547
Pro Ser Glu Arg Gly Ala Arg Ala Ala Tyr Ala Ala Gly Leu Gln Asp
135 140 145

gca tac ttg gaa tac cac aac gca ctc ttt gcc aac ggt gaa aaa ccc 595
Ala Tyr Leu Glu Tyr His Asn Ala Leu Phe Ala Asn Gly Glu Lys Pro
150 155 160 165

agc gaa gac ctg ctc agc gaa gag gga ctt att aag ctt gct ggt gac 643
Ser Glu Asp Leu Leu Ser Glu Glu Gly Leu Ile Lys Leu Ala Gly Asp
170 175 180

ctt gga cta gac gaa tcg aaa ttc act gcc gat ttc caa tcc cct gaa 691
Leu Gly Leu Asp Glu Ser Lys Phe Thr Ala Asp Phe Gln Ser Pro Glu
185 190 195

act gca gtc gca att gcg caa cat caa cag ctg gga atc gat ctt ggc 739
Thr Ala Val Ala Ile Ala Gln His Gln Gln Leu Gly Ile Asp Leu Gly
200 205 210

gcc tac tcc acc cca gct ttc ctc cta ggt ggc cag cca atc atg ggc 787
Ala Tyr Ser Thr Pro Ala Phe Leu Leu Gly Gly Gln Pro Ile Met Gly
215 220 225

gct cag cct gct tct gta ttt gaa gcc gcc ttc gag caa gca ctg gca 835
Ala Gln Pro Ala Ser Val Phe Glu Ala Ala Phe Glu Gln Ala Leu Ala
230 235 240 245

gcg aaa gaa taaacctgg atgtcggcct agt 867
Ala Lys Glu

<210> 2372

<211> 248

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2372

Val Asn Gln Gln Ser Lys Lys Trp Leu Val Pro Thr Leu Val Val Ile

1	5	10	15
Ile Ala Val	Leu Leu	Ile Ala Val	Val Leu Leu Met Tyr Arg Gly Asn
	20		25 30
Ala Ser Asp	Thr Ala	Glu Gly	Val Ser Ala Ala Ala Thr Ser Asp Ser
	35		40 45
Ala Ala Ala	Ser Thr	Ala Ala	Ser Gly Ser Ala Ser Gly Ala Ala Asp
	50		55 60
Ser Asp Leu	Thr Ser	Val Glu	Ala Arg Asp Pro Ser Asp Pro Val Ala
	65		70 75 80
Val Gly Asp	Val Asp	Ala Pro	Val Gly Leu Val Val Phe Ser Asp Tyr
	85		90 95
Gln Cys Pro	Phe Cys	Ala Lys	Trp Ser Asp Glu Thr Leu Pro Gln Met
	100		105 110
Met Lys His	Val Glu	Asp Gly	Asn Leu Arg Ile Glu Trp Arg Glu Val
	115		120 125
Asn Ile Phe	Gly Glu	Pro Ser	Glu Arg Gly Ala Arg Ala Ala Tyr Ala
	130		135 140
Ala Gly Leu	Gln Asp	Ala Tyr	Leu Glu Tyr His Asn Ala Leu Phe Ala
	145		150 155 160
Asn Gly Glu	Lys Pro	Ser Glu	Asp Leu Leu Ser Glu Glu Gly Leu Ile
	165		170 175
Lys Leu Ala	Gly Asp	Leu Gly	Leu Asp Glu Ser Lys Phe Thr Ala Asp
	180		185 190
Phe Gln Ser	Pro Glu	Thr Ala	Val Ala Ile Ala Gln His Gln Gln Leu
	195		200 205
Gly Ile Asp	Leu Gly	Ala Tyr	Ser Thr Pro Ala Phe Leu Leu Gly Gly
	210		215 220
Gln Pro Ile	Met Gly	Ala Gln	Pro Ala Ser Val Phe Glu Ala Ala Phe
	225		230 235 240
Glu Gln Ala	Leu Ala	Ala Lys	Glu
	245		

<210> 2373

<211> 756

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(733)

<223> RXA01681

<400> 2373

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aatcttgcca tcaaaattat cgagtgagtt gaagcattcc gtg gaa gta cta cta 115
Val Glu Val Leu Leu 5
1

ctt atc gca atc gtc gtt ggt ggt ggc gtt ttt gtc gcc tca aag atg 163
Leu Ile Ala Ile Val Val Gly Gly Gly Val Phe Val Ala Ser Lys Met 20
10 15

gga tcc aat aac aat aag aag caa gaa gaa gcc aag ttt gct gac gca 211
Gly Ser Asn Asn Asn Lys Lys Gln Glu Glu Ala Lys Phe Ala Asp Ala 35
25 30

cag gca gat gcg cgt cgg tgg att gag cgt ctt ggt tcc cag gtt ttg 259
Gln Ala Asp Ala Arg Arg Trp Ile Glu Arg Leu Gly Ser Gln Val Leu 45
40 50

acc atc gca ggt aca gat gct gcg tcg acc cag gct att gct gac gcc 307
Thr Ile Ala Gly Thr Asp Ala Ala Ser Thr Gln Ala Ile Ala Asp Ala 65
55 60

tca gag cgc tat acc gct gcg tct tct cag att tct tct gcc act act 355
Ser Glu Arg Tyr Thr Ala Ala Ser Ser Gln Ile Ser Ser Ala Thr Thr 85
70 75 80

cct cgt cag gca gag ttg gct cga gaa tct gca cta gag ggt ctg cat 403
Pro Arg Gln Ala Glu Leu Ala Arg Glu Ser Ala Leu Glu Gly Leu His 100
90 95

tat atg aac gcg gct cgt gag atc atg ggt atg act gct ggc cct gag 451
Tyr Met Asn Ala Ala Arg Glu Ile Met Gly Met Thr Ala Gly Pro Glu 115
105 110

ctg cct cct ctg gaa ggt cag cgc aat gct ggt cgc gtt aca gaa aag 499
Leu Pro Pro Leu Glu Gly Gln Arg Asn Ala Gly Arg Val Thr Glu Lys 125
120 125

cgc acc att gag cag gag ggt cgc cag atc act gct tcc ccc gtc gca 547
Arg Thr Ile Glu Gln Glu Gly Arg Gln Ile Thr Ala Ser Pro Val Ala 145
135 140

aca gat gaa act ccg aac tac tac cct ggc ggt aac gtt gcg ggt cgc 595
Thr Asp Glu Thr Pro Asn Tyr Tyr Pro Gly Gly Asn Val Ala Gly Arg 165
150 155 160

cca gtc cct gct ggt tgg tac tcc gag cct tgg tgg gca agc gca ttg 643
Pro Val Pro Ala Gly Trp Tyr Ser Glu Pro Trp Trp Ala Ser Ala Leu 180
170 175

cgt tcc ggt ctg tgg act gca ggt tcg gtc atg atg ttc tca gca atg 691
Arg Ser Gly Leu Trp Thr Ala Gly Ser Val Met Met Phe Ser Ala Met 195
185 190

ttt aac ggc atg gct ggt gtc ggc tac tcc gct gca gac ctt 733
Phe Asn Gly Met Ala Gly Val Gly Tyr Ser Ala Ala Asp Leu 210
200 205

tgaaaaatgg ctatggcgag ggc 756

<210> 2374

<211> 211

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2374

Val Glu Val Leu Leu 5 Leu Ile Ala Ile Val Val Gly Gly Gly Val Phe
1 10 15

Val Ala Ser Lys Met Gly Ser Asn Asn Lys Lys Gln Glu Glu Ala
20 25 30

Lys Phe Ala Asp Ala Gln Ala Asp Ala Arg Arg Trp Ile Glu Arg Leu
35 40 45

Gly Ser Gln Val Leu Thr Ile Ala Gly Thr Asp Ala Ala Ser Thr Gln
50 55 60

Ala Ile Ala Asp Ala Ser Glu Arg Tyr Thr Ala Ala Ser Ser Gln Ile
65 70 75 80

Ser Ser Ala Thr Thr Pro Arg Gln Ala Glu Leu Ala Arg Glu Ser Ala
85 90 95

Leu Glu Gly Leu His Tyr Met Asn Ala Ala Arg Glu Ile Met Gly Met
100 105 110

Thr Ala Gly Pro Glu Leu Pro Pro Leu Glu Gly Gln Arg Asn Ala Gly
115 120 125

Arg Val Thr Glu Lys Arg Thr Ile Glu Gln Glu Gly Arg Gln Ile Thr
130 135 140

Ala Ser Pro Val Ala Thr Asp Glu Thr Pro Asn Tyr Tyr Pro Gly Gly
145 150 155 160

Asn Val Ala Gly Arg Pro Val Pro Ala Gly Trp Tyr Ser Glu Pro Trp
165 170 175

Trp Ala Ser Ala Leu Arg Ser Gly Leu Trp Thr Ala Gly Ser Val Met
180 185 190

Met Phe Ser Ala Met Phe Asn Gly Met Ala Gly Val Gly Tyr Ser Ala
195 200 205

Ala Asp Leu
210

<210> 2375

<211> 702

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(679)

<223> RXA01685

<400> 2375

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ccccaccaga tgggcgatgt tctttgtcgg gatctttatt atg tcc ttc gcc atc 115

Met Ser Phe Ala Ile
1 5

ggc atc acc gtc cac gca gga cta gga acc acc aca att tca tca ctt 163
Gly Ile Thr Val His Ala Gly Leu Gly Thr Thr Thr Ser Ser Leu
10 15 20

ccc gtg gtg tgg act gct gcc agc gga tta tcc ctg ggc tgg acc aca 211
Pro Val Val Trp Thr Ala Ala Ser Gly Leu Ser Leu Gly Trp Thr Thr
25 30 35

att tac ttc aat ggc ttc atg att ctg tgc caa ata att gtg ctg cgt 259
Ile Tyr Phe Asn Gly Phe Met Ile Leu Cys Gln Ile Val Leu Arg
40 45 50

tcc cag ttc aaa cca caa atg tta gtc caa atc ctg tgg gca ttc ctc 307
Ser Gln Phe Lys Pro Gln Met Leu Val Gln Ile Leu Trp Ala Phe Leu
55 60 65

ttt ggg ttt ctt tgt gat tta agc ctg caa cta acc acc tgg gcg caa 355
Phe Gly Phe Leu Cys Asp Leu Ser Leu Gln Leu Thr Thr Trp Ala Gln
70 75 80 85

act gac aat tat ttt gtg gcc tgg atc tgg gtt att gtg tcc acc att 403
Thr Asp Asn Tyr Phe Val Ala Trp Ile Trp Val Ile Val Ser Thr Ile
90 95 100

ttg atg tcg atc gga gtt ttt att caa gta ctc ccc aac atc act ttc 451
Leu Met Ser Ile Gly Val Phe Ile Gln Val Leu Pro Asn Ile Thr Phe
105 110 115

atc gct ggt gaa ggc att gtc tct gcg ctg gtg aag aaa ttt ccc aac 499
Ile Ala Gly Glu Gly Ile Val Ser Ala Leu Val Lys Lys Phe Pro Asn
120 125 130

gtg gaa ttt ggc acc atg aaa caa atc gtc gac tgg act ttc gtc tcc 547
Val Glu Phe Gly Thr Met Lys Gln Ile Val Asp Trp Thr Phe Val Ser
135 140 145

gtc gct gcc att ttg tcc tgg atc acc atg ggt gga ctt att ggc gtg 595
Val Ala Ala Ile Leu Ser Trp Ile Thr Met Gly Gly Leu Ile Gly Val
150 155 160 165

cgc gaa gga aca gtg ttc gcg gcg ttt ttc atc gga ttc ttc gtc cgc 643
Arg Glu Gly Thr Val Phe Ala Ala Phe Phe Ile Gly Phe Phe Val Arg
170 175 180

cag tgg cgc aaa ctc tac ctc cgc tcc atc ggt cac taaagagctt 689
Gln Trp Arg Lys Leu Tyr Leu Arg Ser Ile Gly His
185 190

gttccaggaa gag 702

<210> 2376

<211> 193

<212> PRT

<213> Corynebacterium glutamicum

<400> 2376

Met Ser Phe Ala Ile Gly Ile Thr Val His Ala Gly Leu Gly Thr Thr

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Thr Ile Ser Ser Leu Pro Val Val Trp	Thr Ala Ala Ser Gly Leu Ser		
20	25	30	
Leu Gly Trp Thr Thr Ile Tyr Phe Asn Gly Phe Met Ile Leu Cys Gln			
35	40	45	
Ile Ile Val Leu Arg Ser Gln Phe Lys Pro Gln Met Leu Val Gln Ile			
50	55	60	
Leu Trp Ala Phe Leu Phe Gly Phe Leu Cys Asp Leu Ser Leu Gln Leu			
65	70	75	80
Thr Thr Trp Ala Gln Thr Asp Asn Tyr Phe Val Ala Trp Ile Trp Val			
85	90	95	
Ile Val Ser Thr Ile Leu Met Ser Ile Gly Val Phe Ile Gln Val Leu			
100	105	110	
Pro Asn Ile Thr Phe Ile Ala Gly Glu Gly Ile Val Ser Ala Leu Val			
115	120	125	
Lys Lys Phe Pro Asn Val Glu Phe Gly Thr Met Lys Gln Ile Val Asp			
130	135	140	
Trp Thr Phe Val Ser Val Ala Ala Ile Leu Ser Trp Ile Thr Met Gly			
145	150	155	160
Gly Leu Ile Gly Val Arg Glu Gly Thr Val Phe Ala Ala Phe Phe Ile			
165	170	175	
Gly Phe Phe Val Arg Gln Trp Arg Lys Leu Tyr Leu Arg Ser Ile Gly			
180	185	190	
His			

<210> 2377

<211> 564

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(541)

<223> RXA01686

<400> 2377

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cgaacgcgggtctttttctcatctacttaagatgtagaac	atg act tca ctc agg	115
	Met Thr Ser Leu Arg	
	1	5

gac tta ctt gtt tcc acc aat gcc gac gca gca	att gca gat atg tca	163
Asp Leu Leu Val Ser Thr Asn Ala Asp Ala Ala	Ile Ala Asp Met Ser	
	10	20

gca ttt atc gaa gaa acc gtg ggc aag caa tcc ggc atc agc ggc atc	211
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Ala Phe Ile Glu Thr Val Gly Lys Gln Ser Gly Ile Ser Gly Ile
25 30 35

gca ctc aaa ggc gca atg ggt gct gca acc aag atc gac tcc gac atc 259
Ala Leu Lys Gly Ala Met Gly Ala Ala Thr Lys Ile Asp Ser Asp Ile
40 45 50

gta gcc aaa ggc tcc agg cgc ctc ctc ccg gaa atc gct gac tcc ctc 307
Val Ala Lys Gly Ser Arg Arg Leu Leu Pro Glu Ile Ala Asp Ser Leu
55 60 65

gac gga ctc tgg cag gaa tac caa aat ggt ggc acc gcc gca gat ttc 355
Asp Gly Leu Trp Gln Glu Tyr Gln Asn Gly Gly Thr Ala Ala Asp Phe
70 75 80 85

ggc gcc cac ctc gag gcc aac agc tcc acc gca ctc gac gcg att ctc 403
Gly Ala His Leu Glu Ala Asn Ser Ser Thr Ala Leu Asp Ala Ile Leu
90 95 100

agc gtt gct gac aaa aac gca gag agc atc aac gtt cca gga ctt ggc 451
Ser Val Ala Asp Lys Asn Ala Glu Ser Ile Asn Val Pro Gly Leu Gly
105 110 115

aag gtc tac aag ggc gtg cgc ggc aag gct gcc aaa gta atc gag cag 499
Lys Val Tyr Lys Gly Val Arg Gly Lys Ala Ala Lys Val Ile Glu Gln
120 125 130

gaa ctt cct gca att ggc cag ttg atc gaa aag aac gca caa 541
Glu Leu Pro Ala Ile Gly Gln Leu Ile Glu Lys Asn Ala Gln
135 140 145

taattaggtg agcaacccta ata 564

<210> 2378
<211> 147
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 2378
Met Thr Ser Leu Arg Asp Leu Leu Val Ser Thr Asn Ala Asp Ala Ala
1 5 10 15

Ile Ala Asp Met Ser Ala Phe Ile Glu Glu Thr Val Gly Lys Gln Ser
20 25 30

Gly Ile Ser Gly Ile Ala Leu Lys Gly Ala Met Gly Ala Ala Thr Lys
35 40 45

Ile Asp Ser Asp Ile Val Ala Lys Gly Ser Arg Arg Leu Leu Pro Glu
50 55 60

Ile Ala Asp Ser Leu Asp Gly Leu Trp Gln Glu Tyr Gln Asn Gly Gly
65 70 75 80

Thr Ala Ala Asp Phe Gly Ala His Leu Glu Ala Asn Ser Ser Thr Ala
85 90 95

Leu Asp Ala Ile Leu Ser Val Ala Asp Lys Asn Ala Glu Ser Ile Asn
100 105 110

Val Pro Gly Leu Gly Lys Val Tyr Lys Gly Val Arg Gly Lys Ala Ala
 115 120
 Lys Val Ile Glu Gln Glu Leu Pro Ala Ile Gly Gln Leu Ile Glu Lys
 130 135 140
 Asn Ala Gln
 145

<210> 2379
 <211> 1545
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1522)
 <223> RXA01693

<400> 2379
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 Met Asn Thr Ala Pro
 1 5

ttc aaa ctc gaa gct gac ttc gca tca gcc ctg ccc acc atg gca gcc 163
 Phe Lys Leu Glu Ala Asp Phe Ala Ser Ala Leu Pro Thr Met Ala Ala
 10 15 20

ccc tgg caa ggt gag gaa gcc ccc aac cct gag ctc gtg att tta aat 211
 Pro Trp Gln Gly Glu Glu Ala Pro Asn Pro Glu Leu Val Ile Leu Asn
 25 30 35

gac gac ctc gcc tac agc ctc ggg ctt gat ccg aca tgg ctt cgc aca 259
 Asp Asp Leu Ala Tyr Ser Leu Gly Leu Asp Pro Thr Trp Leu Arg Thr
 40 45 50

cct gag ggc gtt caa ttt ctt ctc gga ctc aac ccc gag ccc tta aca 307
 Pro Glu Gly Val Gln Phe Leu Leu Gly Leu Asn Pro Glu Pro Leu Thr
 55 60 65

aaa gca gtt gcg cag gcc tat tcc gcc cac caa ttc gga cag ttt gtg 355
 Lys Ala Val Ala Gln Ala Tyr Ser Gly His Gln Phe Gly Gln Phe Val
 70 75 80 85

gca agc ctt ggt gat ggc cga gcg ctt ctt ctc ggc gaa gcc cgc tca 403
 Ala Ser Leu Gly Asp Gly Arg Ala Leu Leu Leu Gly Glu Ala Arg Ser
 90 95 100

gct gac ggc gta ctg cat gat atc cac ctc aaa gga tct gga cga acc 451
 Ala Asp Gly Val Leu His Asp Ile His Leu Lys Gly Ser Gly Arg Thr
 105 110 115

caa ttc tcc cga gga gcc gat gga cgc gcc gtc ctt ggc ccc gtc tta 499
 Gln Phe Ser Arg Gly Ala Asp Gly Arg Ala Val Leu Gly Pro Val Leu
 120 125 130

cgc gaa tac atc atc tcc gaa gcg atg cat gca ctt ggt gtt ccc acc 547
 Arg Glu Tyr Ile Ile Ser Glu Ala Met His Ala Leu Gly Val Pro Thr

135	140	145	
acc agg tca ctt gca gta att agc acc ggt agg aaa atc caa cga gga Thr Arg Ser Leu Ala Val Ile Ser Thr Gly Arg Lys Ile Gln Arg Gly 150 155 160 165			595
agc gta gcc cca ggc gca gtc ctt gtt cga gta gca acc agc ctc att Ser Val Ala Pro Gly Ala Val Leu Val Arg Val Ala Thr Ser Leu Ile 170 175 180			643
cga gtc gga tcc ttc caa tac tcc aac atc tct ggt ggc atc gaa cta Arg Val Gly Ser Phe Gln Tyr Ser Asn Ile Ser Gly Gly Ile Glu Leu 185 190 195			691
tct caa cac ctg gcg aac tat acg atc acc agg cat ttc cct tcg ttg Ser Gln His Leu Ala Asn Tyr Thr Ile Thr Arg His Phe Pro Ser Leu 200 205 210			739
gta gct gaa cta tcc gca cca acc ccc gca act tat gta tca ctg ttt Val Ala Glu Leu Ser Ala Pro Thr Pro Ala Thr Tyr Val Ser Leu Phe 215 220 225			787
aaa gcg att ctt cag cgc caa gca gac acc gtt gga aaa tgg acc agg Lys Ala Ile Leu Gln Arg Gln Ala Asp Thr Val Gly Lys Trp Thr Arg 230 235 240 245			835
ctg ggt ttc gtt cac gga gcc ctc aac aca gac aac acg ttg ata tcc Leu Gly Phe Val His Gly Ala Leu Asn Thr Asp Asn Thr Leu Ile Ser 250 255 260			883
gga gaa act gtt gac tac ggc cca tgc gct ttc atg gag cgc tac cgt Gly Glu Thr Val Asp Tyr Gly Pro Cys Ala Phe Met Glu Arg Tyr Arg 265 270 275			931
ggc gac gcg aaa ttt agc tcc atc gac act tat ggt cgc tac aaa ttt Gly Asp Ala Lys Phe Ser Ser Ile Asp Thr Tyr Gly Arg Tyr Lys Phe 280 285 290			979
gaa aac caa cct atg atc ctc gga tgg aac atg gcc cgc ctc gta gaa Glu Asn Gln Pro Met Ile Leu Gly Trp Asn Met Ala Arg Leu Val Glu 295 300 305			1027
acc ctc ctc cca ctc ctg ggc gcc aca cca gac gaa ggc atg aca gca Thr Leu Leu Pro Leu Leu Gly Ala Thr Pro Asp Glu Gly Met Thr Ala 310 315 320 325			1075
gcc caa gaa gct ctc gta gaa ttc gat gac ctc tgc gaa caa gca atc Ala Gln Glu Ala Leu Val Glu Phe Asp Leu Cys Glu Gln Ala Ile 330 335 340			1123
cga aaa gaa ttc gcc act gca ctg ggc ctt gac gag tca gac acc ggc Arg Lys Glu Phe Ala Thr Ala Leu Gly Leu Asp Glu Ser Asp Thr Gly 345 350 355			1171
acg gta gag cag ttc cgt gaa ctg ctc tac ctc cat aac ccc gac atc Thr Val Glu Gln Phe Arg Glu Leu Leu Tyr Leu His Asn Pro Asp Ile 360 365 370			1219
acc acg ctg ctg cgc gca ctc acc gac aac acc gca cca ccg agt ggc Thr Thr Leu Leu Arg Ala Leu Thr Asp Asn Thr Ala Pro Pro Ser Gly 375 380 385			1267

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ttt gaa gca ttc gtt cac gac tgg aaa acc caa gac cca gat atc gaa 1315
Phe Glu Ala Phe Val His Asp Trp Lys Thr Gln Asp Pro Asp Ile Glu
390 395 400 405

gca atg cga gca gta aat cca ctt ttc att cca cgc aat cac ctc gtg 1363
Ala Met Arg Ala Val Asn Pro Leu Phe Ile Pro Arg Asn His Leu Val
410 415 420

gaa gct gct ctc gca gac gca gtt gaa ggg aat cta gaa aag ttc cac 1411
Glu Ala Ala Leu Ala Asp Ala Val Glu Gly Asn Leu Glu Lys Phe His
425 430 435

gaa ctc ctc gct gct gtc acc aat cct ttt gat cca act cgc ggc ccc 1459
Glu Leu Leu Ala Ala Val Thr Asn Pro Phe Asp Pro Thr Ala Gly Pro
440 445 450

gat gaa cta cgc ctg cca agc gaa gaa gga ttt gaa gaa gac tac atg 1507
Asp Glu Leu Arg Leu Pro Ser Glu Glu Gly Phe Glu Glu Asp Tyr Met
455 460 465

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Thr Phe Cys Gly Thr
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<210> 2380
<211> 474
<212> PRT
<213> Corynebacterium glutamicum

<400> 2380
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20 25 30

Leu Val Ile Leu Asn Asp Asp Leu Ala Tyr Ser Leu Gly Leu Asp Pro
35 40 45

Thr Trp Leu Arg Thr Pro Glu Gly Val Gln Phe Leu Leu Gly Leu Asn
50 55 60

Pro Glu Pro Leu Thr Lys Ala Val Ala Gln Ala Tyr Ser Gly His Gln
65 70 75 80

Phe Gly Gln Phe Val Ala Ser Leu Gly Asp Gly Arg Ala Leu Leu Leu
85 90 95

Gly Glu Ala Arg Ser Ala Asp Gly Val Leu His Asp Ile His Leu Lys
100 105 110

Gly Ser Gly Arg Thr Gln Phe Ser Arg Gly Ala Asp Gly Arg Ala Val
115 120 125

Leu Gly Pro Val Leu Arg Glu Tyr Ile Ile Ser Glu Ala Met His Ala
130 135 140

Leu Gly Val Pro Thr Thr Arg Ser Leu Ala Val Ile Ser Thr Gly Arg
145 150 155 160

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Lys Ile Gln Arg Gly Ser Val Ala Pro Gly Ala Val Leu Val Arg Val
 165 170 175
 Ala Thr Ser Leu Ile Arg Val Gly Ser Phe Gln Tyr Ser Asn Ile Ser
 180 185 190
 Gly Gly Ile Glu Leu Ser Gln His Leu Ala Asn Tyr Thr Ile Thr Arg
 195 200 205
 His Phe Pro Ser Leu Val Ala Glu Leu Ser Ala Pro Thr Pro Ala Thr
 210 215 220
 Tyr Val Ser Leu Phe Lys Ala Ile Leu Gln Arg Gln Ala Asp Thr Val
 225 230 235 240
 Gly Lys Trp Thr Arg Leu Gly Phe Val His Gly Ala Leu Asn Thr Asp
 245 250 255
 Asn Thr Leu Ile Ser Gly Glu Thr Val Asp Tyr Gly Pro Cys Ala Phe
 260 265 270
 Met Glu Arg Tyr Arg Gly Asp Ala Lys Phe Ser Ser Ile Asp Thr Tyr
 275 280 285
 Gly Arg Tyr Lys Phe Glu Asn Gln Pro Met Ile Leu Gly Trp Asn Met
 290 295 300
 Ala Arg Leu Val Glu Thr Leu Leu Pro Leu Leu Gly Ala Thr Pro Asp
 305 310 315 320
 Glu Gly Met Thr Ala Ala Gln Glu Ala Leu Val Glu Phe Asp Asp Leu
 325 330 335
 Cys Glu Gln Ala Ile Arg Lys Glu Phe Ala Thr Ala Leu Gly Leu Asp
 340 345 350
 Glu Ser Asp Thr Gly Thr Val Glu Gln Phe Arg Glu Leu Leu Tyr Leu
 355 360 365
 His Asn Pro Asp Ile Thr Thr Leu Leu Arg Ala Leu Thr Asp Asn Thr
 370 375 380
 Ala Pro Pro Ser Gly Phe Glu Ala Phe Val His Asp Trp Lys Thr Gln
 385 390 395 400
 Asp Pro Asp Ile Glu Ala Met Arg Ala Val Asn Pro Leu Phe Ile Pro
 405 410 415
 Arg Asn His Leu Val Glu Ala Ala Leu Ala Asp Ala Val Glu Gly Asn
 420 425 430
 Leu Glu Lys Phe His Glu Leu Leu Ala Ala Val Thr Asn Pro Phe Asp
 435 440 445
 Pro Thr Ala Gly Pro Asp Glu Leu Arg Leu Pro Ser Glu Glu Gly Phe
 450 455 460
 Glu Glu Asp Tyr Met Thr Phe Cys Gly Thr
 465 470

gtt gaa gcg ttc gca gca gtg ctt gcc tct gtt gct gga ctt ccc cca 691
 Val Glu Ala Phe Ala Ala Val Leu Ala Ser Val Ala Gly Leu Pro Pro
 185 190 195

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<210> 2382

<211> 205

<212> PRT

<213> Corynebacterium glutamicum

<400> 2382

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Arg Ala Arg Leu Arg Pro Glu Leu Thr Leu Gly Thr Ile Arg Pro Pro
 35 40 45

Gln Arg Leu Ala Pro Phe Ser His Ala Ile Gly Leu Glu Val Gly Asn
 50 55 60

Gln Glu Glu Ser Asp Asp Val Ser Thr Asn Ser Glu Gly Asp Ser Phe
 65 70 75 80

Gly Arg Leu Ile Leu Leu His Asp Pro Gly Ala Glu Glu Thr Trp Glu
 85 90 95

Gly Ala Met Arg Leu Val Ala Tyr Ile Gln Ala Asp Met Asp His Ala
 100 105 110

Val Ala Ser Asp Pro Leu Leu Pro Glu Val Ala Trp Gln Trp Leu Asn
 115 120 125

Glu Gly Leu Glu Gln Ala Gly Ala Gly Phe Thr Asn Leu Gly Gly Thr
 130 135 140

Val Thr Ser Thr Thr Ser Val Arg Phe Gly Glu Ile Gly Gly Pro Pro
 145 150 155 160

Ser Ala Tyr Gln Val Glu Met Arg Ala Ser Trp Thr Ala Thr Gly Thr
 165 170 175

Asp Leu Thr Ala His Val Glu Ala Phe Ala Ala Val Leu Ala Ser Val
 180 185 190

Ala Gly Leu Pro Pro Glu Gly Val Thr Glu Leu Arg Arg
 195 200 205

<210> 2383

<211> 819

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(796)

<223> RXA01715

<400> 2383

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				Val	Ser	Glu	Leu	Asp	
				1				5	

att	aaa	cag	ctc	aac	aaa	ctg	cag	cgc	tac	tct	cag	tgg	cgc	gtg	ttc	163
Ile	Lys	Gln	Leu	Asn	Lys	Leu	Gln	Arg	Tyr	Ser	Gln	Trp	Ala	Val	Phe	
				10					15					20		

cgt	gct	att	cct	gga	gcg	ctc	gat	gat	gat	cgc	aca	gaa	gtc	act	gac	211
Arg	Ala	Ile	Pro	Gly	Ala	Leu	Asp	Asp	Asp	Arg	Thr	Glu	Val	Thr	Asp	
			25					30					35			

caa	gca	gcc	aag	ttc	ttt	gcc	gac	ctt	gaa	gca	gaa	ggc	aaa	gtc	act	259
Gln	Ala	Ala	Lys	Phe	Phe	Ala	Asp	Leu	Glu	Ala	Glu	Gly	Lys	Val	Thr	
		40				45						50				

gtc	cgt	ggc	att	tac	aac	gcc	tcc	ggc	ctg	cgc	gca	gac	gct	gac	tac	307
Val	Arg	Gly	Ile	Tyr	Asn	Ala	Ser	Gly	Leu	Arg	Ala	Asp	Ala	Asp	Tyr	
		55				60					65					

atg	atc	tgg	tgg	cac	gca	gaa	gaa	ttc	gaa	gac	att	cag	aag	gcc	ttc	355
Met	Ile	Trp	Trp	His	Ala	Glu	Glu	Phe	Glu	Asp	Ile	Gln	Lys	Ala	Phe	
		70			75					80				85		

gct	gat	ttc	cgc	cgc	acc	acc	att	ttg	ggc	cag	gtt	tct	gag	gtc	ttc	403
Ala	Asp	Phe	Arg	Arg	Thr	Thr	Ile	Leu	Gly	Gln	Val	Ser	Glu	Val	Phe	
					90				95					100		

tgg	atc	gga	aac	gct	ctc	cac	cgt	cca	tct	gag	ttc	aac	aag	gct	cac	451
Trp	Ile	Gly	Asn	Ala	Leu	His	Arg	Pro	Ser	Glu	Phe	Asn	Lys	Ala	His	
			105					110					115			

ttg	cct	tca	ttc	atc	atg	ggt	gaa	gaa	gca	aag	gac	tgg	atc	act	gtt	499
Leu	Pro	Ser	Phe	Ile	Met	Gly	Glu	Glu	Ala	Lys	Asp	Trp	Ile	Thr	Val	
			120				125					130				

tac	ccg	ttc	gtg	cgc	agc	tac	gac	tgg	tac	atc	atg	gag	ccc	ttg	aag	547
Tyr	Pro	Phe	Val	Arg	Ser	Tyr	Asp	Trp	Tyr	Ile	Met	Glu	Pro	Leu	Lys	
			135			140					145					

cgt	tcc	cgc	att	ctc	cgc	gag	cac	gga	caa	gct	gct	gtg	gaa	ttc	cca	595
Arg	Ser	Arg	Ile	Leu	Arg	Glu	His	Gly	Gln	Ala	Ala	Val	Glu	Phe	Pro	
					155				160					165		

gat	gtt	cgt	gcc	aac	act	gtg	ccg	gct	ttc	gca	ctg	ggt	gac	tac	gaa	643
Asp	Val	Arg	Ala	Asn	Thr	Val	Pro	Ala	Phe	Ala	Leu	Gly	Asp	Tyr	Glu	
				170					175					180		

tgg	gtg	ctg	gct	ttc	gag	gct	gat	gag	ttg	cac	cgc	att	gtc	gat	ttg	691
Trp	Val	Leu	Ala	Phe	Glu	Ala	Asp	Glu	Leu	His	Arg	Ile	Val	Asp	Leu	
				185				190					195			

atg	cac	aag	atg	cgt	tac	acc	gag	gct	cgc	ctc	cac	gtc	cgt	gag	gag	739
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Met His Lys Met Arg Tyr Thr Glu Ala Arg Leu His Val Arg Glu Glu
  200                                205                210
ctg cca ttt att tct gga cag cgc gtc gac att gca gat ctg att aag 787
Leu Pro Phe Ile Ser Gly Gln Arg Val Asp Ile Ala Asp Leu Ile Lys
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gtt ctt cct taaaagctgc ttttctaaac gat 819
Val Leu Pro
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<210> 2384

<211> 232

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2384

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Gln Trp Ala Val Phe Arg Ala Ile Pro Gly Ala Leu Asp Asp Asp Arg
  20                                25                30

Thr Glu Val Thr Asp Gln Ala Ala Lys Phe Phe Ala Asp Leu Glu Ala
  35                                40                45

Glu Gly Lys Val Thr Val Arg Gly Ile Tyr Asn Ala Ser Gly Leu Arg
  50                                55                60

Ala Asp Ala Asp Tyr Met Ile Trp Trp His Ala Glu Glu Phe Glu Asp
  65                                70                75                80

Ile Gln Lys Ala Phe Ala Asp Phe Arg Arg Thr Thr Ile Leu Gly Gln
  85                                90                95

Val Ser Glu Val Phe Trp Ile Gly Asn Ala Leu His Arg Pro Ser Glu
  100                               105                110

Phe Asn Lys Ala His Leu Pro Ser Phe Ile Met Gly Glu Glu Ala Lys
  115                               120                125

Asp Trp Ile Thr Val Tyr Pro Phe Val Arg Ser Tyr Asp Trp Tyr Ile
  130                               135                140

Met Glu Pro Leu Lys Arg Ser Arg Ile Leu Arg Glu His Gly Gln Ala
  145                               150                155                160

Ala Val Glu Phe Pro Asp Val Arg Ala Asn Thr Val Pro Ala Phe Ala
  165                               170                175

Leu Gly Asp Tyr Glu Trp Val Leu Ala Phe Glu Ala Asp Glu Leu His
  180                               185                190

Arg Ile Val Asp Leu Met His Lys Met Arg Tyr Thr Glu Ala Arg Leu
  195                               200                205

His Val Arg Glu Glu Leu Pro Phe Ile Ser Gly Gln Arg Val Asp Ile
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Ala Asp Leu Ile Lys Val Leu Pro

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225

230

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 <213> Corynebacterium glutamicum

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 <223> RXA01729

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 Val Lys Leu Arg Thr
 1 5
 atc cca gcc ctg tta gcc gtc gca ctt ctt gca ggc tgt tgc ggt gaa 163
 Ile Pro Ala Leu Leu Ala Val Ala Leu Leu Ala Gly Cys Ser Gly Glu
 10 15 20
 agt gct gat agc caa gcc gtt tcc gct gag gaa acc atg gaa gta acc 211
 Ser Ala Asp Ser Gln Ala Val Ser Ala Glu Glu Thr Met Glu Val Thr
 25 30 35
 act acc tca acc ccg gtg ttc gaa gcc aaa gag gta agc cca atc aca 259
 Thr Thr Ser Thr Pro Val Phe Glu Ala Lys Glu Val Ser Pro Ile Thr
 40 45 50
 gtc cca agc ggc gat atc agg gtt gaa gac cca ggt ctc aat gtt gaa 307
 Val Pro Ser Gly Asp Ile Arg Val Glu Asp Pro Gly Leu Asn Val Glu
 55 60 65
 ttt atc ttc cga ggc acc cgc tac ggc acc aac ggt ggc tca att att 355
 Phe Ile Phe Arg Gly Thr Arg Tyr Gly Thr Asn Gly Gly Ser Ile Ile
 70 75 80 85
 cac atc gcg gtg aaa aac cta aac gac gta gcc ctg cca gcc gac gcc 403
 His Ile Ala Val Lys Asn Leu Asn Asp Val Ala Leu Pro Ala Asp Ala
 90 95 100
 atc gat cca ccc acc ctg gac atc gaa gac tac aac ggc aac aaa acc 451
 Ile Asp Pro Thr Leu Asp Ile Glu Asp Tyr Asn Gly Asn Lys Thr
 105 110 115
 aac atc gaa acc ctc tcc ggc gac gac aac atc cca ctc gac cta cca 499
 Asn Ile Glu Thr Leu Ser Gly Asp Asp Asn Ile Pro Leu Asp Leu Pro
 120 125 130
 ctg ggt gcc ggc gcg aca acg aac ctg caa tac gcg ttc aac acc tca 547
 Leu Gly Ala Gly Ala Thr Thr Asn Leu Gln Tyr Ala Phe Asn Thr Ser
 135 140 145
 aac ggc tca ttg tgc aat gct aaa ttc cag atc gga aac gtc atc tac 595
 Asn Gly Ser Leu Ser Asn Ala Lys Phe Gln Ile Gly Asn Val Ile Tyr
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 tca ggc aat ttg aac agc ttg gcg taagttcaaa aaataatttg aat 642

Ser Gly Asn Leu Asn Ser Leu Ala
170

<210> 2386

<211> 173

<212> PRT

<213> Corynebacterium glutamicum

<400> 2386

Val Lys Leu Arg Thr Ile Pro Ala Leu Leu Ala Val Ala Leu Leu Ala
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Gly Cys Ser Gly Glu Ser Ala Asp Ser Gln Ala Val Ser Ala Glu Glu
20 25 30

Thr Met Glu Val Thr Thr Thr Ser Thr Pro Val Phe Glu Ala Lys Glu
35 40 45

Val Ser Pro Ile Thr Val Pro Ser Gly Asp Ile Arg Val Glu Asp Pro
50 55 60

Gly Leu Asn Val Glu Phe Ile Phe Arg Gly Thr Arg Tyr Gly Thr Asn
65 70 75 80

Gly Gly Ser Ile Ile His Ile Ala Val Lys Asn Leu Asn Asp Val Ala
85 90 95

Leu Pro Ala Asp Ala Ile Asp Pro Pro Thr Leu Asp Ile Glu Asp Tyr
100 105 110

Asn Gly Asn Lys Thr Asn Ile Glu Thr Leu Ser Gly Asp Asn Ile
115 120 125

Pro Leu Asp Leu Pro Leu Gly Ala Gly Ala Thr Thr Asn Leu Gln Tyr
130 135 140

Ala Phe Asn Thr Ser Asn Gly Ser Leu Ser Asn Ala Lys Phe Gln Ile
145 150 155 160

Gly Asn Val Ile Tyr Ser Gly Asn Leu Asn Ser Leu Ala
165 170

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<211> 822

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(799)

<223> RXA01731

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cactcaaggt tggacgttgt gttcatgaat aacttttatg atg aac gca tgg tcc 115
Met Asn Ala Ser Ser
1 5

att tct tcc cga ttc aag gat ctt ttt gtg aca ccc agt att gtt ttt	163
Ile Ser Ser Arg Phe Lys Asp Leu Phe Val Thr Pro Ser Ile Val Phe	
10 15 20	
gat ttc gat ggc acg ctt gcc att ggc cat ggc cct gtc ctt gcg tat	211
Asp Phe Asp Gly Thr Leu Ala Ile Gly His Gly Pro Val Leu Ala Tyr	
25 30 35	
gca ttg tgt gtt gca ccg gag ggt tcc aag gac ttt ctg gag cgt gtg	259
Ala Leu Cys Val Ala Pro Glu Gly Ser Lys Asp Phe Leu Glu Arg Val	
40 45 50	
cgc agg gag ctt cgg cgc tat gac gat ggt cag agt att tac cgt gat	307
Arg Arg Glu Leu Arg Arg Tyr Asp Asp Gly Gln Ser Ile Tyr Arg Asp	
55 60 65	
ggg tat gac att gtg gct aag ttg gcg tcg gaa ttg ggg att gat gat	355
Gly Tyr Asp Ile Val Ala Lys Leu Ala Ser Glu Leu Gly Ile Asp Asp	
70 75 80 85	
ggc acg atg tct gtc gct tat ggc gag agc cgg aag ttg ctt ggt tcg	403
Gly Thr Met Ser Val Ala Tyr Gly Glu Ser Arg Lys Leu Leu Gly Ser	
90 95 100	
gat tta gcg cct gtt gag cat gtg cgg ggt att aag gat att ttg tcc	451
Asp Leu Ala Pro Val Glu His Val Arg Gly Ile Lys Asp Ile Leu Ser	
105 110 115	
tcg ttg aaa ggt cat gct cgg ttg gtt tta gct acc aat gcc ccg gaa	499
Ser Leu Lys Gly His Ala Arg Leu Val Leu Ala Thr Asn Ala Pro Glu	
120 125 130	
aat ggc gtg cat gat ttg ctg cgt cag tgg ggt gtt gct gat ttg ttt	547
Asn Gly Val His Asp Leu Leu Arg Gln Trp Gly Val Ala Asp Leu Phe	
135 140 145	
gat cag ttg cat ttt gtg gtg ggt aag cct gca ggg ttg att tcg atc	595
Asp Gln Leu His Phe Val Val Gly Lys Pro Ala Gly Leu Ile Ser Ile	
150 155 160 165	
att tct gat ttg cag ctt gat ggt ccg gtg ctt gcg gtg ggc gat att	643
Ile Ser Asp Leu Gln Leu Asp Gly Pro Val Leu Ala Val Gly Asp Ile	
170 175 180	
tat gaa ttc gat ctg agt cct gca gcg cag tta ggt gca gat acg gct	691
Tyr Glu Phe Asp Leu Ser Pro Ala Ala Gln Leu Gly Ala Asp Thr Ala	
185 190 195	
ctg gtt gga gct aca gca acc att tct gaa gcg aag gtc tcc atg cgt	739
Leu Val Gly Ala Thr Ala Thr Ile Ser Glu Ala Lys Val Ser Met Arg	
200 205 210	
gga gat tct atc gct gat ctc cct ctc ctt gcc tgg gtt tgt tcc cgg	787
Gly Asp Ser Ile Ala Asp Leu Pro Leu Leu Ala Trp Val Cys Ser Arg	
215 220 225	
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Val Ser Ser Ser	
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 35 40 45
 Phe Leu Glu Arg Val Arg Arg Glu Leu Arg Arg Tyr Asp Asp Gly Gln
 50 55 60
 Ser Ile Tyr Arg Asp Gly Tyr Asp Ile Val Ala Lys Leu Ala Ser Glu
 65 70 75 80
 Leu Gly Ile Asp Asp Gly Thr Met Ser Val Ala Tyr Gly Glu Ser Arg
 85 90 95
 Lys Leu Leu Gly Ser Asp Leu Ala Pro Val Glu His Val Arg Gly Ile
 100 105 110
 Lys Asp Ile Leu Ser Ser Leu Lys Gly His Ala Arg Leu Val Leu Ala
 115 120 125
 Thr Asn Ala Pro Glu Asn Gly Val His Asp Leu Leu Arg Gln Trp Gly
 130 135 140
 Val Ala Asp Leu Phe Asp Gln Leu His Phe Val Val Gly Lys Pro Ala
 145 150 155 160
 Gly Leu Ile Ser Ile Ile Ser Asp Leu Gln Leu Asp Gly Pro Val Leu
 165 170 175
 Ala Val Gly Asp Ile Tyr Glu Phe Asp Leu Ser Pro Ala Ala Gln Leu
 180 185 190
 Gly Ala Asp Thr Ala Leu Val Gly Ala Thr Ala Thr Ile Ser Glu Ala
 195 200 205
 Lys Val Ser Met Arg Gly Asp Ser Ile Ala Asp Leu Pro Leu Leu Ala
 210 215 220
 Trp Val Cys Ser Arg Val Ser Ser Ser
 225 230

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 <212> DNA
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Met Arg Ile Leu Pro
1 5

atc ggc ccc cac gat gaa atc gcc gtc aac gga tca ata gtc ctt cta 163
Ile Gly Pro His Asp Glu Ile Ala Val Asn Gly Ser Ile Val Leu Leu
10 15 20

tcc gag cac gac gga gac atc gta tcg gtc ggc ccc gac ctc ggc acg 211
Ser Glu His Asp Gly Asp Ile Val Ser Val Gly Pro Asp Leu Gly Thr
25 30 35

gtg cga gtt acc ctt gaa gag atc gaa agt tta ggt aca ccg acg gca 259
Val Arg Val Thr Leu Glu Glu Ile Glu Ser Leu Gly Thr Pro Thr Ala
40 45 50

ccc cgc gat ctg ggt tct cgg gaa gtc gac gca tgc gta tcg ttg ctc 307
Pro Arg Asp Leu Gly Ser Arg Glu Val Asp Ala Cys Val Ser Leu Leu
55 60 65

cgc aac cgc gag tta gtg cga ttc gat ccc cac gat ggc agt gaa tta 355
Arg Asn Arg Glu Leu Val Arg Phe Asp Pro His Asp Gly Ser Glu Leu
70 75 80 85

acc tat cgg gaa cat agc gtt gct tac ggt gcg agt ggc aag cca ttg 403
Thr Tyr Arg Glu His Ser Val Ala Tyr Gly Ala Ser Gly Lys Pro Leu
90 95 100

ttt ccc cga ttg gat cca gcg gtg atc ggc att gtg gag ctg cga ggt 451
Phe Pro Arg Leu Asp Pro Ala Val Ile Gly Ile Val Glu Leu Arg Gly
105 110 115

gag gat cgt ttg ctt ctg ggc atg aat gcg cag aaa cgc cca cgc tat 499
Glu Asp Arg Leu Leu Leu Gly Met Asn Ala Gln Lys Arg Gln Arg Tyr
120 125 130

tca tta atc gca ggt tat gtt tcg cat ggt gag tcg ctg gaa gac gca 547
Ser Leu Ile Ala Gly Tyr Val Ser His Gly Glu Ser Leu Glu Asp Ala
135 140 145

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Phe Thr Arg Glu Val Phe Glu Glu Ala Ala Arg Val Ser Glu Ile
150 155 160 165

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Ser Tyr Val Ser Ser Gln Pro Trp Pro Ile Ser Gly Ser Leu Met Leu
170 175 180

ggt atg aag ggc ttc acg gaa gat gag ttg cct caa ggc gaa act gat 691
Gly Met Lys Gly Phe Thr Glu Asp Glu Leu Pro Gln Gly Glu Thr Asp
185 190 195

ggt gaa tta gcg gag aca atc tgg gct tcg cca gat att atc gat 739
Gly Glu Leu Ala Glu Thr Ile Trp Ala Ser Pro Leu Asp Ile Ile Asp
200 205 210

cgt aag att ccg atc gcc cca ccc gga tcg att gcc tac gac atg atc 787

Arg Lys Ile Pro Ile Ala Pro Pro Gly Ser Ile Ala Tyr Asp Met Ile
 215 220 225

aac gcc tgg gcg cga gat aaa caa aac taaggagact tttacagtg 834
 Asn Ala Trp Ala Arg Asp Lys Gln Asn
 230 235

atc 837

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 <212> FRT
 <213> Corynebacterium glutamicum

<400> 2390
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Ser Ile Val Leu Leu Ser Glu His Asp Gly Asp Ile Val Ser Val Gly
 20 25 30

Pro Asp Leu Gly Thr Val Arg Val Thr Leu Glu Glu Ile Glu Ser Leu
 35 40 45

Gly Thr Pro Thr Ala Pro Arg Asp Leu Gly Ser Arg Glu Val Asp Ala
 50 55 60

Cys Val Ser Leu Leu Arg Asn Arg Glu Leu Val Arg Phe Asp Pro His
 65 70 75 80

Asp Gly Ser Glu Leu Thr Tyr Arg Glu His Ser Val Ala Tyr Gly Ala
 85 90 95

Ser Gly Lys Pro Leu Phe Pro Arg Leu Asp Pro Ala Val Ile Gly Ile
 100 105 110

Val Glu Leu Arg Gly Glu Asp Arg Leu Leu Leu Gly Met Asn Ala Gln
 115 120 125

Lys Arg Gln Arg Tyr Ser Leu Ile Ala Gly Tyr Val Ser His Gly Glu
 130 135 140

Ser Leu Glu Asp Ala Phe Thr Arg Glu Val Phe Glu Glu Ala Ala Arg
 145 150 155 160

Arg Val Ser Glu Ile Ser Tyr Val Ser Ser Gln Pro Trp Pro Ile Ser
 165 170 175

Gly Ser Leu Met Leu Gly Met Lys Gly Phe Thr Glu Asp Glu Leu Pro
 180 185 190

Gln Gly Glu Thr Asp Gly Glu Leu Ala Glu Thr Ile Trp Ala Ser Pro
 195 200 205

Leu Asp Ile Ile Asp Arg Lys Ile Pro Ile Ala Pro Pro Gly Ser Ile
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<222> (101)..(898)
<223> RXA01741
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Leu Ala Asn Ser Ala Gln Val Leu Ile Arg Pro Asp Ser Ala Ile Gln
10 15 20

ttc ggc atc gac gcc acc cgc gct ggc gtc tta aat atc gat cca tgc 211
Phe Gly Ile Asp Ala Thr Arg Ala Gly Val Leu Asn Ile Asp Pro Ser
25 30 35

ctg tcg tcg cga gtc gtc ccg gtg ctg cgg aat ctg cgg acc gcc cga 259
Leu Ser Ser Arg Val Val Pro Val Leu Arg Asn Leu Arg Thr Ala Arg
40 45 50

ccg atc gtt gat gtc atc gcc gac ctc acg act gca ggc ctc gca ccc 307
Pro Ile Val Asp Val Ile Ala Asp Leu Thr Thr Ala Gly Leu Ala Pro
55 60 65

acc gct gcg agc agt ttg ctc gag gac ctt tta gaa ttc ggt gtg gtc 355
Thr Ala Ala Ser Ser Leu Leu Glu Asp Leu Leu Glu Phe Gly Val Val
70 75 80 85

cgc gaa tgc gcg gcg gcg cag gtg ttg ctg ttc ggg gac ggt tgc ctt 403
Arg Glu Ser Ala Ala Ala Gln Val Leu Leu Phe Gly Asp Gly Ser Leu
90 95 100

gtc gac gtc acc tcc ttc ctt ttg gaa acc tcc ggc ttt gtt ccc aga 451
Val Asp Val Thr Ser Phe Leu Leu Glu Thr Ser Gly Phe Val Pro Arg
105 110 115

ccc cag atc atc gat gag tgc cct cga gag ttt ttc gag ctt ccc tcc 499
Pro Gln Ile Ile Asp Glu Ser Pro Arg Glu Phe Phe Glu Leu Pro Ser
120 125 130

agc cac att ttg gtt ctc aac aag ctc gca cat tcc caa cgt cta tcc 547
 Ser His Ile Leu Val Leu Asn Lys Leu Ala His Ser Gln Arg Leu Ser
 135 140 145

ccg ctg ctt cac aaa tat gcg ccg acg tat ctg tgc gcc gcg atc gtc 595
Pro Leu Leu His Lys Tyr Ala Pro Thr Tyr Leu Cys Ala Ala Ile Val
150 155 160 165

gat aat cgt ggc atc atc ggc cgg ggc cgg aga tca cga tcg ggg cgg 643
Asp Asn Arg Gly Ile Ile Gly Pro Gly Arg Arg Ser Arg Ser Gly Pro
170 175 180

tgt ttg atg tgt gtg gat ctg cat cgc tgc gat atc gat ccg cat tgg 691
 Cys Leu Met Cys Val Asp Leu His Arg Cys Asp Ile Asp Pro His Trp
 185 190 195

ctc tct att atc aat cag caa ccc aac ggt ccc acc ttt cct gat ccc 739
 Leu Ser Ile Ile Asn Gln Gln Pro Asn Gly Pro Thr Phe Pro Asp Pro
 200 205 210

gtc acg gag atg gcg acg gct gcc cga ctc gtc gcc tgg gtc act gcc 787
 Val Thr Glu Met Ala Thr Ala Ala Arg Leu Val Ala Trp Val Thr Ala
 215 220 225

gat aca tgg ttg ccc ggc gtt gtg gag gaa gta aac ccc cac gat cga 835
 Asp Thr Trp Leu Pro Gly Val Val Glu Glu Val Asn Pro His Asp Arg
 230 235 240 245

aca aac tcg gta cgc acc ctc cct gtg cat cca aaa tgt ccg atg tgt 883
 Thr Asn Ser Val Arg Thr Leu Pro Val Pro Lys Cys Pro Met Cys
 250 255 260

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 Trp Ser Leu Gly Ser
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<210> 2392
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 <212> PRT
 <213> Corynebacterium glutamicum

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Asp Ser Ala Ile Gln Phe Gly Ile Asp Ala Thr Arg Ala Gly Val Leu
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Asn Ile Asp Pro Ser Leu Ser Ser Arg Val Val Pro Val Leu Arg Asn
 35 40 45

Leu Arg Thr Ala Arg Pro Ile Val Asp Val Ile Ala Asp Leu Thr Thr
 50 55 60

Ala Gly Leu Ala Pro Thr Ala Ala Ser Ser Leu Leu Glu Asp Leu Leu
 65 70 75 80

Glu Phe Gly Val Val Arg Glu Ser Ala Ala Gln Val Leu Leu Phe
 85 90 95

Gly Asp Gly Ser Leu Val Asp Val Thr Ser Phe Leu Leu Glu Thr Ser
 100 105 110

Gly Phe Val Pro Arg Pro Gln Ile Ile Asp Glu Ser Pro Arg Glu Phe
 115 120 125

Phe Glu Leu Pro Ser Ser His Ile Leu Val Leu Asn Lys Leu Ala His
 130 135 140

Ser Gln Arg Leu Ser Pro Leu Leu His Lys Tyr Ala Pro Thr Tyr Leu
 145 150 155 160

Cys Ala Ala Ile Val Asp Asn Arg Gly Ile Ile Gly Pro Gly Arg Arg
 165 170 175
 Ser Arg Ser Gly Pro Cys Leu Met Cys Val Asp Leu His Arg Cys Asp
 180 185 190
 Ile Asp Pro His Trp Leu Ser Ile Ile Asn Gln Gln Pro Asn Gly Pro
 195 200 205
 Thr Phe Pro Asp Pro Val Thr Glu Met Ala Thr Ala Ala Arg Leu Val
 210 215 220
 Ala Trp Val Thr Ala Asp Thr Trp Leu Pro Gly Val Val Glu Glu Val
 225 230 235 240
 Asn Pro His Asp Arg Thr Asn Ser Val Arg Thr Leu Pro Val His Pro
 245 250 255
 Lys Cys Pro Met Cys Trp Ser Leu Gly Ser
 260 265

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 <211> 903
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(880)
 <223> RXA01748

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 Met Ala Asp Ala Lys
 1 5
 aag cag gcg gat aaa gcc gcc aag aag cag gta aga gca gcc aag aag 163
 Lys Gln Ala Asp Lys Ala Ala Lys Lys Gln Val Arg Ala Ala Lys Lys
 10 15 20
 gca cag cgc aag gag act cgc tca caa atg tgg cag gtc ttc aac atg 211
 Ala Gln Arg Lys Glu Thr Arg Ser Gln Met Trp Gln Val Phe Asn Met
 25 30 35
 caa cgc aag cag gat aag got ott att ccg ott ctg ttg ctc gct att 259
 Gln Arg Lys Gln Asp Lys Ala Leu Ile Pro Leu Leu Leu Leu Ala Ile
 40 45 50
 ott ggt atc ccg ctg gtc ott ttc ctc atc ggt ttg att tgg ggt ggt 307
 Leu Gly Ile Pro Leu Val Leu Phe Leu Ile Gly Leu Ile Trp Gly Gly
 55 60 65
 cag tgg tgg atg ott ccg atc ggc att gct gca ggt gtt gta gct gca 355
 Gln Trp Trp Met Leu Pro Ile Gly Ile Ala Ala Gly Val Val Ala Ala
 70 75 80 85
 atg ttt att ttc acc cgt cgc gtt gag cgt gac gtg tac aag cgc gcc 403

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Met Phe Ile Phe Thr Arg Arg Val Glu Arg Asp Val Tyr Lys Arg Ala
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gaa ggt cag cag ggt gct gct ggt tgg gct gtg gag aac ctc cgc tct 451
Glu Gly Gln Gln Gly Ala Ala Gly Trp Ala Val Glu Asn Leu Arg Ser
      105      110      115

ggc gtg ggc atg acc tgg cgc acc aag acc gct gtt gca gtg acc act 499
Gly Val Gly Met Thr Trp Arg Thr Lys Thr Ala Val Ala Val Thr Thr
      120      125      130

cag atg gat gca gtg cac cgc gtc att ggt ctg tgt ggt gtt gtg ctg 547
Gln Met Asp Ala Val His Arg Val Ile Gly Leu Cys Gly Val Val Leu
      135      140      145

gtc ggc gag ggc tcc cct cac cgc ctg aag cca atg ctt gcg cag caa 595
Val Gly Glu Gly Ser Pro His Arg Leu Lys Pro Met Leu Ala Gln Gln
      150      155      160      165

aag aag cgc ctg aac cgc gtg gca cct ggt gtt cca gtg tat gaa atc 643
Lys Lys Arg Leu Asn Arg Val Ala Pro Gly Val Pro Val Tyr Glu Ile
      170      175      180

atc acg ggc aac ggc gaa ggc cag acc cct atc gcg aag ctg cag cgt 691
Ile Thr Gly Asn Gly Glu Gly Gln Thr Pro Ile Ala Lys Leu Gln Arg
      185      190      195

gaa ctg gtc aag ctg cct cgc aac tac aag aag aac gac gtc gct gcc 739
Glu Leu Val Lys Leu Pro Arg Asn Tyr Lys Lys Asn Asp Val Ala Ala
      200      205      210

ctg gcc gct cgc att gag gct atg gac aat gtc gga aac gct cct gcc 787
Leu Ala Ala Arg Ile Glu Ala Met Asp Asn Val Gly Asn Ala Pro Gly
      215      220      225

gga tct ttg cct aag ggt cca ttg cca aag ggc gca agc atg tcc ggt 835
Gly Ser Leu Pro Lys Gly Pro Leu Pro Lys Gly Ala Ser Met Ser Gly
      230      235      240      245

atg aac cgc cgc gct cgc cga cag gct gaa cgc aag ggc gag gct 880
Met Asn Arg Arg Ala Arg Arg Gln Ala Glu Arg Lys Gly Glu Ala
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taaagccttt tcgctttgcg ctc 903

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<211> 260

<212> PRT

<213> Corynebacterium glutamicum

<400> 2394

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Arg Ala Ala Lys Lys Ala Gln Arg Lys Glu Thr Arg Ser Gln Met Trp
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Gln Val Phe Asn Met Gln Arg Lys Gln Asp Lys Ala Leu Ile Pro Leu
      35              40              45

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Leu Leu Leu Ala Ile Leu Gly Ile Pro Leu Val Leu Phe Leu Ile Gly
 50 55 60
 Leu Ile Trp Gly Gly Gln Trp Trp Met Leu Pro Ile Gly Ile Ala Ala
 65 70 75 80
 Gly Val Val Ala Ala Met Phe Ile Phe Thr Arg Arg Val Glu Arg Asp
 85 90 95
 Val Tyr Lys Arg Ala Glu Gly Gln Gln Gly Ala Ala Gly Trp Ala Val
 100 105 110
 Glu Asn Leu Arg Ser Gly Val Gly Met Thr Trp Arg Thr Lys Thr Ala
 115 120 125
 Val Ala Val Thr Thr Gln Met Asp Ala Val His Arg Val Ile Gly Leu
 130 135 140
 Cys Gly Val Val Leu Val Gly Glu Gly Ser Pro His Arg Leu Lys Pro
 145 150 155 160
 Met Leu Ala Gln Gln Lys Lys Arg Leu Asn Arg Val Ala Pro Gly Val
 165 170 175
 Pro Val Tyr Glu Ile Ile Thr Gly Asn Gly Glu Gly Gln Thr Pro Ile
 180 185 190
 Ala Lys Leu Gln Arg Glu Leu Val Lys Leu Pro Arg Asn Tyr Lys Lys
 195 200 205
 Asn Asp Val Ala Ala Leu Ala Ala Arg Ile Glu Ala Met Asp Asn Val
 210 215 220
 Gly Asn Ala Pro Gly Gly Ser Leu Pro Lys Gly Pro Leu Pro Lys Gly
 225 230 235 240
 Ala Ser Met Ser Gly Met Asn Arg Arg Ala Arg Arg Gln Ala Glu Arg
 245 250 255
 Lys Gly Glu Ala
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1717)
 <223> RXA01749

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 Val Ser Phe Leu Val
 1 5
 gaa aat caa tta ctc gcg ttg gtt gtc atc atg acg gtc gga cta ttg 163

Glu	Asn	Gln	Leu	Leu	Ala	Leu	Val	Val	Ile	Met	Thr	Val	Gly	Leu	Leu		
				10					15					20			
ctc	ggc	cgc	atc	aaa	att	ttc	ggg	ttc	cgt	ctc	ggc	gtc	gcc	gct	gta	211	
Leu	Gly	Arg	Ile	Lys	Ile	Phe	Gly	Phe	Arg	Leu	Gly	Val	Ala	Ala	Val		
			25					30					35				
ctg	ttt	gta	ggg	cta	gcg	cta	ttc	acc	att	gag	ccg	gat	att	tcc	gtc	259	
Leu	Phe	Val	Gly	Leu	Ala	Leu	Ser	Thr	Ile	Glu	Pro	Asp	Ile	Ser	Val		
			40					45				50					
cca	tcc	ctc	att	tac	gtg	gtt	gga	ctg	tcg	ctt	ttt	gtc	tac	acg	atc	307	
Pro	Ser	Leu	Ile	Tyr	Val	Val	Gly	Leu	Ser	Leu	Phe	Val	Tyr	Thr	Ile		
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Gly	Leu	Glu	Ala	Gly	Pro	Gly	Phe	Phe	Thr	Ser	Met	Lys	Thr	Thr	Gly		
			70			75				80					85		
ctg	cgc	aac	aac	gca	ctg	acc	ttg	ggc	gcc	atc	atc	gcc	acc	acg	gca	403	
Leu	Arg	Asn	Asn	Ala	Leu	Thr	Leu	Gly	Ala	Ile	Ile	Ala	Thr	Thr	Ala		
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ctc	gca	tgg	gca	ctc	atc	aca	gtt	ttg	aac	atc	gat	gcc	gcc	tcc	ggc	451	
Leu	Ala	Trp	Ala	Leu	Ile	Thr	Val	Leu	Asn	Ile	Asp	Ala	Ala	Ser	Gly		
				105				110					115				
gcc	ggc	atg	ctc	acc	ggc	gcg	ctc	acc	aac	acc	cca	gcc	atg	gcc	gca	499	
Ala	Gly	Met	Leu	Thr	Gly	Ala	Leu	Thr	Asn	Thr	Pro	Ala	Met	Ala	Ala		
				120			125					130					
gtt	gtt	gac	gca	ctt	cct	tcg	ctt	atc	gac	gac	acc	ggc	cag	ctt	cac	547	
Val	Val	Asp	Ala	Leu	Pro	Ser	Leu	Ile	Asp	Asp	Thr	Gly	Gln	Leu	His		
				135			140					145					
ctc	atc	gcc	gag	ctg	ccc	gtc	gtc	gca	tat	tcc	ttg	gca	tac	ccc	ctc	595	
Leu	Ile	Ala	Glu	Leu	Pro	Val	Val	Ala	Tyr	Ser	Leu	Ala	Tyr	Pro	Leu		
					150		155			160				165			
ggg	gtg	ctc	atc	gtt	att	ctc	tcc	atc	gcc	atc	ttc	agc	tct	gtg	ttc	643	
Gly	Val	Leu	Ile	Val	Ile	Leu	Ser	Ile	Ala	Ile	Phe	Ser	Ser	Val	Phe		
				170					175					180			
aaa	gtc	gac	cac	aac	aaa	gaa	gcc	gaa	gaa	gcg	ggc	gtt	gcg	gtc	cag	691	
Lys	Val	Asp	His	Asn	Lys	Glu	Ala	Glu	Glu	Ala	Gly	Val	Ala	Val	Gln		
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gaa	ctc	aaa	ggc	cgt	cgc	atc	cgc	gtc	acc	gtc	gct	gat	ctt	cca	gcc	739	
Glu	Leu	Lys	Gly	Arg	Arg	Ile	Arg	Val	Thr	Val	Ala	Asp	Leu	Pro	Ala		
				200			205					210					
ctg	gag	aac	atc	cca	gag	ctg	ctc	aac	ctc	cac	gtc	att	gtg	tcc	cga	787	
Leu	Glu	Asn	Ile	Pro	Glu	Leu	Leu	Asn	Leu	His	Val	Ile	Val	Ser	Arg		
				215		220					225						
gtg	gaa	cga	gac	ggg	gag	caa	ttc	atc	ccg	ctt	tat	ggc	gaa	cac	gca	835	
Val	Glu	Arg	Asp	Gly	Glu	Gln	Phe	Ile	Pro	Leu	Tyr	Gly	Glu	His	Ala		
					230	235				240				245			
cgc	atc	ggc	gat	gtc	tta	aca	gtg	gtg	ggg	gcc	gat	gaa	gaa	ctc	aac	883	
Arg	Ile	Gly	Asp	Val	Leu	Thr	Val	Val	Gly	Ala	Asp	Glu	Glu	Leu	Asn		

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	aat gtg gaa ctt gat tac cga cgc atc ttc gtc tca aac aca gca gtc Asn Val Glu Leu Asp Tyr Arg Arg Ile Phe Val Ser Asn Thr Ala Val 280 285 290			979
	gtg ggc act ccc cta tcc aag ctc cag cca ctg ttt aaa gac atg ctg Val Gly Thr Pro Leu Ser Lys Leu Gln Pro Leu Phe Lys Asp Met Leu 295 300 305			1027
	atc acc cgc atc agg cgc ggc gac aca gat ttg gtg gcc tcc tcc gac Ile Thr Arg Ile Arg Arg Gly Asp Thr Asp Leu Val Ala Ser Ser Asp 310 315 320 325			1075
	atg act ttg cag ctc ggt gac cgt gtc cgc gtt gtc gca cca gca gaa Met Thr Leu Gln Leu Gly Asp Arg Val Arg Val Val Ala Pro Ala Glu 330 335 340			1123
	aaa ctc cgc gaa gca acc caa ttg ctc ggc gat tcc tac aag aaa ctc Lys Leu Arg Glu Ala Thr Gln Leu Leu Gly Asp Ser Tyr Lys Lys Leu 345 350 355			1171
	tcc gat ttc aac ctg ctc cca ctc gct gcc ggc ctc atg atc ggt gtg Ser Asp Phe Asn Leu Leu Pro Leu Ala Ala Gly Leu Met Ile Gly Val 360 365 370			1219
	ctt gtc ggc atg gtg gag ttc cca cta cca ggt gga agc tcc ctg aaa Leu Val Gly Met Val Glu Phe Pro Leu Pro Gly Gly Ser Ser Leu Lys 375 380 385			1267
	ctg ggt aac gca ggt gga ccg cta gtt gtt gcg ctg ctg ctc ggc atg Leu Gly Asn Ala Gly Gly Pro Leu Val Val Ala Leu Leu Leu Gly Met 390 395 400 405			1315
	atc aat cgc aca ggc aag ttc gtc tgg caa atc ccc tac gga gca aac Ile Asn Arg Thr Gly Lys Phe Val Trp Gln Ile Pro Tyr Gly Ala Asn 410 415 420			1363
	ctt gcc ctt cgc caa ctg ggc atc aca cta ttt ttg gct gcc atc ggt Leu Ala Leu Arg Gln Leu Gly Ile Thr Leu Phe Leu Ala Ile Gly 425 430 435			1411
	acc tca gcg ggc gca gga ttt cga tca gcg atc agc gac ccc caa tca Thr Ser Ala Gly Ala Gly Phe Arg Ser Ala Ile Ser Asp Pro Gln Ser 440 445 450			1459
	ctc acc atc atc ggc ttc ggt gcg ctg ctc act ttg ttc atc tcc atc Leu Thr Ile Ile Gly Phe Gly Ala Leu Leu Thr Leu Phe Ile Ser Ile 455 460 465			1507
	acg gtg ctg ttc gtt ggc cac aaa ctg atg aaa atc ccc ttc ggt gaa Thr Val Leu Phe Val Gly His Lys Leu Met Lys Ile Pro Phe Gly Glu 470 475 480 485			1555
	acc gct ggc atc ctc gcc ggt acg caa acc cac cct gct gtg ctg agt Thr Ala Gly Ile Leu Ala Gly Thr Gln Thr His Pro Ala Val Leu Ser 490 495 500			1603

tat gtg tca gat gcc tcc cgc aac gag ctc cct gcc atg ggt tat acc 1651
 Tyr Val Ser Asp Ala Ser Arg Asn Glu Leu Pro Ala Met Gly Tyr Thr
 505 510 515

tct gtg tat ccg ctg gcg atg atc gca aag atc ctg gcc gcc caa acg 1699
 Ser Val Tyr Pro Leu Ala Met Ile Ala Lys Ile Leu Ala Ala Gln Thr
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ttg ttg ttc cta ctt atc tagcattgac cccttaagcg cag 1740
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<210> 2396

<211> 539

<212> PRT

<213> Corynebacterium glutamicum

<400> 2396

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Gly Val Ala Ala Val Leu Phe Val Gly Leu Ala Leu Ser Thr Ile Glu
 35 40 45

Pro Asp Ile Ser Val Pro Ser Leu Ile Tyr Val Val Gly Leu Ser Leu
 50 55 60

Phe Val Tyr Thr Ile Gly Leu Glu Ala Gly Pro Gly Phe Phe Thr Ser
 65 70 75 80

Met Lys Thr Thr Gly Leu Arg Asn Asn Ala Leu Thr Leu Gly Ala Ile
 85 90 95

Ile Ala Thr Thr Ala Leu Ala Trp Ala Leu Ile Thr Val Leu Asn Ile
 100 105 110

Asp Ala Ala Ser Gly Ala Gly Met Leu Thr Gly Ala Leu Thr Asn Thr
 115 120 125

Pro Ala Met Ala Ala Val Val Asp Ala Leu Pro Ser Leu Ile Asp Asp
 130 135 140

Thr Gly Gln Leu His Leu Ile Ala Glu Leu Pro Val Val Ala Tyr Ser
 145 150 155 160

Leu Ala Tyr Pro Leu Gly Val Leu Ile Val Ile Leu Ser Ile Ala Ile
 165 170 175

Phe Ser Ser Val Phe Lys Val Asp His Asn Lys Glu Ala Glu Glu Ala
 180 185 190

Gly Val Ala Val Gln Glu Leu Lys Gly Arg Arg Ile Arg Val Thr Val
 195 200 205

Ala Asp Leu Pro Ala Leu Glu Asn Ile Pro Glu Leu Leu Asn Leu His
 210 215 220

Val Ile Val Ser Arg Val Glu Arg Asp Gly Glu Gln Phe Ile Pro Leu
 225 230 235 240
 Tyr Gly Glu His Ala Arg Ile Gly Asp Val Leu Thr Val Val Gly Ala
 245 250 255
 Asp Glu Glu Leu Asn Arg Ala Glu Lys Ala Ile Gly Glu Leu Ile Asp
 260 265 270
 Gly Asp Pro Tyr Ser Asn Val Glu Leu Asp Tyr Arg Arg Ile Phe Val
 275 280 285
 Ser Asn Thr Ala Val Val Gly Thr Pro Leu Ser Lys Leu Gln Pro Leu
 290 295 300
 Phe Lys Asp Met Leu Ile Thr Arg Ile Arg Arg Gly Asp Thr Asp Leu
 305 310 315 320
 Val Ala Ser Ser Asp Met Thr Leu Gln Leu Gly Asp Arg Val Arg Val
 325 330 335
 Val Ala Pro Ala Glu Lys Leu Arg Glu Ala Thr Gln Leu Leu Gly Asp
 340 345 350
 Ser Tyr Lys Lys Leu Ser Asp Phe Asn Leu Leu Pro Leu Ala Ala Gly
 355 360 365
 Leu Met Ile Gly Val Leu Val Gly Met Val Glu Phe Pro Leu Pro Gly
 370 375 380
 Gly Ser Ser Leu Lys Leu Gly Asn Ala Gly Gly Pro Leu Val Val Ala
 385 390 395 400
 Leu Leu Leu Gly Met Ile Asn Arg Thr Gly Lys Phe Val Trp Gln Ile
 405 410 415
 Pro Tyr Gly Ala Asn Leu Ala Leu Arg Gln Leu Gly Ile Thr Leu Phe
 420 425 430
 Leu Ala Ala Ile Gly Thr Ser Ala Gly Ala Gly Phe Arg Ser Ala Ile
 435 440 445
 Ser Asp Pro Gln Ser Leu Thr Ile Ile Gly Phe Gly Ala Leu Leu Thr
 450 455 460
 Leu Phe Ile Ser Ile Thr Val Leu Phe Val Gly His Lys Leu Met Lys
 465 470 475 480
 Ile Pro Phe Gly Glu Thr Ala Gly Ile Leu Ala Gly Thr Gln Thr His
 485 490 495
 Pro Ala Val Leu Ser Tyr Val Ser Asp Ala Ser Arg Asn Glu Leu Pro
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 Ala Met Gly Tyr Thr Ser Val Tyr Pro Leu Ala Met Ile Ala Lys Ile
 515 520 525
 Leu Ala Ala Gln Thr Leu Leu Phe Leu Leu Ile
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 <213> Corynebacterium glutamicum

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 <222> (101)..(1741)
 <223> RXA01750

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 Met Cys Ile Asn Asp
 1 5

cct aaa ggc gag ttg ctg aag aaa aat tat gtt cgg atg tct aag cgc 163
 Pro Lys Gly Glu Leu Lys Lys Asn Tyr Val Arg Met Ser Lys Arg
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ggt ttt cag gtt gtt cag ttt aac ctg att aac aac ctg aaa act gat 211
 Gly Phe Gln Val Val Gln Phe Asn Leu Ile Asn Asn Leu Lys Thr Asp
 25 30 35

att tat aac ccg ttg gga tta gca gcc gaa gca gct cgc gaa ggt aac 259
 Ile Tyr Asn Pro Leu Gly Leu Ala Ala Glu Ala Ala Arg Glu Gly Asn
 40 45 50

ggg atg aag tgc gca acc tat gtg gaa aat atc gca gag gtg ttc ttt 307
 Gly Met Lys Cys Ala Thr Tyr Val Glu Asn Ile Ala Glu Val Phe Phe
 55 60 65

ccg gtg gac ggt gcc gat gat ccg gta tgg ccg aat cgc gcc aac aat 355
 Pro Val Asp Gly Ala Asp Asp Pro Val Trp Pro Asn Ala Ala Asn Asn
 70 75 80 85

gcc ttc aag cgt gca gcc tat ggt ctt atc gac ttc tat ttg gaa gag 403
 Ala Phe Lys Arg Ala Ala Tyr Gly Leu Ile Asp Phe Tyr Leu Glu Glu
 90 95 100

gag cgc gag atg cgc aag cag gct gca gct gag aat tgg gat gcc aag 451
 Glu Arg Glu Met Arg Lys Gln Ala Ala Glu Asn Trp Asp Ala Lys
 105 110 115

gtg ctt gat aca cgt att gat cag atg tgg ggt aag gtc acg ctc tac 499
 Val Leu Asp Thr Arg Ile Asp Gln Met Trp Gly Lys Val Thr Leu Tyr
 120 125 130

aac tgc tac cag ctc ttt gtg cag ctt tcg gca aag aag ctg aag aat 547
 Asn Cys Tyr Gln Leu Phe Val Gln Leu Ser Ala Lys Lys Leu Lys Asn
 135 140 145

ccc gtt gag cga ctc aat gaa cgt gca cgt gcc ggt gaa ttc ggt aac 595
 Pro Val Glu Arg Leu Asn Glu Arg Ala Arg Ala Gly Glu Phe Gly Asn
 150 155 160 165

tta gag act gat gaa aat gca gcc atg atg ttc cag gat gct gtg aca 643
 Leu Glu Thr Asp Glu Asn Ala Ala Met Met Phe Gln Asp Ala Val Thr
 170 175 180

gag gcc gaa gag aac gaa atg ttt ctg tgg gag ggt gag aaa gaa aaa	691
Glu Ala Glu Glu Asn Glu Met Phe Leu Trp Glu Gly Glu Lys Glu Lys	
185 190 195	
gac atg ctc acc ttg ttc ttt agt gcc aca gac ggt ctg cca aag tcc	739
Asp Met Leu Thr Leu Phe Phe Ser Ala Thr Asp Gly Leu Pro Lys Ser	
200 205 210	
agt gtt cgt act ctg gtg ggc aac gca gat aag gcc ctg aaa gca atg	787
Ser Val Arg Thr Leu Val Gly Asn Ala Asp Lys Ala Leu Lys Ala Met	
215 220 225	
ggt ggc gct gaa aaa atg atg gcg tcg gtc tac ggt atc gcg att aca	835
Gly Gly Ala Glu Lys Met Met Ala Ser Val Tyr Tyr Gly Ile Ala Ile Thr	
230 235 240 245	
gcg atg tcc ttc ttt aca gac ccc aca att tca acg tta acc tca ggc	883
Ala Met Ser Phe Phe Thr Asp Pro Thr Ile Ser Thr Leu Thr Ser Gly	
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aca cta agt cag aac gtt gac ttg gcc gga ttg tcg ttt cca cgg cgc	931
Thr Leu Ser Gln Asn Val Asp Leu Ala Gly Leu Ser Phe Pro Arg Arg	
265 270 275	
atg ggt gtt cgt ttt gcg gcc ccc tat gtg aag cgc tac aac ctg gtt	979
Met Gly Val Arg Phe Ala Ala Pro Tyr Val Lys Arg Tyr Asn Leu Val	
280 285 290	
gga tca cag gtg aaa tgg gat gcg tat agt gac gcc aag ttc acc aag	1027
Gly Ser Gln Val Lys Trp Asp Ala Tyr Ser Asp Ala Lys Phe Thr Lys	
295 300 305	
ccg ttg ggt aag aat ttt gtt cat gat gac acg ctg tcg gtt gag ggt	1075
Pro Leu Gly Lys Asn Phe Val His Asp Asp Thr Leu Ser Val Glu Gly	
310 315 320 325	
tgg gcg cgg ttc tat att aaa gac tcg ttc ccg agt aat act gcg tac	1123
Trp Ala Arg Phe Tyr Ile Lys Asp Ser Phe Pro Ser Asn Thr Ala Tyr	
330 335 340	
ctg cgt ttg cgg att ctc aat ggt act tct ggc acg ttg atc aag act	1171
Leu Arg Leu Arg Ile Leu Asn Gly Thr Ser Gly Thr Leu Ile Lys Thr	
345 350 355	
ctg tac ttc aag ttc acc aag ggc tac caa acg aac ctt aaa ggc cgt	1219
Leu Tyr Phe Lys Phe Thr Lys Gly Tyr Gln Thr Asn Leu Lys Gly Arg	
360 365 370	
gcg ttt att act gat ccg gtg acc gat gag aag atc att aag aat ggt	1267
Ala Phe Ile Thr Asp Pro Val Thr Asp Glu Lys Ile Ile Lys Asn Gly	
375 380 385	
ctg ctg atc gag ctg gtg aaa aac gat gct ggt gac ttt gtt cca ggt	1315
Leu Leu Ile Glu Leu Val Lys Asn Asp Ala Gly Asp Phe Val Pro Gly	
390 395 400 405	
cat gtg cag ttt aag acg aag aaa ctg aat ctt gac caa ctc acg cag	1363
His Val Gln Phe Lys Thr Lys Lys Leu Asn Leu Asp Gln Leu Thr Gln	
410 415 420	

gaa cag atc aat atg ccg ggt cat gac atg atc aag cag gtt gat gcg 1411
 Glu Gln Ile Asn Met Pro Gly His Asp Met Ile Lys Gln Val Asp Ala
 425 430 435

atg gtt gat gcg gtg tcg gct ctg aat gtg cgg tat tcg gag aag cct 1459
 Met Val Asp Ala Val Ser Ala Leu Asn Val Arg Tyr Ser Glu Lys Pro
 440 445 450

aag gca gtg ttc ttc gta acg cct ccg cat ctt atg aaa tat gcg aag 1507
 Lys Ala Val Phe Phe Val Thr Pro Pro His Leu Met Lys Tyr Ala Lys
 455 460 465

ttg att ttg att ctc atc aaa cag ctt gtg gat ctg aac ttc gat tcc 1555
 Leu Ile Leu Ile Leu Ile Lys Gln Leu Val Asp Leu Asn Phe Asp Ser
 470 475 480 485

tcg tat atg acg cgt gag aat cag aag ccg gat tat aag act cgt ttc 1603
 Ser Tyr Met Thr Arg Glu Asn Gln Lys Pro Asp Tyr Lys Thr Arg Phe
 490 495 500

atg ttg gac gag ttg gga aac ctt cag agt gag ggt cat ggt att gcg 1651
 Met Leu Asp Glu Leu Gly Asn Leu Gln Ser Glu Gly His Gly Ile Ala
 505 510 515

gga ttt gaa acc atg ctc tcg atc ggt ctg gga caa gaa caa caa ttt 1699
 Gly Phe Glu Thr Met Leu Ser Ile Gly Leu Gly Gln Glu Gln Phe
 520 525 530

agt gcg acc agt tgc gta gcg aaa aac tac gct ctt gca gct 1741
 Ser Ala Thr Ser Cys Val Ala Lys Asn Tyr Ala Leu Ala Ala
 535 540 545

taaagttgca agaaactgtt tca 1764

<210> 2398

<211> 547

<212> FRT

<213> *Corynebacterium glutamicum*

<400> 2398

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Asn Leu Lys Thr Asp Ile Tyr Asn Pro Leu Gly Leu Ala Ala Glu Ala
 35 40 45

Ala Arg Glu Gly Asn Gly Met Lys Cys Ala Thr Tyr Val Glu Asn Ile
 50 55 60

Ala Glu Val Phe Phe Pro Val Asp Gly Ala Asp Asp Pro Val Trp Pro
 65 70 75 80

Asn Ala Ala Asn Asn Ala Phe Lys Arg Ala Ala Tyr Gly Leu Ile Asp
 85 90 95

Phe Tyr Leu Glu Glu Glu Arg Glu Met Arg Lys Gln Ala Ala Ala Glu
 100 105 110

Asn Trp Asp Ala Lys Val Leu Asp Thr Arg Ile Asp Gln Met Trp Gly
 115 120 125
 Lys Val Thr Leu Tyr Asn Cys Tyr Gln Leu Phe Val Gln Leu Ser Ala
 130 135 140
 Lys Lys Leu Lys Asn Pro Val Glu Arg Leu Asn Glu Arg Ala Arg Ala
 145 150 155 160
 Gly Glu Phe Gly Asn Leu Glu Thr Asp Glu Asn Ala Ala Met Met Phe
 165 170 175
 Gln Asp Ala Val Thr Glu Ala Glu Glu Asn Glu Met Phe Leu Trp Glu
 180 185 190
 Gly Glu Lys Glu Lys Asp Met Leu Thr Leu Phe Phe Ser Ala Thr Asp
 195 200 205
 Gly Leu Pro Lys Ser Ser Val Arg Thr Leu Val Gly Asn Ala Asp Lys
 210 215 220
 Ala Leu Lys Ala Met Gly Gly Ala Glu Lys Met Met Ala Ser Val Tyr
 225 230 235 240
 Gly Ile Ala Ile Thr Ala Met Ser Phe Phe Thr Asp Pro Thr Ile Ser
 245 250 255
 Thr Leu Thr Ser Gly Thr Leu Ser Gln Asn Val Asp Leu Ala Gly Leu
 260 265 270
 Ser Phe Pro Arg Arg Met Gly Val Arg Phe Ala Ala Pro Tyr Val Lys
 275 280 285
 Arg Tyr Asn Leu Val Gly Ser Gln Val Lys Trp Asp Ala Tyr Ser Asp
 290 295 300
 Ala Lys Phe Thr Lys Pro Leu Gly Lys Asn Phe Val His Asp Asp Thr
 305 310 315 320
 Leu Ser Val Glu Gly Trp Ala Arg Phe Tyr Ile Lys Asp Ser Phe Pro
 325 330 335
 Ser Asn Thr Ala Tyr Leu Arg Leu Arg Ile Leu Asn Gly Thr Ser Gly
 340 345 350
 Thr Leu Ile Lys Thr Leu Tyr Phe Lys Phe Thr Lys Gly Tyr Gln Thr
 355 360 365
 Asn Leu Lys Gly Arg Ala Phe Ile Thr Asp Pro Val Thr Asp Glu Lys
 370 375 380
 Ile Ile Lys Asn Gly Leu Leu Ile Glu Leu Val Lys Asn Asp Ala Gly
 385 390 395 400
 Asp Phe Val Pro Gly His Val Gln Phe Lys Thr Lys Lys Leu Asn Leu
 405 410 415
 Asp Gln Leu Thr Gln Glu Gln Ile Asn Met Pro Gly His Asp Met Ile
 420 425 430

Lys Gln Val Asp Ala Met Val Asp Ala Val Ser Ala Leu Asn Val Arg
 435 440 445
 Tyr Ser Glu Lys Pro Lys Ala Val Phe Phe Val Thr Pro Pro His Leu
 450 455 460
 Met Lys Tyr Ala Lys Leu Ile Leu Ile Leu Ile Lys Gln Leu Val Asp
 465 470 475 480
 Leu Asn Phe Asp Ser Ser Tyr Met Thr Arg Glu Asn Gln Lys Pro Asp
 485 490 495
 Tyr Lys Thr Arg Phe Met Leu Asp Glu Leu Gly Asn Leu Gln Ser Glu
 500 505 510
 Gly His Gly Ile Ala Gly Phe Glu Thr Met Leu Ser Ile Gly Leu Gly
 515 520 525
 Gln Glu Gln Gln Phe Ser Ala Thr Ser Cys Val Ala Lys Asn Tyr Ala
 530 535 540

Leu Ala Ala
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<210> 2399

<211> 652

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(652)

<223> RXA01752

<400> 2399

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ttggccgtca gatcgtggca gaacaacagg tggggagggtc atg atg gaa caa gat 115
 Met Met Glu Gln Asp
 1 5

ctc agc tac cgt gaa att ctt ccc ctc aac gcg agt gag gag aag aaa 163
 Leu Ser Tyr Arg Glu Ile Leu Pro Leu Asn Ala Ser Glu Glu Lys Lys
 10 15 20

aag gct gca ctg att gat gcc att gaa ggg tta agg gtg cgc gat ccg 211
 Lys Ala Ala Leu Ile Asp Ala Ile Glu Gly Leu Arg Val Arg Asp Pro
 25 30 35

cta ctc tct gcc tcg att gca ttt act aga ggg cag aaa gtc gcc ttc 259
 Leu Leu Ser Ala Ser Ile Ala Phe Thr Arg Gly Gln Lys Val Ala Phe
 40 45 50

att gct gtg gtg gtg ggc ttt atc ttg atg ctc att ttt gct cgg caa 307
 Ile Ala Val Val Val Gly Phe Ile Leu Met Leu Ile Phe Ala Arg Gln
 55 60 65

gca gca ctt att gga ctg tca gca acg tgt acg ttc atg tac ctc att 355
 Ala Ala Leu Ile Gly Leu Ser Ala Thr Cys Thr Phe Met Tyr Leu Ile
 70 75 80 85

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aca ttg ttg gac aga ttt atc atg ttt tcc aga ggt atc cgc gcg gaa 403
Thr Leu Leu Asp Arg Phe Ile Met Phe Ser Arg Gly Ile Arg Ala Glu
          90                      95          100

tcc atc atc cag gta tcg gat gaa gat gcg ctg gct ttc cct gag gac 451
Ser Ile Ile Gln Val Ser Asp Glu Asp Ala Leu Ala Phe Pro Glu Asp
          105                      110          115

aag ctg aaa acc tac acg gtg ttg gtg ccc gcc tat gcc gaa cct gag 499
Lys Leu Lys Thr Tyr Thr Val Leu Val Pro Ala Tyr Gly Glu Pro Glu
          120                      125          130

gtg att gcg cag ctg ctg gca tcc atg cac gct ttt gat tac ccc aag 547
Val Ile Ala Gln Leu Leu Ala Ser Met His Ala Phe Asp Tyr Pro Lys
          135                      140          145

cat ctt ctg cag gta ttg ctc atg ttg gag gaa gat gat ctg ccc acg 595
His Leu Leu Gln Val Leu Leu Met Leu Glu Glu Asp Asp Leu Pro Thr
          150                      155          160          165

atc gcc gcg gca gag gca gcg gga gtg gat cag gtg gca acg atc att 643
Ile Ala Ala Ala Glu Ala Ala Gly Val Asp Gln Val Ala Thr Ile Ile
          170                      175          180

aag gtg ccg 652
Lys Val Pro

<210> 2400
<211> 184
<212> PRT
<213> Corynebacterium glutamicum

<400> 2400
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Ser Glu Glu Lys Lys Lys Ala Ala Leu Ile Asp Ala Ile Glu Gly Leu
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Arg Val Arg Asp Pro Leu Leu Ser Ala Ser Ile Ala Phe Thr Arg Gly
          35          40          45

Gln Lys Val Ala Phe Ile Ala Val Val Val Gly Phe Ile Leu Met Leu
          50          55          60

Ile Phe Ala Arg Gln Ala Ala Leu Ile Gly Leu Ser Ala Thr Cys Thr
          65          70          75          80

Phe Met Tyr Leu Ile Thr Leu Leu Asp Arg Phe Ile Met Phe Ser Arg
          85          90          95

Gly Ile Arg Ala Glu Ser Ile Ile Gln Val Ser Asp Glu Asp Ala Leu
          100          105          110

Ala Phe Pro Glu Asp Lys Leu Lys Thr Tyr Thr Val Leu Val Pro Ala
          115          120          125

Tyr Gly Glu Pro Glu Val Ile Ala Gln Leu Leu Ala Ser Met His Ala

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130          135          140
Phe Asp Tyr Pro Lys His Leu Leu Gln Val Leu Met Leu Glu Glu
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Asp Asp Leu Pro Thr Ile Ala Ala Ala Glu Ala Ala Gly Val Asp Gln
165          170          175
Val Ala Thr Ile Ile Lys Val Pro
180

<210> 2401
<211> 1662
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1639)
<223> RXA01753

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Met Ser Asn Pro Ser
1 5
cta gaa cct cta gaa ccg atc gag ctt tct gac ggt act gaa att gaa 163
Leu Glu Pro Leu Glu Pro Ile Glu Leu Ser Asp Gly Thr Glu Ile Glu
10 15 20
gtt tca gac gtt gat cca gaa ccg caa gct ggc aat gcg cag atg gaa 211
Val Ser Asp Val Asp Pro Glu Pro Gln Ala Gly Asn Ala Gln Met Glu
25 30 35
gta ccc agc tta cgg aca tat gtt ttt cgc gga atc att gcc att gcc 259
Val Pro Ser Leu Arg Thr Tyr Val Phe Arg Gly Ile Ala Ile Ala
40 45 50
tgt ttg atc att ggt ttt tat gag agc ttt gtg ctg atg tgg caa aac 307
Cys Leu Ile Ile Gly Phe Tyr Glu Ser Phe Val Leu Met Trp Gln Asn
55 60 65
ctc cga atc ggc gtg gcc aac tac tca cta ctt gtg gtg ctc atg gcg 355
Leu Arg Ile Gly Val Ala Asn Tyr Ser Leu Leu Val Val Leu Met Ala
70 75 80 85
atc gtg ttg ttt atc gga ctg gac cgc aag cgt gct cgt gca ttg aac 403
Ile Val Leu Phe Ile Gly Leu Asp Arg Lys Arg Ala Arg Ala Leu Asn
90 95 100
att cac gac cgc gaa gtc gac tac atc att ggt ggc att gtc gta ctg 451
Ile His Asp Arg Glu Val Asp Tyr Ile Ile Gly Gly Ile Val Val Leu
105 110 115
ata gcc atc acg att aag agc cag ctt ctg cca cgt ttt gtg gac tgg 499
Ile Ala Ile Thr Ile Lys Ser Gln Leu Leu Pro Arg Phe Val Asp Trp
120 125 130

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gaa act ctg ctg cgc ttg gat atg ttc gca ctg tta ttc ttt gcg ttt	547
Glu Thr Leu Leu Arg Leu Asp Met Phe Ala Leu Leu Phe Phe Ala Phe	
135 140 145	
ggg att tcc ggc ctg gtg ttt ggc atg cgc tct acc ttt tct ttt gca	595
Gly Ile Ser Gly Leu Val Phe Gly Met Arg Ser Thr Phe Ser Phe Ala	
150 155 160 165	
ccc ggc tgg att ttg ctg ttt ggc tac aac gcg gtg gca cac ctg atc	643
Pro Gly Trp Ile Leu Leu Phe Gly Tyr Asn Ala Val Ala His Leu Ile	
170 175 180	
atc tcg gtg att ttc ggt ggt ggc ttt tgg ggc ccg gtg atg gca aac	691
Ile Ser Val Ile Phe Gly Gly Gly Phe Trp Gly Pro Val Met Ala Asn	
185 190 195	
atc att gga ctg tct ctt gcg gtg ttg gtg tcc tcc aac agg gac ctg	739
Ile Ile Gly Leu Ser Leu Ala Val Leu Val Ser Ser Asn Arg Asp Leu	
200 205 210	
gtt cag gcc acc tat ttg gca ctg atg acg gtg ttg ttt ggc gtc att	787
Val Gln Ala Thr Tyr Leu Ala Leu Met Thr Val Leu Phe Gly Val Ile	
215 220 225	
att gcc atc atc gtg tgg gcg ctg acc gat gcc agt aag ttc ctc acc	835
Ile Ala Ile Ile Val Trp Ala Leu Thr Asp Gly Ser Lys Phe Leu Thr	
230 235 240 245	
ttg gtc cca gca gtg ctg gca acc atc act gtg gtg ttg gtg tct tcg	883
Leu Val Pro Ala Val Leu Ala Thr Ile Thr Val Val Leu Val Ser Ser	
250 255 260	
cgt tgg agg ctt ggt cag tgg aaa att cgt cgt aga caa ccc acg gtg	931
Arg Trp Arg Leu Gly Gln Trp Lys Ile Arg Arg Arg Gln Pro Thr Val	
265 270 275	
gaa aaa gcc gga ccc gcg ctt atc gcg gtc gtg gtt gcg aca gca ctc	979
Glu Lys Ala Gly Pro Ala Leu Ile Ala Val Val Val Ala Thr Ala Leu	
280 285 290	
ttg gcg tgg att cct act cct tat gtg gag cgc gtc aac aac ctc ccc	1027
Leu Ala Trp Ile Pro Thr Pro Tyr Val Glu Arg Arg Asn Asn Leu Pro	
295 300 305	
ggg ctt caa atg ctg gca aag cct gcc cca ggt gtt atc gca cct att	1075
Gly Leu Gln Met Leu Ala Lys Pro Ala Pro Gly Val Ile Ala Pro Ile	
310 315 320 325	
ggg tgg cac atc gac gat gtg cag tat tac aac tgg gct tcg cgc tac	1123
Gly Trp His Ile Asp Asp Val Gln Tyr Tyr Asn Trp Ala Ser Arg Tyr	
330 335 340	
ttc ggc ccc ggt tcc tct ctg ctt agg cag acg atg acg gca gat oat	1171
Phe Gly Pro Gly Ser Ser Leu Leu Arg Gln Thr Met Thr Ala Asp His	
345 350 355	
tac aac gag gcg tgg gat cca gat gga ctc gac cga act gtt gtg gtg	1219
Tyr Asn Glu Ala Trp Asp Pro Asp Gly Leu Asp Arg Thr Val Val Val	
360 365 370	
gat acc ctc caa tcg gcg gaa cgg ttc cag cag cgt gcc ttt ggt gac	1267

Asp Thr Leu Gln Ser Ala Glu Arg Phe Gln Gln Arg Ala Phe Gly Asp
 375 380 385
 gag acg ctg tat tcc act ctg aga ggt cga aag tca gat acc gtc cag 1315
 Glu Thr Leu Tyr Ser Thr Leu Arg Gly Arg Lys Ser Asp Thr Val Gln
 390 395 400 405
 gtg gat ctg gga tac ggc gtg gac gga cgc gcc tac acg gtg ctc gat 1363
 Val Asp Leu Gly Tyr Gly Val Asp Gly Arg Ala Tyr Thr Val Leu Asp
 410 415 420
 gaa act gac ttc ttg acg tac acc aag ctg gtt ttt gaa tgg cag acc 1411
 Glu Thr Asp Phe Leu Thr Thr Lys Leu Val Phe Glu Trp Gln Thr
 425 430 435
 acc aac aac acc gtg gag aag atc tcc gtc atc cgc gtg gat gat cac 1459
 Thr Asn Asn Thr Val Glu Lys Ile Ser Val Ile Ala Val Asp Asp His
 440 445 450
 cgc gca gaa cgc aag ttc ccg gag ctt gca cca tgc gtt acc aga atg 1507
 Arg Ala Glu Ala Lys Phe Pro Glu Leu Ala Pro Ser Val Thr Arg Met
 455 460 465
 ttt atc cag gtg gct acc att ttg ttc cgt gga aat gac gtg acc atc 1555
 Phe Ile Gln Val Ala Thr Ile Leu Phe Arg Gly Asn Asp Val Thr Ile
 470 475 480 485
 gat acc aat acc caa ttg aaa gat ctt gac ctg gtc agc caa gtt ggc 1603
 Asp Thr Asn Thr Gln Leu Lys Asp Leu Asp Leu Val Ser Gln Val Gly
 490 495 500
 cgt cag atc gtg gca gaa caa cag gtg ggg agg tca tgatggaaca 1649
 Arg Gln Ile Val Ala Glu Gln Gln Val Gly Arg Ser
 505 510
 agatctcagc tac 1662
 <210> 2402
 <211> 513
 <212> PRT
 <213> *Corynebacterium glutamicum*
 <400> 2402
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 20 25 30
 Asn Ala Gln Met Glu Val Pro Ser Leu Arg Thr Tyr Val Phe Arg Gly
 35 40 45
 Ile Ile Ala Ile Ala Cys Leu Ile Ile Gly Phe Tyr Glu Ser Phe Val
 50 55 60
 Leu Met Trp Gln Asn Leu Arg Ile Gly Val Ala Asn Tyr Ser Leu Leu
 65 70 75 80
 Val Val Leu Met Ala Ile Val Leu Phe Ile Gly Leu Asp Arg Lys Arg
 85 90 95

Ala Arg Ala Leu Asn Ile His Asp Arg Glu Val Asp Tyr Ile Ile Gly
 100 105 110
 Gly Ile Val Val Leu Ile Ala Ile Thr Ile Lys Ser Gln Leu Leu Pro
 115 120 125
 Arg Phe Val Asp Trp Glu Thr Leu Leu Arg Leu Asp Met Phe Ala Leu
 130 135 140
 Leu Phe Phe Ala Phe Gly Ile Ser Gly Leu Val Phe Gly Met Arg Ser
 145 150 155 160
 Thr Phe Ser Phe Ala Pro Gly Trp Ile Leu Leu Phe Gly Tyr Asn Ala
 165 170 175
 Val Ala His Leu Ile Ile Ser Val Ile Phe Gly Gly Gly Phe Trp Gly
 180 185 190
 Pro Val Met Ala Asn Ile Ile Gly Leu Ser Leu Ala Val Leu Val Ser
 195 200 205
 Ser Asn Arg Asp Leu Val Gln Ala Thr Tyr Leu Ala Leu Met Thr Val
 210 215 220
 Leu Phe Gly Val Ile Ile Ala Ile Ile Val Trp Ala Leu Thr Asp Gly
 225 230 235 240
 Ser Lys Phe Leu Thr Leu Val Pro Ala Val Leu Ala Thr Ile Thr Val
 245 250 255
 Val Leu Val Ser Ser Arg Trp Arg Leu Gly Gln Trp Lys Ile Arg Arg
 260 265 270
 Arg Gln Pro Thr Val Glu Lys Ala Gly Pro Ala Leu Ile Ala Val Val
 275 280 285
 Val Ala Thr Ala Leu Leu Ala Trp Ile Pro Thr Pro Tyr Val Glu Arg
 290 295 300
 Val Asn Asn Leu Pro Gly Leu Gln Met Leu Ala Lys Pro Ala Pro Gly
 305 310 315 320
 Val Ile Ala Pro Ile Gly Trp His Ile Asp Asp Val Gln Tyr Tyr Asn
 325 330 335
 Trp Ala Ser Arg Tyr Phe Gly Pro Gly Ser Ser Leu Leu Arg Gln Thr
 340 345 350
 Met Thr Ala Asp His Tyr Asn Glu Ala Trp Asp Pro Asp Gly Leu Asp
 355 360 365
 Arg Thr Val Val Val Asp Thr Leu Gln Ser Ala Glu Arg Phe Gln Gln
 370 375 380
 Arg Ala Phe Gly Asp Glu Thr Leu Tyr Ser Thr Leu Arg Gly Arg Lys
 385 390 395 400
 Ser Asp Thr Val Gln Val Asp Leu Gly Tyr Gly Val Asp Gly Arg Ala
 405 410 415

Tyr Thr Val Leu Asp Glu Thr Asp Phe Leu Thr Tyr Thr Lys Leu Val
 420 425 430
 Phe Glu Trp Gln Thr Thr Asn Asn Thr Val Glu Lys Ile Ser Val Ile
 435 440 445
 Ala Val Asp Asp His Arg Ala Glu Ala Lys Phe Pro Glu Leu Ala Pro
 450 455 460
 Ser Val Thr Arg Met Phe Ile Gln Val Ala Thr Ile Leu Phe Arg Gly
 465 470 475 480
 Asn Asp Val Thr Ile Asp Thr Asn Thr Gln Leu Lys Asp Leu Asp Leu
 485 490 495
 Val Ser Gln Val Gly Arg Gln Ile Val Ala Glu Gln Gln Val Gly Arg
 500 505 510
 Ser

<210> 2403
 <211> 405
 <212> DNA
 <213> Corynebacterium glutamicum
 <220>
 <221> CDS
 <222> (101)..(382)
 <223> RXA01760

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 Met Ala Ala Phe Leu
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 gag atc acc ttg aaa atc aat gac gaa ggc cgc cca tca gca gct ggc 163
 Glu Ile Thr Leu Lys Ile Asn Asp Glu Gly Arg Pro Ser Ala Ala Gly
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 gtc tac cag gaa tac aag caa cca ttc ctc agc tca att gct ggc gct 211
 Val Tyr Gln Glu Tyr Lys Gln Pro Phe Leu Ser Ser Ile Ala Gly Ala
 25 30 35
 aca agc aaa gaa ctc ctc atc cga gaa gaa gac gtg cag gtg ctc cac 259
 Thr Ser Lys Glu Leu Leu Ile Arg Glu Glu Asp Val Gln Val Leu His
 40 45 50
 ggc tgt gac acc gta gct aat gct gaa gat tat ctt gtc agc gaa ctg 307
 Gly Cys Asp Thr Val Ala Asn Ala Glu Asp Tyr Leu Val Ser Glu Leu
 55 60 65
 ttc acg gcc gat gtt gtc ggt ggt cta gct cca cta ttg cag gct gat 355
 Phe Thr Ala Asp Val Val Gly Gly Leu Ala Pro Leu Leu Gln Ala Asp
 70 75 80 85
 cca gag att cgt att tac cag gtc gcg taactgctgt ggcaggctca 402
 Pro Glu Ile Arg Ile Tyr Gln Val Ala

90

tcg

405

<210> 2404

<211> 94

<212> PRT

<213> Corynebacterium glutamicum

<400> 2404

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Pro Ser Ala Ala Gly Val Tyr Gln Glu Tyr Lys Gln Pro Phe Leu Ser
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Ser Ile Ala Gly Ala Thr Ser Lys Glu Leu Leu Ile Arg Glu Glu Asp
 35 40 45

Val Gln Val Leu His Gly Cys Asp Thr Val Ala Asn Ala Glu Asp Tyr
 50 55 60

Leu Val Ser Glu Leu Phe Thr Ala Asp Val Val Gly Gly Leu Ala Pro
 65 70 75 80

Leu Leu Gln Ala Asp Pro Glu Ile Arg Ile Tyr Gln Val Ala
 85 90

<210> 2405

<211> 501

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(478)

<223> RXA01768

<400> 2405

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gcactctccc gtactcattt ctgaaaggt ttttccgctc atg tct gaa tct act 115
 Met Ser Glu Ser Thr
 1 5

tct tct get aac tcc acc acc atc ctc aac gac acc ttc aac cag aag 163
 Ser Ser Ala Asn Ser Thr Thr Ile Leu Asn Asp Thr Phe Asn Pro Lys
 10 15 20

cct ggc gta cct tat gca cgc gtc gat aat ctc gaa ttt gcc aca cgt 211
 Pro Gly Val Pro Tyr Ala Arg Val Asp Asn Leu Glu Phe Ala Thr Arg
 25 30 35

gac gaa ttc cgc gct tgg gct acc gca gag atg gag gcc ggt aac gtt 259
 Asp Glu Phe Arg Ala Trp Ala Thr Ala Glu Met Glu Ala Gly Asn Val
 40 45 50

atc tct gca acc atc gcc aat gcc cca cgc gaa gac cgc atc aag tct 307
 Ile Ser Ala Thr Ile Ala Asn Ala Pro Arg Glu Asp Arg Ile Lys Ser

55	60	65	
ttt gtc atg gat ctt gtt cga gac ggt att gac gac gct gct gag gaa			355
Phe Val Met Asp Leu Val Arg Asp Gly Ile Asp Asp Ala Ala Glu Glu			
70	75	80	85
atc gtc tca cgc att gat agc ggt gac ttc act atg aag gaa gct ctc			403
Ile Val Ser Arg Ile Asp Ser Gly Asp Phe Thr Met Lys Glu Ala Leu			
	90	95	100
acc gcg atc gcg gca tca atc aac gac ctc gat gct gac gat gta gtc			451
Thr Ala Ile Ala Ala Ser Ile Asn Asp Leu Asp Ala Asp Asp Val Val			
	105	110	115
agc gac atc gtt gaa aac cac ttc aac tagtcaacac accagccctc			498
Ser Asp Ile Val Glu Asn His Phe Asn			
	120	125	
cac			501

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<211> 126

<212> PRT

<213> Corynebacterium glutamicum

<400> 2406

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35 40 45

Glu Ala Gly Asn Val Ile Ser Ala Thr Ile Ala Asn Ala Pro Arg Glu
50 55 60

Asp Arg Ile Lys Ser Phe Val Met Asp Leu Val Arg Asp Gly Ile Asp
65 70 75 80

Asp Ala Ala Glu Glu Ile Val Ser Arg Ile Asp Ser Gly Asp Phe Thr
85 90 95

Met Lys Glu Ala Leu Thr Ala Ile Ala Ala Ser Ile Asn Asp Leu Asp
100 105 110

Ala Asp Asp Val Val Ser Asp Ile Val Glu Asn His Phe Asn
115 120 125

<210> 2407

<211> 3888

<212> DNA

<213> Corynebacterium glutamicum

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<223> RXA01770

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 Met Pro Ile Ile Ile 5
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 Asp Asn Leu Asn Ser Asp Asp Ser Thr Ile Gly Thr Ala Thr Glu 10 15 20
 tac aac cct gac act gac gcc gat tta ctt gat gct att aac gct gat 211
 Tyr Asn Pro Asp Thr Asp Ala Asp Leu Leu Asp Ala Ile Asn Ala Asp 25 30 35
 gct gac ctt gat ggc gac gcc acc atc agc act aac gcg aca gaa gaa 259
 Ala Asp Leu Asp Gly Asp Ala Thr Ile Ser Thr Asn Ala Thr Glu Glu 40 45 50
 ggt gta gac gca gca gct gaa aaa cct aag aaa aag cgt aaa gcc cct 307
 Gly Val Asp Ala Ala Ala Glu Lys Pro Lys Lys Lys Arg Lys Ala Pro 55 60 65
 gct ctg aag cct aaa gga ctc acg gca aag ttc ttc cac cgt gat ctt 355
 Ala Leu Lys Pro Lys Gly Leu Thr Ala Lys Phe His Arg Asp Leu 70 75 80 85
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 Thr Gly Val Gly Gly Arg Thr Gly Arg Leu Asn Lys Asn Val His Pro 90 95 100
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 Thr Asn Pro Asp Leu Ser Tyr Gln Pro Val Ser Asp Val Tyr Thr Pro 105 110 115
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 Gln Ser Ala Asp His Lys Gly Ile Lys Thr Arg Tyr Ile Leu Thr His 120 125 130
 cca acc ccc gct gtt gtt ctc agt gag tcc atc agc aac gcg ttt cat 547
 Pro Thr Pro Ala Val Val Leu Ser Glu Ser Ile Ser Asn Ala Phe His 135 140 145
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 Gln Met Ile Asn Val Ala Asp Ile Cys Asp Tyr His Phe His Gly Tyr 185 190 195
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 Asn Leu Trp Val Asp Phe Thr Pro Gln Thr Ile Ala Leu Arg Ser Gly 200 205 210
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Lys 215	Thr	Val	Leu	Asp	Asp	Gly 220	Thr	Thr	Ala	Ser	Asp 225	Asn	Thr	Thr	His	
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Val	Tyr	Tyr	Arg	Val	Thr	Val	His	Val	Ile	Ala	Gly	Gln	Asp	His	Gly	
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Ser	Thr	Leu	Leu	Asp	Asp	Gln	Gly	Asn	Gln	Val	Leu	Asp	Arg	Asp	Asp	
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aat	cct	att	tct	acc	cca	agt	atc	aag	cgt	att	ggc	gct	gtc	act	gat	931
Asn	Pro	Ile	Ser	Thr	Pro	Ser	Ile	Lys	Arg	Ile	Gly	Ala	Val	Thr	Asp	
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Leu	Phe	Val	His	Asn	Pro	Phe	Gly	Phe	Ala	Ser	Val	Asn	Ser	Phe	Ala	
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Pro	Thr	Pro	Ile	Ala	Leu	Asp	Met	Val	Val	Leu	Asn	Glu	Trp	Ser	Glu	
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Lys	Ser	Tyr	Gln	Leu	Cys	Glu	Arg	Val	Val	Ala	Gln	Ala	Lys	Leu	Ile	
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gcc	cac	aat	atc	ttg	tgg	ttt	acc	gaa	cag	atg	aac	cct	ggc	acc	acc	1267
Ala	His	Asn	Ile	Leu	Trp	Phe	Thr	Glu	Gln	Met	Asn	Pro	Gly	Thr	Thr	
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aac	ctc	agc	gag	gta	cct	atc	tcc	aag	aag	tct	atg	ctg	ccg	atg	tct	1315
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Ser	Ala	Leu	Phe	Trp	Thr	Val	Ser	Ala	Ile	Lys	Asn	Glu	Ser	Met	Val	
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Gln	Tyr	Leu	Val	Arg	Gln	Asn	Met	Gln	Leu	Thr	Leu	Ser	Ser	Asn	Leu	
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Asp	Ala	Leu	Asn	Ser	Ile	Val	Ser	Gln	Leu	Pro	Val	Pro	Asp	Lys	Asp	

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Leu Cys Ala Ala Gly Thr Asn Pro Glu Glu Ile Ala Val Leu Ser Phe			
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Thr Asn Ala Ala Ala Asp Asn Ile Thr Ala Lys Asn Asp Lys Val Thr			
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Ser Met Thr Ile Ser Lys Met Val His Glu Ile Tyr Ala His Asn Phe			
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Pro Asp His Glu Ile Ser Thr Ile Asp Thr Ile Ile Asn Thr Leu Asp			
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Ile Glu Tyr Gly Asp Gln Met Val Thr Ser Asp Tyr Met Ile Gln Leu			
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Cys Tyr Leu Leu Asp Lys Leu Ile Glu Pro His Ala Ser Pro Lys			
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Tyr Leu Ile Ile Asp Glu Val Gln Asp Asn Ser Val Phe Glu Phe Val			
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Phe Ala Leu Arg Phe Ala Ala Lys His Asn Thr Ser Leu Tyr Leu Val			
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Gly Asp Ser Ser Gln Thr Leu Tyr Glu Phe Arg Ser Ala Asn Pro Lys			
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Thr Thr Asn Tyr Arg Ser Asn Gln Glu Ile Leu Asp Phe Ala Asn Ile	
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His Leu Ser Asp Ile Glu Ala Asn Gln Phe Ala Gly Ile Gln Leu Tyr	
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760 765 770	
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Glu Leu Asp Met His His Val Ser Lys Gln Ser Glu Phe Thr Asp Ser	
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 Lys Arg Lys Ala Pro Ala Leu Lys Pro Lys Gly Leu Thr Ala Lys Phe
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 Phe His Arg Asp Leu Thr Gly Val Gly Gly Arg Thr Gly Arg Leu Asn
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 Lys Asn Val His Pro Thr Asn Pro Asp Leu Ser Tyr Gln Pro Val Ser
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 Asp Val Tyr Thr Pro Gln Ser Ala Asp His Lys Gly Ile Lys Thr Arg
 115 120 125
 Tyr Ile Leu Thr His Pro Thr Pro Ala Val Val Leu Ser Glu Ser Ile
 130 135 140
 Ser Asn Ala Phe His Val Ser Thr Leu Arg Arg Asn Asn Asn Val Asn
 145 150 155 160
 Asn Ser Asp Ser Glu Leu Ala Ala Trp Pro Tyr Leu Tyr Gln Leu Asp
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 Ile Pro Gln Leu Asp Gln Met Ile Asn Val Ala Asp Ile Cys Asp Tyr
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His	Phe	His	Gly	Tyr	Asn	Leu	Trp	Val	Asp	Phe	Thr	Pro	Gln	Thr	Ile	195	200	205
Ala	Leu	Arg	Ser	Gly	Lys	Thr	Val	Leu	Asp	Asp	Gly	Thr	Thr	Ala	Ser	210	215	220
Asp	Asn	Thr	Thr	His	Val	Tyr	Tyr	Arg	Val	Thr	Val	His	Val	Ile	Ala	225	230	235
Gly	Gln	Asp	His	Gly	Ser	Thr	Leu	Leu	Asp	Asp	Gln	Gly	Asn	Gln	Val	245	250	255
Leu	Asp	Arg	Asp	Asp	Asn	Pro	Ile	Ser	Thr	Pro	Ser	Ile	Lys	Arg	Ile	260	265	270
Gly	Ala	Val	Thr	Asp	Leu	Phe	Asp	His	Asn	Pro	Phe	Gly	Phe	Ala	Ser	275	280	285
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Val	Pro	Asp	Lys	Asp	Val	Val	Ala	Ala	Ser	Gly	Tyr	Gln	Ile	Gln	Pro	465	470	475
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Glu Arg Ile Glu Tyr Leu Cys Ala Ala Gly Thr Asn Pro Glu Glu Ile
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 Tyr Ala His Asn Phe Pro Asp His Glu Ile Ser Thr Ile Asp Thr Ile
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 Gly Asn Ala Asn Leu Thr Ala Leu Ser Ile Phe Met Glu Ser His Ile
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 740 745 750
 Gly Ile Gln Leu Tyr Ala Asn Ser Phe Asp Ala Pro Thr Ala Asp Ser
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 770 775 780
 Glu Phe Thr Asp Ser Ile Pro Tyr Phe Met Glu Ser Asn Lys Ala Arg
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 Phe Asp Ala Ala Ile Leu Asn Asn Glu Gln Thr Ile Val Leu Ala His
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Val	Ile	Arg	Ser	Met	Ala	Ala	Trp	Trp	Arg	Glu	Asn	Glu	Arg	Asp	Ile	Val	Ile	Arg	Ser	Met	Ala	Ala	Trp	Trp	Arg	Glu	Asn	Glu	Arg	Asp	Ile	Val	Ile	Arg	Ser	Met	Ala	Ala	Trp	Trp	Arg	Glu	Asn	Glu	Arg	Asp	Ile
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Gln	Gly	Trp	Val	Gln	Gln	Thr	Gln	Ser	Gly	Ala	Ile	Thr	Asn	Glu	Glu	Gln	Gly	Trp	Val	Gln	Gln	Thr	Gln	Ser	Gly	Ala	Ile	Thr	Asn	Glu	Glu	Gln	Gly	Trp	Val	Gln	Gln	Thr	Gln	Ser	Gly	Ala	Ile	Thr	Asn	Glu	Glu
915										920										925																											
Phe	Phe	Tyr	Arg	Leu	Arg	Gln	Cys	Ile	Leu	Asp	Tyr	Glu	Ile	Arg	Asn	Phe	Phe	Tyr	Arg	Leu	Arg	Gln	Cys	Ile	Leu	Asp	Tyr	Glu	Ile	Arg	Asn	Phe	Phe	Tyr	Arg	Leu	Arg	Gln	Cys	Ile	Leu	Asp	Tyr	Glu	Ile	Arg	Asn
930										935										940																											
Asn	Arg	Ala	Arg	Gln	Ser	Met	Leu	Asn	Ala	Arg	Asn	Asn	Ala	Asn	Lys	Asn	Arg	Ala	Arg	Gln	Ser	Met	Leu	Asn	Ala	Arg	Asn	Asn	Ala	Asn	Lys	Asn	Arg	Ala	Arg	Gln	Ser	Met	Leu	Asn	Ala	Arg	Asn	Asn	Ala	Asn	Lys
945										950										955																											
Glu	Ala	Val	Ala	Gln	Glu	Lys	Pro	Leu	Leu	Met	Val	Ser	Thr	Ile	His	Glu	Ala	Val	Ala	Gln	Glu	Lys	Pro	Leu	Leu	Met	Val	Ser	Thr	Ile	His	Glu	Ala	Val	Ala	Gln	Glu	Lys	Pro	Leu	Leu	Met	Val	Ser	Thr	Ile	His
965										970										975																											
Ser	Ala	Lys	Gly	Leu	Glu	Phe	Asp	Asn	Val	Ile	Val	Leu	Gln	Lys	Pro	Ser	Ala	Lys	Gly	Leu	Glu	Phe	Asp	Asn	Val	Ile	Val	Leu	Gln	Lys	Pro	Ser	Ala	Lys	Gly	Leu	Glu	Phe	Asp	Asn	Val	Ile	Val	Leu	Gln	Lys	Pro
980										985										990																											
Ser	Ser	Asp	Ala	Glu	Met	Thr	Glu	Glu	Gly	Lys	Arg	Ala	Thr	Tyr	Val	Ser	Ser	Asp	Ala	Glu	Met	Thr	Glu	Glu	Gly	Lys	Arg	Ala	Thr	Tyr	Val	Ser	Ser	Asp	Ala	Glu	Met	Thr	Glu	Glu	Gly	Lys	Arg	Ala	Thr	Tyr	Val
995										1000										1005																											
Ala	Leu	Thr	Arg	Ala	Lys	Lys	Arg	Glu	Leu	Ile	Ile	Ala	Gly	Ser	Thr	Ala	Leu	Thr	Arg	Ala	Lys	Lys	Arg	Glu	Leu	Ile	Ile	Ala	Gly	Ser	Thr	Ala	Leu	Thr	Arg	Ala	Lys	Lys	Arg	Glu	Leu	Ile	Ile	Ala	Gly	Ser	Thr
1010										1015										1020																											
Arg	Ala	Tyr	Pro	Arg	Ile	Val	Thr	Asp	Tyr	Glu	Gln	Ile	Val	Asp	Leu	Arg	Ala	Tyr	Pro	Arg	Ile	Val	Thr																								

Asp Val Thr Val Gln Ser Ser Thr Ala Pro Val Thr Pro Val Val Ala
1170 1175 1180

Asp Leu Glu Val Thr Thr Val Ala Ala Asp Pro Val Glu Pro Thr Ile
1185 1190 1195 1200

Val Ala Ala Gln Pro Glu Val Asp Asp Asn Leu Val Tyr Ser Thr Ser
1205 1210 1215

Thr Pro Asn Ser His Ser Asp Val Ile Ala Val Asn Ser Asp Thr Ser
1220 1225 1230

Glu Asn Ala Ala Val Asn Pro Val Leu Ser Asp Ile Glu Ala Leu Arg
1235 1240 1245

Ala Ile Phe Asn Asn Gln Asp
1250 1255

<210> 2409

<211> 467

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (34)..(444)

<223> RXA01773

<400> 2409

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Met Ile Thr His Ile Gln Ala
1 5

ggc ctg cat ctt ggt ggc tgc cgc gca gca ggt tta ctg cct ata cca 102
Gly Leu His Leu Gly Gly Cys Arg Ala Ala Gly Leu Leu Pro Ile Pro
10 15 20

gca cat att gat cat att gtg cgc ctg aca gcc gca gat ttc tat gac 150
Ala His Ile Asp His Ile Val Arg Leu Thr Ala Ala Asp Phe Tyr Asp
25 30 35

acc cag tca gca ccg cag ctg ctc agc aac act gtg ctt gat gta ttg 198
Thr Gln Ser Ala Pro Gln Leu Leu Ser Asn Thr Val Leu Asp Val Leu
40 45 50 55

gac acc acc act caa gac ttg aag gca ttg tgg cct gtt gca gaa cat 246
Asp Thr Thr Thr Gln Asp Leu Lys Ala Leu Trp Pro Val Ala Glu His
60 65 70

att gct aca acc att cct gaa tct gag aac gtg ctt atc cac tgc cag 294
Ile Ala Thr Thr Ile Pro Glu Ser Glu Asn Val Leu Ile His Cys Gln
75 80 85

atg ggt atc aac cgc tca gct gca ctc atg aca cgg gtg ttg atg ttg 342
Met Gly Ile Asn Arg Ser Ala Ala Leu Met Thr Arg Val Leu Met Leu
90 95 100

cgc aac gat tgc acc gcc gat gaa gca att gca ctg ctg cgt gat cga 390
Arg Asn Asp Cys Thr Ala Asp Glu Ala Ile Ala Leu Leu Arg Asp Arg

105	110	115	
cgc tca ccg ttt gta ctg ttc aat gag cat ttt gtg gaa caa ctt cga			438
Arg Ser Pro Phe Val Leu Phe Asn Glu His Phe Val Glu Gln Leu Arg			
120	125	130	135

gca ctg taagcgctca aagacccatt acc	467
Ala Leu	

<210> 2410

<211> 137

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2410

Met Ile Thr His Ile Gln Ala Gly Leu His Leu Gly Gly Cys Arg Ala
1 5 10 15

Ala Gly Leu Leu Pro Ile Pro Ala His Ile Asp His Ile Val Arg Leu
20 25 30

Thr Ala Ala Asp Phe Tyr Asp Thr Gln Ser Ala Pro Gln Leu Leu Ser
35 40 45

Asn Thr Val Leu Asp Val Leu Asp Thr Thr Thr Gln Asp Leu Lys Ala
50 55 60

Leu Trp Pro Val Ala Glu His Ile Ala Thr Thr Ile Pro Glu Ser Glu
65 70 75 80

Asn Val Leu Ile His Cys Gln Met Gly Ile Asn Arg Ser Ala Ala Leu
85 90 95

Met Thr Arg Val Leu Met Leu Arg Asn Asp Cys Thr Ala Asp Glu Ala
100 105 110

Ile Ala Leu Leu Arg Asp Arg Ser Pro Phe Val Leu Phe Asn Glu
115 120 125

His Phe Val Glu Gln Leu Arg Ala Leu
130 135

<210> 2411

<211> 687

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(664)

<223> RXA01775

<400> 2411	
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ttttattccc cgagaatgtc ctagaaagga actegacccc	atg tcc tat tca ctc	115
	Met Ser Tyr Ser Leu	
	1 5	

att att tct aaa gca cca acc cac tcc atg cct ttt aat gag gct gaa 163
 Ile Ile Ser Lys Ala Pro Thr His Ser Met Pro Phe Asn Glu Ala Glu
 10 15 20
 ctc cta gag ctt gtc gat gaa ctg cac tcc gac aac acc gtg aaa aag 211
 Leu Leu Glu Leu Val Asp Glu Leu His Ser Asp Asn Thr Val Lys Lys
 25 30 35
 ccg gtt att gtg cca ctc ccc gat gat ttc tcc tac acc gta gat agc 259
 Pro Val Ile Val Pro Leu Pro Asp Asp Phe Ser Tyr Thr Val Asp Ser
 40 45 50
 gcc gtg cga cta cat gat ttg ggt gtt gac cag gaa ctg act gac tgg 307
 Ala Val Arg Leu His Asp Leu Gly Val Asp Gln Glu Leu Thr Asp Trp
 55 60 65
 att act gca caa gtt gct gca gcc tat cca aac cag atc gtc tca gag 355
 Ile Thr Thr Ala Gln Val Ala Ala Tyr Pro Asn Gln Ile Val Ser Glu
 70 75 80 85
 att gct gct gcc cct gat ccg caa gcc aag acc tta ttc tcc gcc aat 403
 Ile Ala Ala Ala Pro Asp Pro Gln Ala Lys Thr Leu Phe Ser Ala Asn
 90 95 100
 gcg tat aac acc agg tct ttt ggt act ttt tgg act gag cac cct att 451
 Ala Tyr Asn Thr Arg Ser Phe Gly Thr Phe Trp Thr Glu His Pro Ile
 105 110 115
 aca cag ctc caa tac aag cgc tgc tac caa att gtc atc gag aac gtt 499
 Thr Gln Leu Gln Tyr Lys Arg Cys Tyr Gln Ile Val Ile Glu Asn Val
 120 125 130
 acg ggt gtc tat cat ccg tta cct gtt gat aac tac cgc tac gta ccc 547
 Thr Gly Val Tyr His Pro Leu Pro Val Asp Asn Tyr Arg Tyr Val Pro
 135 140 145
 cct gtc acg ccc tca ttg cca cag ccg gtc tac cac gaa gct atc gcc 595
 Pro Val Thr Pro Ser Leu Pro Gln Pro Val Tyr His Glu Ala Ile Ala
 150 155 160 165
 tta aat gag tct gat gtc gct gat cac ggt act cgt gca gcc aag cac 643
 Leu Asn Glu Ser Asp Val Ala Asp His Gly Thr Arg Ala Ala Lys His
 170 175 180
 gca atg atc aac cgc aac gta taaccacaca cgccacagat act 687
 Ala Met Ile Asn Arg Asn Val
 185

<210> 2412

<211> 188

<212> PRT

<213> Corynebacterium glutamicum

<400> 2412

Met Ser Tyr Ser Leu Ile Ile Ser Lys Ala Pro Thr His Ser Met Pro
 1 5 10 15

Phe Asn Glu Ala Glu Leu Leu Glu Leu Val Asp Glu Leu His Ser Asp
 20 25 30

Asn Thr Val Lys Lys Pro Val Ile Val Pro Leu Pro Asp Asp Phe Ser
35 40 45

Tyr Thr Val Asp Ser Ala Val Arg Leu His Asp Leu Gly Val Asp Gln
50 55 60

Glu Leu Thr Asp Trp Ile Thr Ala Gln Val Ala Ala Tyr Pro Asn
65 70 75 80

Gln Ile Val Ser Glu Ile Ala Ala Ala Pro Asp Pro Gln Ala Lys Thr
85 90 95

Leu Phe Ser Ala Asn Ala Tyr Asn Thr Arg Ser Phe Gly Thr Phe Trp
100 105 110

Thr Glu His Pro Ile Thr Gln Leu Gln Tyr Lys Arg Cys Tyr Gln Ile
115 120 125

Val Ile Glu Asn Val Thr Gly Val Tyr His Pro Leu Pro Val Asp Asn
130 135 140

Tyr Arg Tyr Val Pro Pro Val Thr Pro Ser Leu Pro Gln Pro Val Tyr
145 150 155 160

His Glu Ala Ile Ala Leu Asn Glu Ser Asp Val Ala Asp His Gly Thr
165 170 175

Arg Ala Ala Lys His Ala Met Ile Asn Arg Asn Val
180 185

<210> 2413

<211> 1575

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1552)

<223> RXA01776

<400> 2413

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tctcaccat ccccatcac tattaagaa aatcaccatc atg acc cac act gat 115
Met Thr His Thr Asp
1 5

acc cca gcc cct gca cac ggc gta aca ccg agt gaa ttc gct gtt acc 163
Thr Pro Ala Pro Ala His Gly Val Thr Pro Ser Glu Phe Ala Val Thr
10 15 20

tca cac gaa ctc acc acc tca cca aca cct agt ccg aca cag gtc gct 211
Ser His Glu Leu Thr Thr Ser Pro Thr Pro Ser Pro Thr Gln Val Ala
25 30 35

att gca gcc cag gaa aaa att cgc cag cgc aag ctc gaa gag ctt aaa 259
Ile Ala Ala Gln Glu Lys Ile Arg Gln Arg Lys Leu Glu Glu Leu Lys
40 45 50

gca aaa aag cgc aca gac acg aca gct caa cca ctt cta cct gca cct	307
Ala Lys Lys Arg Thr Asp Thr Thr Ala Gln Pro Leu Pro Ala Pro	
55 60 65	
gtg ctg cat aca cgc cca ctc ccc tca ccg aat cca ccg cga cca tct	355
Val Leu His Thr Arg Pro Leu Pro Ser Pro Asn Pro Pro Arg Pro Ser	
70 75 80 85	
cca ccg gca cct acc act gga cac tgg gaa ctt ctt att gtc agg tca	403
Pro Pro Ala Pro Thr Thr Gly His Trp Glu Leu Leu Ile Val Arg Ser	
90 95 100	
cag cag aag aaa atg acc gca gcc aat ccc ttt ctc aaa ttc ctt cat	451
Gln Gln Lys Lys Met Thr Ala Ala Asn Pro Phe Leu Lys Phe Leu His	
105 110 115	
ctc ggt aaa gcc ttc aac gtg aaa gac cta ggg ctc acc tgc gat cgc	499
Leu Gly Lys Ala Phe Asn Val Lys Asp Leu Gly Thr Cys Asp Arg	
120 125 130	
acc act gat gtt gac ctc tca ccg ctt ggc aag ctc aat ccg ccc agc	547
Thr Thr Asp Val Asp Leu Ser Arg Leu Gly Lys Leu Asn Pro Pro Ser	
135 140 145	
tca ctt atc ctt gaa cta gca acg gca ctt gac ctg cat cca ttc ctc	595
Ser Leu Ile Leu Glu Leu Ala Thr Ala Leu Asp Leu His Pro Phe Leu	
150 155 160 165	
tca gtc gca ctc tct tgc cac agt gcg gtc aac gcc cgt cgc aac caa	643
Ser Val Ala Leu Ser Ser His Ser Ala Val Asn Ala Arg Arg Asn Gln	
170 175 180	
ctt gaa tta acc ctg cac aac cat gac act cag ggc aca gca tta ggt	691
Leu Glu Leu Thr Leu His Asn His Asp Thr Gln Gly Thr Ala Leu Gly	
185 190 195	
cac agc gtt act atg gtc cag cta ccc gag gtc att aat cga gct gct	739
His Ser Val Thr Met Val Gln Leu Pro Glu Val Ile Asn Arg Ala Ala	
200 205 210	
gta gag ccc tat atc aaa ccc aag ggc tgc ggc aat gac ccg ctt gac	787
Val Glu Pro Tyr Ile Lys Pro Lys Gly Ser Gly Asn Asp Pro Leu Asp	
215 220 225	
caa agc ctg aac cac cgc gca ccc acc gta agt gac gtg caa aaa gcc	835
Gln Ser Leu Asn His Arg Ala Pro Thr Val Ser Asp Val Gln Lys Ala	
230 235 240 245	
ctt gtg cag gaa aac aca ggc acg gca aca gac agc aac aac tac ctg	883
Leu Val Gln Glu Asn Thr Gly Thr Ala Thr Asp Ser Asn Asn Tyr Leu	
250 255 260	
ctt cct ttt gat cct gat tct ggt gca cca aaa acc acc gcg ctt aat	931
Leu Pro Phe Asp Pro Asp Ser Gly Ala Pro Lys Thr Thr Ala Leu Asn	
265 270 275	
gcg cct aat aag gat ctc cta cag gcc agg cat gag ctt gcc tat att	979
Ala Pro Asn Lys Asp Leu Leu Gln Ala Arg His Glu Leu Ala Tyr Ile	
280 285 290	
ccc gag atc ccc gcc att gca tgc tgg ctc gat cac ctt gac ccc atc	1027

[illegible]

<400> 2414
Met Thr His Thr Asp Thr Pro Ala Pro Ala His Gly Val Thr Pro Ser
1 5 10 15
Glu Phe Ala Val Thr Ser His Glu Leu Thr Thr Ser Pro Thr Pro Ser
20 25 30

Pro Thr Gln Val Ala Ile Ala Ala Gln Glu Lys Ile Arg Gln Arg Lys
 35 40 45
 Leu Glu Glu Leu Lys Ala Lys Lys Arg Thr Asp Thr Thr Ala Gln Pro
 50 55 60
 Leu Leu Pro Ala Pro Val Leu His Thr Arg Pro Leu Pro Ser Pro Asn
 65 70 75 80
 Pro Pro Arg Pro Ser Pro Pro Ala Pro Thr Thr Gly His Trp Glu Leu
 85 90 95
 Leu Ile Val Arg Ser Gln Gln Lys Lys Met Thr Ala Ala Asn Pro Phe
 100 105 110
 Leu Lys Phe Leu His Leu Gly Lys Ala Phe Asn Val Lys Asp Leu Gly
 115 120 125
 Leu Thr Cys Asp Arg Thr Thr Asp Val Asp Leu Ser Arg Leu Gly Lys
 130 135 140
 Leu Asn Pro Pro Ser Ser Leu Ile Leu Glu Leu Ala Thr Ala Leu Asp
 145 150 155 160
 Leu His Pro Phe Leu Ser Val Ala Leu Ser Ser His Ser Ala Val Asn
 165 170 175
 Ala Arg Arg Asn Gln Leu Glu Leu Thr Leu His Asn His Asp Thr Gln
 180 185 190
 Gly Thr Ala Leu Gly His Ser Val Thr Met Val Gln Leu Pro Glu Val
 195 200 205
 Ile Asn Arg Ala Ala Val Glu Pro Tyr Ile Lys Pro Lys Gly Ser Gly
 210 215 220
 Asn Asp Pro Leu Asp Gln Ser Leu Asn His Arg Ala Pro Thr Val Ser
 225 230 235 240
 Asp Val Gln Lys Ala Leu Val Gln Glu Asn Thr Gly Thr Ala Thr Asp
 245 250 255
 Ser Asn Asn Tyr Leu Leu Pro Phe Asp Pro Asp Ser Gly Ala Pro Lys
 260 265 270
 Thr Thr Ala Leu Asn Ala Pro Asn Lys Asp Leu Leu Gln Ala Arg His
 275 280 285
 Glu Leu Ala Tyr Ile Pro Glu Ile Pro Ala Ile Ala Ser Trp Leu Asp
 290 295 300
 His Leu Asp Pro Ile Met Arg Val His Arg Ser Leu Ala Leu Ser Ile
 305 310 315 320
 Phe Pro Val Gln Leu Leu Arg Ala Ala Val Glu Asn Leu Pro His Asn
 325 330 335
 Val Thr Asp Leu His Asn His Leu Asp Pro Glu Asp Leu Leu Pro Glu
 340 345 350

Glu Leu Thr Thr Trp Leu Asp His Leu Phe Asp Ala Asp Leu Thr Ala
 355 360 365
 Leu Ala Ser Cys Pro Gln Leu Ala Pro Pro Ile Val Arg Ser His Asn
 370 375 380
 His Ala Lys Ala Ile Ala Ala Ile Thr Val Thr Ser Val Met Asp Ala
 385 390 395 400
 Leu Ile Ala Lys Thr Leu Asp Ala His Asp Asp Pro Leu Pro Ser Leu
 405 410 415
 Pro Glu Phe Val Glu Leu Leu Arg Asp Ala Val Ala Gln Leu Ala Ala
 420 425 430
 His Phe Lys Gln Gln Arg Gly Glu Val Leu Pro Gln Pro Asn Gly Leu
 435 440 445
 Arg Tyr Ala Thr Asp Phe Gly Leu Leu Ser Tyr Ile Ala Asp Gly Leu
 450 455 460
 His Glu Tyr Ala Leu Ala Ile Asp Phe Gly Leu Ile Tyr Pro Asn Glu
 465 470 475 480

Leu Ile Thr Glu

<210> 2415

<211> 582

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(559)

<223> RXA01777

<400> 2415

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tcataccgca gtaaacccac tcctagaaag gtctttaccc atg tct cgt atc atc 115
 Met Ser Arg Ile Ile
 1 5

act gct ccc gtc cac aag cct tat att att gct cgt gaa gtc aag ggg 163
 Thr Ala Pro Val His Lys Pro Tyr Ile Ile Ala Arg Glu Val Lys Gly
 10 15 20

gtc tcc cat gtc cac gac act gtt ggc ggc aag tgg cag gcc acc ttg 211
 Val Ser His Val His Asp Thr Val Gly Gly Lys Trp Gln Ala Thr Leu
 25 30 35

cac aca ctt aaa ccg ggg ccc tcc tgg ccg aaa ccg tca cag ttc act 259
 His Thr Leu Lys Pro Gly Pro Ser Trp Pro Lys Pro Ser Gln Phe Thr
 40 45 50

gcg cct aaa tcc acg tcc atc tgg ttt att gcg gta gca acc cac cca 307
 Ala Pro Lys Ser Thr Ser Ile Trp Phe Ile Ala Val Ala Thr His Pro
 55 60 65

cgt aac cca cgg gca cgc aaa ggt acc cta ctt ggt cgc ggt ggt ctt 355
 Arg Asn Pro Arg Ala Arg Lys Gly Thr Leu Leu Gly Arg Gly Gly Leu 85
 70 75 80

tac gaa ctc aaa gac act gat ctg aac ttt ctc aca gag cga cag gat 403
 Tyr Glu Leu Lys Asp Thr Asp Leu Asn Phe Leu Thr Glu Arg Gln Asp 100
 90 95

ttg ctc gcc aca tct acc tct cgt gac cca gag gat tgc cgt tta cgc 451
 Leu Leu Ala Thr Ser Thr Ser Arg Asp Pro Glu Asp Cys Arg Leu Arg 115
 105 110

ttt aat tcg cgt cac gat gca gca gca ttt tta cat gct aac gcc cgc 499
 Phe Asn Ser Arg His Asp Ala Ala Ala Phe Leu His Ala Asn Ala Arg 130
 120 125

cac atc aac aag ctt ttt cat cca gca cta ggt cat gct cgc tac gat 547
 His Ile Asn Lys Leu Phe His Pro Ala Leu Gly His Ala Arg Tyr Asp 145
 135 140

ctc ata gat gtg taagcacaac gcttagctta tga 582
 Leu Ile Asp Val 150
 150

<210> 2416
 <211> 153
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 2416
 Met Ser Arg Ile Ile Thr Ala Pro Val His Lys Pro Tyr Ile Ile Ala 15
 1 5 10

Arg Glu Val Lys Gly Val Ser His Val His Asp Thr Val Gly Gly Lys 30
 20 25

Trp Gln Ala Thr Leu His Thr Leu Lys Pro Gly Pro Ser Trp Pro Lys 45
 35 40

Pro Ser Gln Phe Thr Ala Pro Lys Ser Thr Ser Ile Trp Phe Ile Ala 60
 50 55

Val Ala Thr His Pro Arg Asn Pro Arg Ala Arg Lys Gly Thr Leu Leu 80
 65 70 75

Gly Arg Gly Gly Leu Tyr Glu Leu Lys Asp Thr Asp Leu Asn Phe Leu 95
 85 90

Thr Glu Arg Gln Asp Leu Leu Ala Thr Ser Thr Ser Arg Asp Pro Glu 110
 100 105

Asp Cys Arg Leu Arg Phe Asn Ser Arg His Asp Ala Ala Ala Phe Leu 125
 115 120

His Ala Asn Ala Arg His Ile Asn Lys Leu Phe His Pro Ala Leu Gly 140
 130 135

His Ala Arg Tyr Asp Leu Ile Asp Val 150
 145 150

<210> 2417
 <211> 1260
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1237)
 <223> RXA01778

<400> 2417
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tccatacata actgcgaaat tggtttagt ctttttcagt atg ctc tac caa cac 115
 Met Leu Tyr Gln His
 1 5

acc aca cgc ggc ctg atc att agt gac gcg atc atc gcg aaa atc agc 163
 Thr Thr Arg Gly Leu Ile Ile Ser Asp Ala Ile Ile Ala Lys Ile Ser
 10 15 20

caa gtc aac caa ctg ctg cta cta aga ccc acg ctg ttg caa gac aaa 211
 Gln Val Asn Gln Leu Leu Leu Leu Arg Pro Thr Leu Leu Gln Asp Lys
 25 30 35

gat atg cac cat gcg aca ttg agt agc gac acc cca tca att cgc agt 259
 Asp Met His His Ala Thr Leu Ser Ser Asp Thr Pro Ser Ile Arg Ser
 40 45 50

gcg cgt cgc tcc tat cgc gag aat aaa gcc gcc tat gcg acc acg agc 307
 Arg Arg Arg Ser Tyr Arg Gln Asn Lys Ala Ala Tyr Ala Thr Thr Ser
 55 60 65

acc atc aga aac cgt gag acc ttt ttc agc aca tct gat att gat ttc 355
 Thr Ile Arg Asn Arg Glu Thr Phe Phe Ser Thr Ser Asp Ile Asp Phe
 70 75 80 85

gcc ata ctc atg att cag gac gta caa gaa tct ctc gta tct ttt gac 403
 Ala Ile Leu Met Ile Gln Asp Val Gln Glu Ser Leu Val Ser Phe Asp
 90 95 100

ccc acc ttg gct caa gat atg aag cca aga acc aac gca gtc att tct 451
 Pro Thr Leu Ala Gln Asp Met Lys Pro Arg Thr Asn Ala Val Ile Ser
 105 110 115

gca ctc aat gag cta cgc gag cca ctg gat acc ttc tac cgt gcc cat 499
 Ala Leu Asn Glu Leu Arg Glu Pro Leu Asp Thr Phe Tyr Arg Ala His
 120 125 130

gaa tac ggt gac atc atc agc gat ggt gct tat gag ttc gat cat gct 547
 Glu Tyr Gly Asp Ile Ile Ser Asp Gly Ala Tyr Glu Phe Asp His Ala
 135 140 145

gcc att gat gca caa cac agc ctt agt gaa ctc gtt gcc ggt ctg cat 595
 Ala Ile Asp Ala Gln His Ser Leu Ser Glu Leu Val Ala Gly Leu His
 150 155 160 165

aat tat gac aac ctc atg ttt ccc cag gaa acc gct cgc ttg atg agt 643
 Asn Tyr Asp Asn Leu Met Phe Pro Gln Glu Thr Ala Pro Leu Met Ser
 170 175 180

gaa tcc aat ggc att cag ctg gct cag tac tat aag tcc acc aaa ctc 691
 Glu Ser Asn Gly Ile Gln Leu Ala Gln Tyr Tyr Lys Ser Thr Lys Leu
 185 190 195

gat gag tca caa ttg acg gtg gaa cct aat gag cct ggt atc agc att 739
 Asp Glu Ser Gln Leu Thr Val Glu Pro Asn Glu Pro Gly Ile Ser Ile
 200 205 210

atg tgg cac gcc cat gat ttc acc tgg tct tgc cta gtg cgc tat gac 787
 Met Trp His Ala His Asp Phe Thr Trp Ser Cys Leu Val Arg Tyr Asp
 215 220 225

gac atg aac cgt tac cct gag cat ttc agc att tct ttt aaa gac atg 835
 Asp Met Asn Arg Tyr Pro Glu His Phe Ser Ile Ser Phe Lys Asp Met
 230 235 240 245

ctg atc cct gaa cag atc tat act ttc cac ttc acc cca cgt gag gca 883
 Leu Ile Pro Glu Gln Ile Tyr Thr Phe His Phe Thr Pro Arg Glu Ala
 250 255 260

atg caa ctg cgc aag gga ctt ttt aat gcc atc gct gcc tac aag tct 931
 Met Gln Leu Arg Lys Gly Leu Phe Asn Ala Ile Ala Ala Tyr Lys Ser
 265 270 275

cag aca tgg ggt gat gag aac act gat ctc acc aag gct gaa ctc gaa 979
 Gln Thr Trp Gly Asp Glu Asn Thr Asp Leu Thr Lys Ala Glu Leu Glu
 280 285 290

ttt ggt ggc acc tcc atg acc ttc cgc gcc ggc ctc tca cag ctt agc 1027
 Phe Gly Gly Thr Ser Met Thr Phe Arg Ala Gly Leu Ser Gln Leu Ser
 295 300 305

gtc acc gga cct cct gat cac cgc cag gtg ttc tgc ttg tgc tct tct 1075
 Val Thr Gly Pro Pro Asp His Arg Gln Val Phe Cys Leu Ser Ser Ser
 310 315 320 325

ggt cgt gag gat cac aac acc ccg cca aac atg cga gac gga cat gtc 1123
 Gly Arg Glu Asp His Asn Thr Pro Pro Asn Met Arg Asp Gly His Val
 330 335 340

att gat att gcg gtt act caa ttg tcc acc ctg cgt aac ctc att cgg 1171
 Ile Asp Ile Ala Val Thr Gln Leu Ser Thr Leu Arg Asn Leu Ile Arg
 345 350 355

gta ctg tgc acc act cac ccg gat cat tca cca gca ctg cta cct tat 1219
 Val Leu Cys Thr Thr His Pro Asp His Ser Pro Ala Leu Leu Pro Tyr
 360 365 370

ggt cag cag tac acc atc taacatgctc taactcgacc ccg 1260
 Gly Gln Gln Tyr Thr Ile
 375

<210> 2418
 <211> 379
 <212> PRT
 <213> *Corynebacterium glutamicum*
 <400> 2418
 Met Leu Tyr Gln His Thr Thr Arg Gly Leu Ile Ile Ser Asp Ala Ile

1	5	10	15
Ile Ala Lys	Ile Ser Gln Val	Asn Gln Leu Leu Leu	Arg Pro Thr
	20	25	30
Leu Leu Gln	Asp Lys Asp Met	His His Ala Thr	Leu Ser Ser Asp Thr
	35	40	45
Pro Ser Ile	Arg Ser Arg Arg	Arg Ser Tyr Arg	Glu Asn Lys Ala Ala
	50	55	60
Tyr Ala Thr	Thr Ser Thr Ile	Arg Asn Arg Glu	Thr Phe Phe Ser Thr
	65	70	75
Ser Asp Ile	Asp Phe Ala Ile	Leu Met Ile Gln	Asp Val Gln Glu Ser
	85	90	95
Leu Val Ser	Phe Asp Pro Thr	Leu Ala Gln Asp	Met Lys Pro Arg Thr
	100	105	110
Asn Ala Val	Ile Ser Ala Leu	Asn Glu Leu Arg	Glu Pro Leu Asp Thr
	115	120	125
Phe Tyr Arg	Ala His Glu Tyr	Gly Asp Ile Ile	Ser Asp Gly Ala Tyr
	130	135	140
Glu Phe Asp	His Ala Ala Ile	Asp Ala Gln His	Ser Leu Ser Glu Leu
	145	150	155
Val Ala Gly	Leu His Asn Tyr	Asp Asn Leu Met	Phe Pro Gln Glu Thr
	165	170	175
Ala Pro Leu	Met Ser Glu Ser	Asn Gly Ile Gln	Leu Ala Gln Tyr Tyr
	180	185	190
Lys Ser Thr	Lys Leu Asp Glu	Ser Gln Leu Thr	Val Glu Pro Asn Glu
	195	200	205
Pro Gly Ile	Ser Ile Met Trp	His Ala His Asp	Phe Thr Trp Ser Cys
	210	215	220
Leu Val Arg	Tyr Asp Asp Met	Asn Arg Tyr Pro	Glu His Phe Ser Ile
	225	230	235
Ser Phe Lys	Asp Met Leu Ile	Pro Glu Gln Ile	Tyr Thr Phe His Phe
	245	250	255
Thr Pro Arg	Glu Ala Met Gln	Leu Arg Lys Gly	Leu Phe Asn Ala Ile
	260	265	270
Ala Ala Tyr	Lys Ser Gln Thr	Trp Gly Asp Glu	Asn Thr Asp Leu Thr
	275	280	285
Lys Ala Glu	Leu Glu Phe Gly	Gly Thr Ser Met	Thr Phe Arg Ala Gly
	290	295	300
Leu Ser Gln	Leu Ser Val Thr	Gly Pro Pro Asp	His Arg Gln Val Phe
	305	310	315
Cys Leu Ser	Ser Ser Gly Arg	Glu Asp His Asn	Thr Pro Pro Asn Met
	325	330	335

Arg Asp Gly His Val Ile Asp Ile Ala Val Thr Gln Leu Ser Thr Leu
340 345 350

Arg Asn Leu Ile Arg Val Leu Cys Thr Thr His Pro Asp His Ser Pro
355 360 365

Ala Leu Leu Pro Tyr Gly Gln Gln Tyr Thr Ile
370 375

<210> 2419

<211> 1542

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1519)

<223> RXA01779

<400> 2419

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ttgtcgcgct taaaatacta gaaagtaata taaaaaactc atg cgt tat act ccc 115
Met Arg Tyr Thr Pro
1 5

cgt acc cac cgc gca ctc gga ctt gct gca ctt acc gct aca gct ctc 163
Arg Thr His Arg Ala Leu Gly Leu Ala Ala Leu Thr Ala Thr Ala Leu
10 15 20

cta ctg agc tca tgc tgc acc acc gct gac ctt ctc ggc gcc gat tct 211
Leu Leu Ser Ser Cys Ser Thr Thr Ala Asp Leu Leu Gly Ala Asp Ser
25 30 35

gtg gcg cag gct gtc acc gat ggt ggc tct gcc ctt gat ccc act gca 259
Val Ala Gln Ala Val Thr Asp Gly Gly Ser Ala Leu Asp Pro Thr Ala
40 45 50

gct cat gtg ctc acc atc acc aat gcc act gca atg act ctt gct gag 307
Ala His Val Leu Thr Ile Thr Asn Ala Thr Ala Met Thr Leu Ala Glu
55 60 65

cta cca gaa aac acc gac cct gac gca gcc aat aac acg gag cca aca 355
Leu Pro Glu Asn Thr Asp Pro Asp Ala Ala Asn Asn Thr Glu Pro Thr
70 75 80 85

atg gcc caa agc gcc ctc aag cgt att tac ggt ctc gaa att gcc gcc 403
Met Ala Gln Ser Ala Leu Lys Arg Ile Tyr Gly Leu Glu Ile Ala Ala
90 95 100

gat ggc act ctg att gct gtc gca gcg cca tta acc tcg cga aat agt 451
Asp Gly Thr Leu Ile Ala Val Ala Pro Leu Thr Ser Arg Asn Ser
105 110 115

ggt tct gag cag cct act gtc gca gca atg gct gat cca gaa aac aat 499
Gly Ser Glu Gln Pro Thr Val Ala Ala Met Ala Asp Pro Glu Asn Asn
120 125 130

gct gaa ctc acc aca gca cat att ctt gag atc gac cca gcc aca gga 547

Ala Glu Leu Thr Thr	Ala His Ile Leu Glu Ile	Asp Pro Ala Thr Gly	
135	140	145	
act gcc aca cca cgt	caa gat att gct ctg act	gaa gat ttt cag acc	595
Thr Ala Thr Pro Arg	Gln Asp Ile Ala Leu Thr	Glu Asp Phe Gln Thr	
150	155	160	165
atg gct agc tct ttt	agc cag atc cgt aat	ggc tgg ggt act acc caa	643
Met Ala Ser Ser Phe	Ser Gln Ile Arg Asn	Gly Trp Gly Thr Thr Gln	
	170	175	180
ctc atc gga caa cac	cct gat gat ccc aag	caa cct att cgt tca gct	691
Leu Ile Gly Gln His	Pro Asp Asp Pro Lys	Gln Pro Ile Arg Ser Ala	
	185	190	195
gat acc tgg act gtc	acc ggc tcc act cag	atc acc ggc ttt aac acc	739
Asp Thr Trp Thr Val	Thr Gly Ser Thr Gln	Ile Thr Gly Phe Asn Thr	
	200	205	210
aac acc cca acg gga	acc gaa gat gct gcc	tac acc atg ccg gcg act	787
Asn Thr Pro Thr Gly	Thr Glu Asp Ala Ala	Tyr Thr Met Pro Ala Thr	
	215	220	225
gag cca gct gtg gga	ctg tgc gct cta gaa	tca ggc tcc gat gca cca	835
Glu Pro Ala Val Gly	Leu Cys Ala Leu Glu	Ser Gly Ser Asp Ala Pro	
	230	235	240
ctg gat gaa cac cgt	gag ctc agc acc agt	gca ttg cgt acc gca tca	883
Leu Asp Glu His Arg	Glu Leu Ser Thr Ser	Ala Leu Arg Thr Ala Ser	
	250	255	260
gta ttg tcg agc tct	gga tct gcc acc ctc	aag ctg cat gat cct atg	931
Val Leu Ser Ser Ser	Gly Ser Ala Thr Leu	Lys Leu His Asp Pro Met	
	265	270	275
gtc atg tct gct act	ggc att gtc caa gca	cgc gcc tat gtc gat ggc	979
Val Met Ser Ala Thr	Gly Ile Val Gln Ala	Arg Ala Tyr Val Asp Gly	
	280	285	290
gaa gtc att aac cag	cac gag att ggc gat	ctc cgc gag cag ctc ggt	1027
Glu Val Ile Asn Gln	His Glu Ile Gly Asp	Leu Arg Glu Gln Leu Gly	
	295	300	305
atc acc atc gaa gaa	tct gag gct gct caa	gca gaa tcg gat gcc caa	1075
Ile Thr Ile Glu Glu	Ser Glu Ala Ala Gln	Ala Glu Ser Asp Ala Gln	
	310	315	320
gca gcc acc gat cac	cca ctt gca gcc ctg	ggc tta agc aac ccc acc	1123
Ala Ala Thr Asp His	Pro Leu Ala Ala Leu	Gly Leu Ser Asn Pro Thr	
	330	335	340
agc tca gcg ttg gtt	cca ggt ctt gct gag	ctt gat tgt ctc agt gct	1171
Ser Ser Ala Leu Val	Pro Gly Leu Ala Glu	Leu Asp Cys Leu Ser Ala	
	345	350	355
gac cag gct gcc acc	tgg cat aac cgc gac	acc agc att ggc acc ggt	1219
Asp Gln Ala Ala Thr	Trp His Asn Arg Asp	Thr Ser Ile Gly Thr Gly	
	360	365	370
aag ccc agc gtg ctt	gct gtc atc aac	gcg gaa atg gcc gat gac ttt	1267
Lys Pro Ser Val Leu	Ala Val Ile Asn	Ala Glu Met Ala Asp Asp Phe	

375	380	385	
acc ctg cag ctg ttg agc tca ggt gcc acc act gcc gaa acg cag ctt			1315
Thr Leu Gln Leu Leu Ser Ser Gly Ala Thr Thr Ala Glu Thr Gln Leu			
390	395	400	405
gcc cag ctg ccg gat gaa acc gcg ttc gtg ctc att gac cca tca tct			1363
Ala Gln Leu Pro Asp Glu Thr Ala Phe Val Leu Ile Asp Pro Ser Ser			
	410	415	420
ggg gct gtt act gac ctg ttc ttt atc caa agt ctc aac act gat ctg			1411
Gly Ala Val Thr Asp Leu Phe Phe Ile Gln Ser Leu Asn Thr Asp Leu			
	425	430	435
ccg gca cca aca acc cag att aat tct att gct gtt gat gag cgc gac			1459
Pro Ala Pro Thr Thr Gln Ile Asn Ser Ile Ala Val Asp Glu Arg Asp			
	440	445	450
ccc aac atc atc tac gcc act ttt agc ggc gat gac cac ctg tac caa			1507
Pro Asn Ile Ile Tyr Ala Thr Phe Ser Gly Asp Asp His Leu Tyr Gln			
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atg atg ctg ggt tagttacaca actaactaac cag			1542
Met Met Leu Gly			
470			
<210> 2420			
<211> 473			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 2420			
Met Arg Tyr Thr Pro Arg Thr His Arg Ala Leu Gly Leu Ala Ala Leu			
1 5 10 15			
Thr Ala Thr Ala Leu Leu Leu Ser Ser Cys Ser Thr Thr Ala Asp Leu			
	20	25	30
Leu Gly Ala Asp Ser Val Ala Gln Ala Val Thr Asp Gly Gly Ser Ala			
	35	40	45
Leu Asp Pro Thr Ala Ala His Val Leu Thr Ile Thr Asn Ala Thr Ala			
	50	55	60
Met Thr Leu Ala Glu Leu Pro Glu Asn Thr Asp Pro Asp Ala Ala Asn			
	65	70	75
Asn Thr Glu Pro Thr Met Ala Gln Ser Ala Leu Lys Arg Ile Tyr Gly			
	85	90	95
Leu Glu Ile Ala Ala Asp Gly Thr Leu Ile Ala Val Ala Ala Pro Leu			
	100	105	110
Thr Ser Arg Asn Ser Gly Ser Glu Gln Pro Thr Val Ala Ala Met Ala			
	115	120	125
Asp Pro Glu Asn Asn Ala Glu Leu Thr Thr Ala His Ile Leu Glu Ile			
	130	135	140
Asp Pro Ala Thr Gly Thr Ala Thr Pro Arg Gln Asp Ile Ala Leu Thr			

145						150									155																		160
Glu	Asp	Phe	Gln	Thr	Met	Ala	Ser	Ser	Phe	Ser	Gln	Ile	Arg	Asn	Gly																		
				165						170					175																		
Trp	Gly	Thr	Thr	Gln	Leu	Ile	Gly	Gln	His	Pro	Asp	Asp	Pro	Lys	Gln																		
			180					185																									
Pro	Ile	Arg	Ser	Ala	Asp	Thr	Trp	Thr	Val	Thr	Gly	Ser	Thr	Gln	Ile																		
			195				200					205																					
Thr	Gly	Phe	Asn	Thr	Asn	Thr	Pro	Thr	Gly	Thr	Glu	Asp	Ala	Ala	Tyr																		
			210			215					220																						
Thr	Met	Pro	Ala	Thr	Glu	Pro	Ala	Val	Gly	Leu	Cys	Ala	Leu	Glu	Ser																		
			225		230					235																							
Gly	Ser	Asp	Ala	Pro	Leu	Asp	Glu	His	Arg	Glu	Leu	Ser	Thr	Ser	Ala																		
			245						250																								
Leu	Arg	Thr	Ala	Ser	Val	Leu	Ser	Ser	Ser	Gly	Ser	Ala	Thr	Leu	Lys																		
			260					265																									
Leu	His	Asp	Pro	Met	Val	Met	Ser	Ala	Thr	Gly	Ile	Val	Gln	Ala	Arg																		
			275					280																									
Ala	Tyr	Val	Asp	Gly	Glu	Val	Ile	Asn	Gln	His	Glu	Ile	Gly	Asp	Leu																		
			290			295					300																						
Arg	Glu	Gln	Leu	Gly	Ile	Thr	Ile	Glu	Glu	Ser	Glu	Ala	Ala	Gln	Ala																		
			305		310					315																							
Glu	Ser	Asp	Ala	Gln	Ala	Ala	Thr	Asp	His	Pro	Leu	Ala	Ala	Leu	Gly																		
			325						330																								
Leu	Ser	Asn	Pro	Thr	Ser	Ser	Ala	Leu	Val	Pro	Gly	Leu	Ala	Glu	Leu																		
			340					345																									
Asp	Cys	Leu	Ser	Ala</																													


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His Leu Thr Asp Leu Gly Leu Asp Pro Glu Gln Leu Ile Asn Glu Leu
      20      25      30

Pro Thr Ile Thr Tyr Asp Val Gln Pro His Asn Val Phe Val Leu Gln
      35      40      45

Phe Ser Thr Ala Asp Val Arg Val Tyr Gln Glu Gly Asn Thr Leu Phe
      50      55      60

Ile Arg Ser Ala Glu Leu Ile Asn Pro Glu Leu Arg Gln Arg Gln Arg
      65      70      75      80

Thr Gln Leu Asn Asp Asp Leu Asn Asn Pro Ala Ser Leu Arg Val Cys
      85      90      95

Asp Glu Ile Ser Gly Arg Ser Thr Val Phe Leu Lys Asp Lys Ser Val
      100     105     110

Val Thr His Asp His Gly Thr Asn Cys Cys Asp Ser Ala
      115     120     125

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<210> 2423
<211> 384
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(361)
<223> RXA01781

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<400> 2423
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gagatcagtg gccgcagcac cgtgttcttc aaagacaaaa gtg ttg tca ctc acg 115
Val Leu Ser Leu Thr
1 5

atc acg gga cca att gct gtg att ccg cat aat cct gat gaa gcc agc 163
Ile Thr Gly Pro Ile Ala Val Ile Pro His Asn Pro Asp Glu Ala Ser
10 15 20

gcc aag gct gtc gct acc aaa cat aag cac acc ttg tcc gcc gct acc 211
Ala Lys Ala Val Ala Thr Lys His Lys His Thr Leu Ser Gly Ala Thr
25 30 35

tct gat cac cct tat gcc gcc atg acg ctt aaa gac atg att gaa cag 259
Ser Asp His Pro Tyr Ala Gly Met Thr Leu Lys Asp Met Ile Glu Gln
40 45 50

ggc ttt acg ctc aca ccg ctg gaa ttc ccg ctc tgt gct gtc gat gat 307
Gly Phe Thr Leu Thr Pro Leu Glu Phe Pro Leu Cys Ala Val Asp Asp
55 60 65

cca aca gat tct gat cgc acc atg cac gtg atc aat gtt cgc gag cac 355
Pro Thr Asp Ser Asp Arg Thr Met His Val Ile Asn Val Arg Glu His
70 75 80 85

agt atg tagattctaa agtgcggtac aac 384
Ser Met

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<210> 2424

<211> 87

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2424

Val Leu Ser Leu Thr Ile Thr Gly Pro Ile Ala Val Ile Pro His Asn
 1 5 10 15

Pro Asp Glu Ala Ser Ala Lys Ala Val Ala Thr Lys His Lys His Thr
 20 25 30

Leu Ser Gly Ala Thr Ser Asp His Pro Tyr Ala Gly Met Thr Leu Lys
 35 40 45

Asp Met Ile Glu Gln Gly Phe Thr Leu Thr Pro Leu Glu Phe Pro Leu
 50 55 60

Cys Ala Val Asp Asp Pro Thr Asp Ser Asp Arg Thr Met His Val Ile
 65 70 75 80

Asn Val Arg Glu His Ser Met
 85

<210> 2425

<211> 519

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(496)

<223> RXA01782

<400> 2425

acgtgtgcaa ttgtgcgcgag cacagtatgt agattctaaa gtgcggtaca acctgtaccg 60

cccacacaat tccacccttt aagaaaagga cttagccatc atg acc acc ttc gcc 115
 Met Thr Thr Phe Ala
 1 5

ctt att gct agc ccc aac aat gtt gat ccc act gct gag tcc cca ctc 163
 Leu Ile Ala Ser Pro Asn Asn Val Asp Pro Thr Ala Glu Ser Pro Leu
 10 15 20

gcc att gaa atc cat acc gat gag gac agc agc tat cca cta ggg ctt 211
 Ala Ile Glu Ile His Thr Asp Glu Asp Ser Ser Tyr Pro Leu Gly Leu
 25 30 35

att gac tca gac cac ctg gtt cct gct gtg att tac ggc gat atg gtg 259
 Ile Asp Ser Asp His Leu Val Pro Ala Val Ile Tyr Gly Asp Met Val
 40 45 50

atc tac acc aaa aca ctg ctc gca cag acc cca cca gat gat gtg tcc 307
 Ile Tyr Thr Lys Thr Leu Leu Ala Gln Thr Pro Pro Asp Asp Val Ser
 55 60 65

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act gct agc gcc ttc ttc gac aaa ctc acc gca ctt gac gct cag ggt 355
Thr Ala Ser Ala Phe Phe Asp Lys Leu Thr Ala Leu Asp Ala Gln Gly
  70                75                80                85

cgc acc cgt gat ctg gtc tac agc gcc acc tac agc caa ctt gtt att 403
Arg Thr Arg Asp Leu Val Tyr Ser Ala Thr Tyr Ser Gln Leu Val Ile
                90                95                100

gcc ggc cac aac cgc act gta tta act gac gac tca gag ttc tac gat 451
Ala Gly His Asn Arg Thr Val Leu Thr Asp Asp Ser Glu Phe Tyr Asp
                105                110                115

gag ttt tac cag gtt att gag gct gct cct ggg gtg atc ttg aaa 496
Glu Phe Tyr Gln Val Ile Glu Ala Ala Pro Gly Val Ile Leu Lys
                120                125                130

tgatgtttat cgggcaacac ctc 519

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<210> 2426

<211> 132

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2426

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Met Thr Thr Phe Ala Leu Ile Ala Ser Pro Asn Asn Val Asp Pro Thr
  1                5                10                15

Ala Glu Ser Pro Leu Ala Ile Glu Ile His Thr Asp Glu Asp Ser Ser
                20                25                30

Tyr Pro Leu Gly Leu Ile Asp Ser Asp His Leu Val Pro Ala Val Ile
  35                40                45

Tyr Gly Asp Met Val Ile Tyr Thr Lys Thr Leu Leu Ala Gln Thr Pro
  50                55                60

Pro Asp Asp Val Ser Thr Ala Ser Ala Phe Phe Asp Lys Leu Thr Ala
  65                70                75                80

Leu Asp Ala Gln Gly Arg Thr Arg Asp Leu Val Tyr Ser Ala Thr Tyr
                85                90                95

Ser Gln Leu Val Ile Ala Gly His Asn Arg Thr Val Leu Thr Asp Asp
                100                105                110

Ser Glu Phe Tyr Asp Glu Phe Tyr Gln Val Ile Glu Ala Ala Pro Gly
                115                120                125

Val Ile Leu Lys
  130

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<210> 2427

<211> 360

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(337)

<223> RXA01783

<400> 2427

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cacacttagg ctaggctctt aacatgaagc agatagcgcc atg atc aat ctt ttt 115
 Met Ile Asn Leu Phe
 1 5

gct gca gcc ctg ccc gca ttc gag cct ttg agt att acc tcc ata ctc 163
 Ala Ala Ala Leu Pro Ala Phe Glu Pro Leu Ser Ile Thr Ser Ile Leu
 10 15 20

gtg ctc ggt gct gtg gca ttg atc tgt ggc ctc cct gtt ttt ctc gca 211
 Val Leu Gly Ala Val Ala Leu Ile Cys Gly Leu Pro Val Phe Leu Ala
 25 30 35

ctg gaa aaa agc gct gag ctc gat gat ctc ttc gca gca ctc atc atc 259
 Leu Glu Lys Ser Ala Glu Leu Asp Asp Leu Phe Ala Ala Leu Ile Ile
 40 45 50

gct gta ctt tta ggt ttt gct gct tat acg ttt gtg ctc ccc aag ctc 307
 Ala Val Leu Leu Gly Phe Ala Ala Tyr Thr Phe Val Leu Pro Lys Leu
 55 60 65

gtt gaa ttg ggc tgt act att tgc cag ctc tgactagcga cacttacact 357
 Val Glu Leu Gly Cys Thr Ile Cys Gln Leu
 70 75

ttc 360

<210> 2428

<211> 79

<212> PRT

<213> Corynebacterium glutamicum

<400> 2428

Met Ile Asn Leu Phe Ala Ala Ala Leu Pro Ala Phe Glu Pro Leu Ser
 1 5 10 15

Ile Thr Ser Ile Leu Val Leu Gly Ala Val Ala Leu Ile Cys Gly Leu
 20 25 30

Pro Val Phe Leu Ala Leu Glu Lys Ser Ala Glu Leu Asp Asp Leu Phe
 35 40 45

Ala Ala Leu Ile Ile Ala Val Leu Leu Gly Phe Ala Ala Tyr Thr Phe
 50 55 60

Val Leu Pro Lys Leu Val Glu Leu Gly Cys Thr Ile Cys Gln Leu
 65 70 75

<210> 2429

<211> 699

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(676)

<223> RXA01785

<400> 2429

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 Val Asp Gln Phe Val 5
 1

gag ttc ggc ggt gga caa gca aac att aac cct gat gga tca gcg acc 163
 Glu Phe Gly Gly Gln Ala Asn Ile Asn Pro Asp Gly Ser Ala Thr 20
 10 15

gtt gat tgg gag ggt tct ttc agc atc aac ttc tac gat ggt ttg gtg 211
 Val Asp Trp Glu Gly Ser Phe Ser Ile Asn Phe Tyr Asp Gly Leu Val 35
 25 30

ccg ttt acc atc acg aat ccg cac ctc gag gtt tct gta gct ggt act 259
 Pro Phe Thr Ile Thr Asn Pro His Leu Glu Val Ser Val Ala Gly Thr 50
 40 45

ggc gtt ttg act ggt gac ctc act agc tat gca gtg gag atg tgc aac 307
 Gly Val Leu Thr Gly Asp Leu Thr Ser Tyr Ala Val Glu Met Ser Asn 65
 55 60

ccg aat gag aaa acc ccg ttg act gac ttg tat gag gat gtc acg atc 355
 Pro Asn Glu Lys Thr Pro Leu Thr Asp Leu Tyr Glu Asp Val Thr Ile 85
 70 75 80

aca acg ttt ggg gga gtg aac ctt gat cct gaa ggt gtt gtg aca agc 403
 Thr Thr Phe Gly Gly Val Asn Leu Asp Pro Glu Gly Val Val Thr Ser 100
 90 95

aat cct gat tat gac gga gtg att gtt gat gtc cca ctg gat gcc acc 451
 Asn Pro Asp Tyr Asp Gly Val Ile Val Asp Val Pro Leu Asp Ala Thr 115
 105 110

tct cag gtt act tcc ggt gca ggt tgg gga gcg tgg ccg cag gcc ttc 499
 Ser Gln Val Thr Ser Gly Ala Gly Trp Gly Ala Trp Pro Gln Gly Phe 130
 120 125

ctt gat ttc cac ttt gat acc aac ttg cct tcc tac tgg tat tcc tca 547
 Leu Asp Phe His Phe Asp Thr Asn Leu Pro Ser Tyr Trp Tyr Ser Ser 145
 135 140

gat ggc gca ggt gat cct aag aag gcg cct atg agc ttt aat gtt gat 595
 Asp Gly Ala Gly Asp Pro Lys Lys Ala Pro Met Ser Phe Asn Val Asp 165
 150 155 160

ttc act aat ggt cca ggt ctg gtg aac agc caa ttg ctc cac agg caa 643
 Phe Thr Asn Gly Pro Gly Leu Val Asn Ser Gln Leu Leu His Arg Gln 180
 170 175

gtg atc tca atg ccg gaa acc aag gca gtc tgc tagttccatc ggaggcagaa 696
 Val Ile Ser Met Pro Glu Thr Lys Ala Val Ser 190
 185 190

gct 699

<210> 2430

<211> 192

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2430

Val Asp Gln Phe Val Glu Phe Gly Gly Gly Gln Ala Asn Ile Asn Pro
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Asp Gly Ser Ala Thr Val Asp Trp Glu Gly Ser Phe Ser Ile Asn Phe
 20 25 30

Tyr Asp Gly Leu Val Pro Phe Thr Ile Thr Asn Pro His Leu Glu Val
 35 40 45

Ser Val Ala Gly Thr Gly Val Leu Thr Gly Asp Leu Thr Ser Tyr Ala
 50 55 60

Val Glu Met Ser Asn Pro Asn Glu Lys Thr Pro Leu Thr Asp Leu Tyr
 65 70 75 80

Glu Asp Val Thr Ile Thr Thr Phe Gly Gly Val Asn Leu Asp Pro Glu
 85 90 95

Gly Val Val Thr Ser Asn Pro Asp Tyr Asp Gly Val Ile Val Asp Val
 100 105 110

Pro Leu Asp Ala Thr Ser Gln Val Thr Ser Gly Ala Gly Trp Gly Ala
 115 120 125

Trp Pro Gln Gly Phe Leu Asp Phe His Phe Asp Thr Asn Leu Pro Ser
 130 135 140

Tyr Trp Tyr Ser Ser Asp Gly Ala Gly Asp Pro Lys Lys Ala Pro Met
 145 150 155 160

Ser Phe Asn Val Asp Phe Thr Asn Gly Pro Gly Leu Val Asn Ser Gln
 165 170 175

Leu Leu His Arg Gln Val Ile Ser Met Pro Glu Thr Lys Ala Val Ser
 180 185 190

<210> 2431

<211> 564

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> {101}..(541)

<223> RXA01788

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cggaaactaa tcccgacgat gagaagcag gacgctagcc atg tct cgc agc tac 115
 Met Ser Arg Ser Tyr

1

5

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ccc atc tac atc att tct ttt gcc cca gcg gat gat ctc cac gcc gtt 163
Pro Ile Tyr Ile Ile Ser Phe Ala Pro Ala Asp Asp Leu His Gly Val
      10      15      20

gga gga ttc gag tgg gtt cca gca tca aca cca gaa aac aaa gct gcc 211
Gly Gly Phe Glu Trp Val Pro Ala Ser Thr Pro Glu Asn Lys Ala Ala
      25      30      35

gcc ttc acg acc ttt gat cgt caa ttc gat gat tct cgt aac aat ggt 259
Ala Phe Thr Thr Phe Asp Arg Gln Phe Asp Asp Ser Arg Asn Asn Gly
      40      45      50

ggc tgc cat att gtg cgt cta ctc aat atc tct gat ccc aat atc aca 307
Gly Ser His Ile Val Arg Leu Leu Asn Ile Ser Asp Pro Asn Ile Thr
      55      60      65

gcg gat atg acc caa gac gat att acc gcg tac ctc gac tca aac atc 355
Ala Asp Met Thr Gln Asp Asp Ile Thr Ala Tyr Leu Asp Ser Asn Ile
      70      75      80      85

gac cgc tgg gaa tcc acg gaa cat gcg ctc aag cag ttt gtc cca ctt 403
Asp Arg Trp Glu Ser Thr Glu His Ala Leu Lys Gln Phe Val Pro Leu
      90      95      100

aac gcg ggt gct gat cgc gta cct acc ggt ggt gcc gac gag cac att 451
Asn Ala Gly Ala Asp Arg Val Pro Thr Gly Gly Ala Asp Glu His Ile
      105      110      115

acc cac gcc tgc cgc ata ata act gtg cag cgt agc tgc aca cgg att 499
Thr His Ala Cys Arg Ile Ile Thr Val Gln Arg Ser Cys Thr Arg Ile
      120      125      130

cac ctg cgc tgt gga tgc atc cca aca cca caa cac cgc ccc 541
His Leu Arg Cys Gly Cys Ile Pro Thr Pro Gln His Arg Pro
      135      140      145

tagtgccata aatgctaggg gtg 564

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<210> 2432

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<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2432

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Met Ser Arg Ser Tyr Pro Ile Tyr Ile Ile Ser Phe Ala Pro Ala Asp
 1      5      10      15

Asp Leu His Gly Val Gly Gly Phe Glu Trp Val Pro Ala Ser Thr Pro
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Glu Asn Lys Ala Ala Ala Phe Thr Thr Phe Asp Arg Gln Phe Asp Asp
      35      40      45

Ser Arg Asn Asn Gly Gly Ser His Ile Val Arg Leu Leu Asn Ile Ser
      50      55      60

Asp Pro Asn Ile Thr Ala Asp Met Thr Gln Asp Asp Ile Thr Ala Tyr
      65      70      75      80

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[illegible]

gca ctc atg cgt gcg gtg aca cga aca ttg tgc act gca aac aac cct 499
Ala Leu Met Arg Ala Val Thr Arg Thr Leu Cys Thr Ala Asn Asn Pro
120 125 130

gta gaa gcg gcg act atc ttc cct gtg tct gtc gct aat gcc tta agc 547
Val Glu Arg Ala Thr Ile Phe Pro Val Ser Val Ala Asn Ala Leu Ser
135 140 145

atc gaa gcg ctg tgt tcc gaa tat cat gcg ttc cgc acc aag cag gtg 595
Ile Glu Ala Leu Cys Ser Glu Tyr His Ala Phe Arg Thr Lys Gln Val
150 155 160 165

ctc aac act gct gca ctc atc aat cct gat aac act ctt ata ccc atg 643
Leu Asn Thr Ala Ala Leu Ile Asn Pro Asp Asn Thr Leu Ile Pro Met
170 175 180

ttg ttg agc aaa gcg tat gag gca tac gcc tgg cac aag ggt gtc gaa 691
Leu Leu Ser Lys Ala Tyr Glu Ala Tyr Ala Trp His Lys Gly Val Glu
185 190 195

tcc gcg caa cga ggt agc aac cta gct cgt gag tac tac gca gga ctt 739
Ser Ala Gln Arg Gly Ser Asn Leu Ala Arg Glu Tyr Tyr Ala Gly Leu
200 205 210

atc tgaaaattca ctactcaact ctg 765
Ile

<210> 2434
<211> 214
<212> PRT
<213> Corynebacterium glutamicum

<400> 2434
Met Pro His Asn Pro Ile Glu Leu His Thr Asn Asp Val Leu Asp Ala
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Leu Asp Ile Asp Ala Ile Cys Asp Asp Val Phe Leu Tyr Thr Asp Phe
20 25 30
Glu His Thr Pro Gly Gln Leu Asp Arg Phe Glu Gln Leu Ala Phe Thr
35 40 45
Lys Ile Tyr Asp Met Leu Glu Thr Ala Ala Glu Lys Phe Pro Asp Val
50 55 60
Ala Ile Asn Asp Thr Leu Ser Thr Gly Asn His Ala Ala Glu Gln Tyr
65 70 75 80
Phe Leu Ala Asn Pro Gly Asn Ile Ile Val Leu Thr Ser Phe Ala Leu
85 90 95
Asn Gln Thr Asp Leu Arg Asp Leu Ile Ile Ser Pro Cys Ile Lys Tyr
100 105 110
Thr Ala His Ala Arg Ala Leu Met Arg Ala Val Thr Arg Thr Leu Cys
115 120 125
Thr Ala Asn Asn Pro Val Glu Arg Ala Thr Ile Phe Pro Val Ser Val


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130
135
140
Ala Asn Ala Leu Ser Ile Glu Ala Leu Cys Ser Glu Tyr His Ala Phe
145 150 155 160
Arg Thr Lys Gln Val Leu Asn Thr Ala Ala Leu Ile Asn Pro Asp Asn
165 170 175
Thr Leu Ile Pro Met Leu Leu Ser Lys Ala Tyr Glu Ala Tyr Ala Trp
180 185 190
His Lys Gly Val Glu Ser Ala Gln Arg Gly Ser Asn Leu Ala Arg Glu
195 200 205
Tyr Tyr Ala Gly Leu Ile
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tgatgatgat tcccctgata tcgatgagga cgataaacacc gtg ctc atc gcc gaa 115
Val Leu Ile Ala Glu
1 5
gac atc cgt gat atg gat gac tat ggc gaa gat cat cct gat ctt 160
Asp Ile Arg Asp Met Asp Asp Tyr Gly Glu Asp His Pro Asp Leu
10 15 20
taaagctcac tgттаagccc gca 183
<210> 2436
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<213> Corynebacterium glutamicum
<400> 2436
Val Leu Ile Ala Glu Asp Ile Arg Asp Met Asp Asp Tyr Gly Glu Asp
1 5 10 15
His Pro Asp Leu
20
<210> 2437
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<213> Corynebacterium glutamicum
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<223> RXA01791

<400> 2437

ccgcctgtgc aactaaccct gttgtgcagg cggttttctc tatctacacc aacaactcca 60

caacactatc	cggtc	caaat	ctagaaa	aga	gacaaccccc	atg	acc	tcc	ccc	acc	115
						Met	Thr	Ser	Pro	Thr	
						1				5	

acg	tta	aag	ccc	tgg	tct	att	cgc	gga	ccc	atc	gac	ggt	gaa	tac	acc	163
Thr	Leu	Lys	Pro	Trp	Ser	Ile	Arg	Gly	Pro	Ile	Asp	Gly	Glu	Tyr	Thr	
			10						15					20		

atg	ctt	gag	gca	tat	ccg	ttt	cag	tat	gta	gca	aat	act	cgc	ccg	gcc	211
Met	Leu	Glu	Ala	Tyr	Pro	Phe	Gln	Tyr	Val	Ala	Asn	Thr	Arg	Pro	Ala	
			25				30						35			

atc	atg	ctc	tac	gca	ctc	gat	gaa	aac	ggt	gta	ccg	gaa	caa	tat	gcc	259
Ile	Met	Leu	Tyr	Ala	Leu	Asp	Glu	Asn	Gly	Val	Pro	Glu	Gln	Tyr	Ala	
		40				45						50				

gac	ctc	acc	atc	aac	ctt	gcc	gat	gtg	gag	ctc	aag	caa	ctt	aac	cac	307
Asp	Leu	Thr	Ile	Asn	Leu	Ala	Asp	Val	Glu	Leu	Lys	Gln	Leu	Asn	His	
		55			60						65					

gtc	atc	att	aac	cca	gat	ctg	cac	gct	gat	gtt	acc	gaa	ctg	tgc	att	355
Val	Ile	Ile	Asn	Pro	Asp	Leu	His	Ala	Asp	Val	Thr	Glu	Leu	Cys	Ile	
	70				75					80				85		

agc	gcc	ggc	ctg	ctg	cga	cct	ggt	gtt	ctg	ggc	cag	cac	caa	gtc	ggg	403
Ser	Ala	Gly	Leu	Leu	Arg	Pro	Gly	Val	Leu	Gly	Gln	His	Gln	Val	Gly	
			90					95						100		

agc	acc	acc	gcc	aag	gtc	tac	cga	ctc	act	gag	cgt	gct	gat	ggc	tggt	451
Ser	Thr	Thr	Ala	Lys	Val	Tyr	Arg	Leu	Thr	Glu	Arg	Ala	Asp	Gly	Trp	
			105				110						115			

cta	cag	ctg	ttt	tagcagctac	ctgcgcctaa	tcc										486
Leu	Gln	Leu	Phe													
			120													

<210> 2438

<211> 121

<212> PRT

<213> Corynebacterium glutamicum

<400> 2438

Met	Thr	Ser	Pro	Thr	Thr	Leu	Lys	Pro	Trp	Ser	Ile	Arg	Gly	Pro	Ile
1				5					10					15	

Asp	Gly	Glu	Tyr	Thr	Met	Leu	Glu	Ala	Tyr	Pro	Phe	Gln	Tyr	Val	Ala
			20					25						30	

Asn	Thr	Arg	Pro	Ala	Ile	Met	Leu	Tyr	Ala	Leu	Asp	Glu	Asn	Gly	Val
		35				40					45				

Pro	Glu	Gln	Tyr	Ala	Asp	Leu	Thr	Ile	Asn	Leu	Ala	Asp	Val	Glu	Leu
	50					55					60				

Lys Gln Leu Asn His Val Ile Ile Asn Pro Asp Leu His Ala Asp Val
65 70 75 80

Thr Glu Leu Cys Ile Ser Ala Gly Leu Leu Arg Pro Gly Val Leu Gly
85 90 95

Gln His Gln Val Gly Ser Thr Thr Ala Lys Val Tyr Arg Leu Thr Glu
100 105 110

Arg Ala Asp Gly Trp Leu Gln Leu Phe
115 120

<210> 2439

<211> 396

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(373)

<223> RXA01792

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ccccaccca tactcaactcc aaaacaagaa agtagtcatc atg cct cag tac acc 115
Met Pro Gln Tyr Thr
1 5

atc aca atc acc gac gag cag aaa gct gtt cta cac agc ctc acc aac 163
Ile Thr Ile Thr Asp Glu Gln Lys Ala Val Leu His Ser Leu Thr Asn
10 15 20

ccc cat atc gcc act gct gaa cac gcc gct atc acc gca atc gag att 211
Pro His Ile Ala Thr Ala Glu His Gly Ala Ile Thr Ala Ile Glu Ile
25 30 35

cat gac gac cac gat gtt gtt gtc tat cac gtt caa cca gac gcc aca 259
His Asp Asp His Asp Val Val Val Tyr His Val Gln Pro Asp Gly Thr
40 45 50

cta act tac gag cgc ctt gtt gaa gcc ttc cat tac gcc tgg aca cgt 307
Leu Thr Tyr Glu Arg Leu Val Glu Gly Phe His Tyr Gly Trp Thr Arg
55 60 65

ttt gac agc gaa ggt ttt gag atc gac tcc gac aat aac cgc gtt gta 355
Phe Asp Ser Glu Gly Phe Glu Ile Asp Ser Asp Asn Asn Arg Val Val
70 75 80 85

gac gga ctc cgc gac gaa tagttaacaa caacgaccgc aca 396
Asp Gly Leu Arg Asp Glu
90

<210> 2440

<211> 91

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2440

Met Pro Gln Tyr Thr Ile Thr Ile Thr Asp Glu Gln Lys Ala Val Leu
 1 5 10 15

His Ser Leu Thr Asn Pro His Ile Ala Thr Ala Glu His Gly Ala Ile
 20 25 30

Thr Ala Ile Glu Ile His Asp Asp His Asp Val Val Val Tyr His Val
 35 40 45

Gln Pro Asp Gly Thr Leu Thr Tyr Glu Arg Leu Val Glu Gly Phe His
 50 55 60

Tyr Gly Trp Thr Arg Phe Asp Ser Glu Gly Phe Glu Ile Asp Ser Asp
 65 70 75 80

Asn Asn Arg Val Val Asp Gly Leu Arg Asp Glu
 85 90

<210> 2441

<211> 357

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

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<222> (101)..(334)

<223> RXA01793

<400> 2441

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gccactaaac acccaaacac aacaagaag aaacaccact atg gca caa tac cgc 115
 Met Ala Gln Tyr Arg
 1 5

gtc agt ttt atc gcg ctc gcc gag tca acc atc gag gtc gaa gca gac 163
 Val Ser Phe Ile Ala Leu Ala Glu Ser Thr Ile Glu Val Glu Ala Asp
 10 15 20

agt cct gaa gaa gca ctc gac cta gcc aat gca gaa ttt gac tac ccg 211
 Ser Pro Glu Glu Ala Leu Asp Leu Ala Asn Ala Glu Phe Asp Tyr Pro
 25 30 35

gtc acc ttg gcc ggc gat ccc tat gag ctg cac gac tgg gaa gca cgc 259
 Val Thr Leu Ala Gly Asp Pro Tyr Glu Leu His Asp Trp Glu Ala Arg
 40 45 50

gct gaa att gaa tgg ctc gat acc agc tcg acc ccg cag caa cgc ctt 307
 Ala Glu Ile Glu Trp Leu Asp Thr Ser Ser Thr Pro Gln Gln Arg Leu
 55 60 65

gga gaa cat gtc gtc aag atc gaa gat taaactcgat cattaacac 354
 Gly Glu His Val Val Lys Ile Glu Asp
 70 75

act 357

<210> 2442

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<211> 78
<212> PRT
<213> Corynebacterium glutamicum

<400> 2442
Met Ala Gln Tyr Arg Val Ser Phe Ile Ala Leu Ala Glu Ser Thr Ile
  1             5             10             15

Glu Val Glu Ala Asp Ser Pro Glu Glu Ala Leu Asp Leu Ala Asn Ala
      20             25             30

Glu Phe Asp Tyr Pro Val Thr Leu Ala Gly Asp Pro Tyr Glu Leu His
      35             40             45

Asp Trp Glu Ala Arg Ala Glu Ile Glu Trp Leu Asp Thr Ser Ser Thr
      50             55             60

Pro Gln Gln Arg Leu Gly Glu His Val Val Lys Ile Glu Asp
      65             70             75

<210> 2443
<211> 357
<212> DNA
<213> Corynebacterium glutamicum

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<223> RXA01794

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ctcgatcatt aaacacactc ttaagataag gacactaatt atg gca acc cac cgc 115
                                     Met Ala Thr His Arg
                                     1             5

gtt cat ttt gtc gca acc gca tcc gcc tac atc gac gtt gag gca gat 163
Val His Phe Val Ala Thr Ala Ser Ala Tyr Ile Asp Val Glu Ala Asp
      10             15             20

tcc ccc gaa gat gct ata gaa aaa gcg tat gat ctc gcc ggt gat ctg 211
Ser Pro Glu Asp Ala Ile Glu Lys Ala Tyr Asp Leu Ala Gly Asp Leu
      25             30             35

ccc gcc ctc atc gcc gac aac gaa ttt gat ctc ggt gaa tgg gag gta 259
Pro Gly Leu Ile Ala Asp Asn Glu Phe Asp Leu Gly Glu Trp Glu Val
      40             45             50

cag gcc gat gtc cag tgg cct gat aac tct gta cct cgc gag caa cgc 307
Gln Ala Asp Val Gln Trp Pro Asp Asn Ser Val Pro Arg Glu Gln Arg
      55             60             65

ctt gaa gag gcc gtt gac ctg ctc gat taaacagaat taactcaaac 354
Leu Glu Glu Gly Val Asp Leu Leu Asp
      70             75

ccc 357

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<210> 2444
 <211> 78
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2444
 Met Ala Thr His Arg Val His Phe Val Ala Thr Ala Ser Ala Tyr Ile
 1 5 10 15
 Asp Val Glu Ala Asp Ser Pro Glu Asp Ala Ile Glu Lys Ala Tyr Asp
 20 25 30
 Leu Ala Gly Asp Leu Pro Gly Leu Ile Ala Asp Asn Glu Phe Asp Leu
 35 40 45
 Gly Glu Trp Glu Val Gln Ala Asp Val Gln Trp Pro Asp Asn Ser Val
 50 55 60
 Pro Arg Glu Gln Arg Leu Glu Glu Gly Val Asp Leu Leu Asp
 65 70 75

<210> 2445
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1294)
 <223> RXA01799

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 aaaatcccca tagtttcccc cgggtgcatat cottaaaggt atg gaa att ccg ctg 115
 Met Glu Ile Pro Leu
 1 5
 ccc aca tcc ctt atc gat gtc atc act gat ggt gcc ctc ggc caa acc 163
 Pro Thr Ser Leu Ile Asp Val Ile Thr Asp Gly Ala Leu Gly Gln Thr
 10 15 20
 tgc att gat cag gca ttt gct gcc caa ttg ggg cga gtt act gga gtc 211
 Cys Ile Asp Gln Ala Phe Ala Ala Gln Leu Gly Arg Val Thr Gly Val
 25 30 35
 gaa ttc aac ctt tct gac gat aaa acc gcg gct gaa gtg agg atc aat 259
 Glu Phe Asn Leu Ser Asp Asp Lys Thr Ala Ala Glu Val Arg Ile Asn
 40 45 50
 aag gcg tcg ggg agt cct ttt gat acc acc ggt gaa gtc att gcg tgg 307
 Lys Ala Ser Gly Ser Pro Phe Asp Thr Thr Gly Glu Val Ile Ala Trp
 55 60 65
 att aat aat cag gaa ttt gag tgg gtc agc acg cgc ggt gag gat ttg 355
 Ile Asn Asn Gln Glu Phe Glu Trp Val Ser Thr Arg Gly Glu Asp Leu
 70 75 80 85
 gga ctg cct gaa ttg cag ggc att cag ccg ctc gac gat gat ctg atc 403
 Gly Leu Pro Glu Leu Gln Gly Ile Gln Pro Leu Asp Asp Asp Leu Ile

90										95					100					
acc	gcc	gca	cgc	acg	ctg	tat	agc	aat	gcg	ccg	gcg	ttc	atc	gcc	ccg	451				
Thr	Ala	Ala		Thr	Leu	Tyr	Ser	Asn	Ala	Pro	Ala	Phe	Ile	Ala	Pro					
105																				
ttg	cgc	gat	ggc	cgc	agg	gcg	ttg	gtt	gcg	atc	aat	cac	acg	cca	aaa	499				
Leu	Arg	Asp	Gly	Arg	Arg	Ala	Leu	Val	Ala	Ile	Asn	His	Thr	Pro	Lys					
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ctg	gtt	ggc	atc	cgt	cgc	acg	ctc	atc	gaa	ggc	ctg	cag	gcg	ctg	aag	547				
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Pro	Gly	Thr	Asp	Leu	Lys	Arg	Ala	Leu	Thr	Ser	Phe	Ala	Ala	Phe	Cys					
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gaa	ctg	ggc	atc	cga	ttc	gat	gac	aac	cgc	atc	tcc	ttc	agc	gat	ggc	643				
Glu	Leu	Gly	Ile	Arg	Phe	Asp	Asp	Asn	Arg	Ile	Ser	Phe	Ser	Asp	Gly					
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acc	tgc	ctg	ttg	ctt	cgt	ggc	ggc	aaa	gtc	atc	gaa	atc	gca	ggc	ggg	691				
Thr	Ser	Leu	Leu	Leu	Arg	Gly	Gly	Lys	Val	Ile	Glu	Ile	Ala	Gly	Gly					
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Leu	Ser	Leu	Arg	Asp	Val	Arg	Ala	Asp	Ala	Ala	Phe	Met	Ser	Ala	Glu					
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gac	cca	cac	acc	aac	gtg	gcg	acc	gtg	gca	aac	gaa	cac	caa	gtt	cac	835				
Asp	Pro	His	Thr	Asn	Val	Ala	Thr	Val	Ala	Asn	Glu	His	Gln	Val	His					
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Ala	Ile	Pro	Leu	Ala	Val	Ile	Asp	Gly	Thr	Arg	Trp	Val	Trp	Thr	Trp					
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Ser	Leu	Lys	Glu	Leu	Asn	Gly	Gln	Ala	Thr	Glu	Gly	Leu	Ala	Arg	Phe					
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ggc	ttc	gat	aac	ggc	cta	cta	ctg	ctc	acc	aat	gca	gag	atc	ctt	gct	979				
Gly	Phe	Asp	Asn	Gly	Leu	Leu	Leu	Leu	Leu	Asn	Ala	Glu	Ile	Leu	Ala					
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gag	gaa	gcc	acc	gca	ttc	aac	ctg	att	gat	gtg	gct	aaa	cag	gtg	ctc	1027				
Glu	Glu	Ala	Thr	Ala	Phe	Asn	Leu	Ile	Asp	Val	Ala	Lys	Gln	Val	Leu					
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Asn	Thr	Trp	Thr	His	Thr	Ile	Val	Gln	Gln	Pro	Asp	Gly	Thr	Gly	Ile					
310																				
gtc	ctg	ctg	ctg	gat	cat	cct	cgg	ctg	cag	ctt	ccg	cca	gca	tca	cat	1123				
Val	Leu	Leu	Leu	Asp	His	Pro	Arg	Leu	Gln	Leu	Pro	Pro	Ala	Ser	His					
330																				

gca gct gtt gag gcc acg ctg tat cac cag cta cca ggc gat att gat 1171
 Ala Ala Val Glu Ala Thr Leu Tyr His Gln Leu Pro Gly Asp Ile Asp
 345 350 355

gcc cgc cgc gcg gtg gcg tcc tat gca gct cac cga cag ctt cct ttt 1219
 Ala Arg Arg Ala Val Ala Ser Tyr Ala Ala His Arg Gln Leu Pro Phe
 360 365 370

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 Asp Gly Tyr Ala Leu Thr Val Glu Gly Gln Val Gly Val Thr Phe
 375 380 385

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 Asp Gly Glu His Leu Thr Lys Val Gly
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acc 1317

<210> 2446

<211> 398

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2446

Met Glu Ile Pro Leu Pro Thr Ser Leu Ile Asp Val Ile Thr Asp Gly
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Ala Leu Gly Gln Thr Cys Ile Asp Gln Ala Phe Ala Ala Gln Leu Gly
 20 25 30

Arg Val Thr Gly Val Glu Phe Asn Leu Ser Asp Asp Lys Thr Ala Ala
 35 40 45

Glu Val Arg Ile Asn Lys Ala Ser Gly Ser Pro Phe Asp Thr Thr Gly
 50 55 60

Glu Val Ile Ala Trp Ile Asn Asn Gln Glu Phe Glu Trp Val Ser Thr
 65 70 75 80

Arg Gly Glu Asp Leu Gly Leu Pro Glu Leu Gln Gly Ile Gln Pro Leu
 85 90 95

Asp Asp Asp Leu Ile Thr Ala Ala Arg Thr Leu Tyr Ser Asn Ala Pro
 100 105 110

Ala Phe Ile Ala Pro Leu Arg Asp Gly Arg Arg Ala Leu Val Ala Ile
 115 120 125

Asn His Thr Pro Lys Leu Val Gly Ile Arg Arg Thr Leu Ile Glu Gly
 130 135 140

Leu Gln Ala Leu Lys Pro Gly Thr Asp Leu Lys Arg Ala Leu Thr Ser
 145 150 155 160

Phe Ala Ala Phe Cys Glu Leu Gly Ile Arg Phe Asp Asp Asn Arg Ile
 165 170 175

Ser Phe Ser Asp Gly Thr Ser Leu Leu Leu Arg Gly Gly Lys Val Ile
 180 185 190

Glu Ile Ala Gly Gly Leu Ser Leu Arg Asp Val Arg Ala Asp Ala Ala
 195 200 205
 Phe Met Ser Ala Glu His Gln Leu Leu Phe Asp Ala Ile Ser Ser Ser
 210 215 220
 His Asn Val Thr Phe Asp Pro His Thr Asn Val Ala Thr Val Ala Asn
 225 230 235 240
 Glu His Gln Val His Ala Ile Pro Leu Ala Val Ile Asp Gly Thr Arg
 245 250 255
 Trp Val Trp Thr Trp Ser Leu Lys Glu Leu Asn Gly Gln Ala Thr Glu
 260 265 270
 Gly Leu Ala Arg Phe Gly Phe Asp Asn Gly Leu Leu Leu Thr Asn
 275 280 285
 Ala Glu Ile Leu Ala Glu Glu Ala Thr Ala Phe Asn Leu Ile Asp Val
 290 295 300
 Ala Lys Gln Val Leu Asn Thr Trp Thr His Thr Ile Val Gln Gln Pro
 305 310 315 320
 Asp Gly Thr Gly Ile Val Leu Leu Leu Asp His Pro Arg Leu Gln Leu
 325 330 335
 Pro Pro Ala Ser His Ala Ala Val Glu Ala Thr Leu Tyr His Gln Leu
 340 345 350
 Pro Gly Asp Ile Asp Ala Arg Arg Ala Val Ala Ser Tyr Ala Ala His
 355 360 365
 Arg Gln Leu Pro Phe Asp Gly Tyr Ala Leu Thr Val Glu Gly Gln Gln
 370 375 380
 Val Gly Val Thr Phe Asp Gly Glu His Leu Thr Lys Val Gly
 385 390 395

<210> 2447

<211> 843

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(820)

<223> RXA01800

<400> 2447

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tggggcccatg ttgtcacaaat gcttgaagaa gggtagggca gtg aag ccg ctg ggc 115
 Val Lys Pro Leu Gly
 1 5

aag atc gcc gtt cct tgg act tgg tac ctg gga att gtt ggg gtc atc 163
 Lys Ile Ala Val Pro Trp Thr Trp Tyr Leu Gly Ile Val Gly Val Ile
 10 15 20

ata ttt gat gtg gtg gca gca ata acg atg ctc acc ctc gtg ccc aac 211
 Ile Phe Asp Val Val Ala Ala Ile Thr Met Leu Thr Leu Val Pro Asn
 25 30 35

aaa atg ccc gaa aga gtc aac agt ggg ctt gtc gcg ctg ggt gga tcg 259
 Lys Met Pro Glu Arg Val Asn Ser Gly Leu Val Ala Leu Gly Gly Ser
 40 45 50

tat gca ccc ccg atg agc cgg gaa aca ctc att gcc aga gtc att gcc 307
 Tyr Ala Pro Pro Met Ser Arg Glu Thr Leu Ile Ala Arg Val Ile Ala
 55 60 65

ggt gca gtg ctg gtt ctg gtg att tct tta ggt att tcg ctg ctg att 355
 Gly Ala Val Leu Val Leu Val Ile Ser Leu Gly Ile Ser Leu Leu Ile
 70 75 80 85

tcc gcg cag tcc aag aac ctc gcg tcc gat cac ccg gat gca tct gcc 403
 Ser Ala Gln Ser Lys Asn Leu Ala Ser Asp His Pro Asp Ala Ser Ala
 90 95 100

att cag att gct cgg cgt tgg gcg ttt ttg aac aat att caa agc tgt 451
 Ile Gln Ile Ala Arg Arg Trp Ala Phe Leu Asn Asn Ile Gln Ser Cys
 105 110 115

atc ggc tgg ttt agt ttc ttc ctc gca gcg att ttg agc atc tca tcg 499
 Ile Gly Trp Phe Ser Phe Phe Leu Ala Ala Ile Leu Ser Ile Ser Ser
 120 125 130

cta aga ctc aac ggc cca ggt gcc acc acg cat ctt gag atg gcc gtt 547
 Leu Arg Leu Leu Asn Gly Pro Gly Ala Thr Thr His Leu Glu Met Ala Val
 135 140 145

tac atc atc gct gtg tcg gtg ttg gct tgg gcg ttg atg att tcc ttg 595
 Tyr Ile Ile Ala Val Ser Val Leu Ala Trp Ala Leu Met Ile Ser Leu
 150 155 160 165

cga cgc ggc cag gtg gcg att gat cgt gcc att cca att ccg gaa gat 643
 Arg Arg Gly Gln Val Ala Ile Asp Arg Ala Ile Pro Ile Arg Glu Asp
 170 175 180

gat tcc gaa ctg aaa tgg ggc atg atc tac cac gat gct tca gac aaa 691
 Asp Ser Glu Leu Lys Trp Gly Met Ile Tyr His Asp Ala Ser Asp Lys
 185 190 195

cga gtt ttc gtg gaa ctc gat gat ggc cac acg acc gtc atc aac atg 739
 Arg Val Phe Val Glu Leu Asp Asp Gly His Thr Thr Val Ile Asn Met
 200 205 210

gcg cgc ggg gga gcg tgg ctg ctc atc gca gtg atg gtg ctg cct gcg 787
 Ala Arg Gly Gly Ala Trp Leu Leu Ile Ala Val Met Val Leu Pro Ala
 215 220 225

ctg gcc atc gtc ggt tgg gtt ttg cta gaa aac tagccccacct ttgttaaatg 840
 Leu Ala Ile Val Gly Trp Val Leu Leu Glu Asn
 230 235 240

ctc 843

<211> 240

<212> PRT

<213> Corynebacterium glutamicum

<400> 2448

Val Lys Pro Leu Gly Lys Ile Ala Val Pro Trp Thr Trp Tyr Leu Gly
 1 5 10 15

Ile Val Gly Val Ile Ile Phe Asp Val Val Ala Ala Ile Thr Met Leu
 20 25 30

Thr Leu Val Pro Asn Lys Met Pro Glu Arg Val Asn Ser Gly Leu Val
 35 40 45

Ala Leu Gly Gly Ser Tyr Ala Pro Pro Met Ser Arg Glu Thr Leu Ile
 50 55 60

Ala Arg Val Ile Ala Gly Ala Val Leu Val Leu Val Ile Ser Leu Gly
 65 70 75 80

Ile Ser Leu Leu Ile Ser Ala Gln Ser Lys Asn Leu Ala Ser Asp His
 85 90 95

Pro Asp Ala Ser Ala Ile Gln Ile Ala Arg Arg Trp Ala Phe Leu Asn
 100 105 110

Asn Ile Gln Ser Cys Ile Gly Trp Phe Ser Phe Phe Leu Ala Ala Ile
 115 120 125

Leu Ser Ile Ser Ser Leu Arg Leu Asn Gly Pro Gly Ala Thr Thr His
 130 135 140

Leu Glu Met Ala Val Tyr Ile Ile Ala Val Ser Val Leu Ala Trp Ala
 145 150 155 160

Leu Met Ile Ser Leu Arg Arg Gly Gln Val Ala Ile Asp Arg Ala Ile
 165 170 175

Pro Ile Arg Glu Asp Asp Ser Glu Leu Lys Trp Gly Met Ile Tyr His
 180 185 190

Asp Ala Ser Asp Lys Arg Val Phe Val Glu Leu Asp Asp Gly His Thr
 195 200 205

Thr Val Ile Asn Met Ala Arg Gly Gly Ala Trp Leu Leu Ile Ala Val
 210 215 220

Met Val Leu Pro Ala Leu Ala Ile Val Gly Trp Val Leu Leu Glu Asn
 225 230 235 240

<210> 2449

<211> 444

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(421)

<223> RXA01804

<400> 2449

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ttttgggtca aagttttgtg aaacgaagta agcttaagtt atg cat atc gtc aac 115
 Met His Ile Val Asn
 1 5

att cgc ttc aag ccc aag gct aag tac gtg gat aca ttc cgc tac aca 163
 Ile Arg Phe Lys Pro Lys Ala Lys Tyr Val Asp Thr Phe Arg Tyr Thr
 10 15 20

gtc gac aaa ttc act gag tca acc agg aca gag gaa ggc tgt ctc tac 211
 Val Asp Lys Phe Thr Glu Ser Thr Arg Thr Glu Glu Gly Cys Leu Tyr
 25 30 35

ttt gat tgg ttc cgc aac acc gat tac cca ggc gag tac ctt gta att 259
 Phe Asp Trp Phe Arg Asn Thr Asp Tyr Pro Gly Glu Tyr Leu Val Ile
 40 45 50

ggg ggt tgg acg gat gaa ggt gcg acg gaa cat aag aag agc gag cac 307
 Gly Val Trp Thr Asp Glu Gly Ala Thr Glu His Lys Lys Ser Glu His
 55 60 65

ttc ttg cga gct caa gaa aca ctt cca ccg ttg ctg caa caa act cca 355
 Phe Leu Arg Ala Gln Glu Thr Leu Pro Pro Leu Leu Gln Gln Thr Pro
 70 75 80 85

atg att att cag agt gag ttt tcc aag aag aag ggt tgg gaa cgt ttc 403
 Met Ile Ile Gln Ser Glu Phe Ser Lys Lys Lys Gly Trp Glu Arg Phe
 90 95 100

agc gat ttc acc gtc tac taaggagccc gcaaaagctt tgt 444
 Ser Asp Phe Thr Val Tyr
 105

<210> 2450

<211> 107

<212> PRT

<213> Corynebacterium glutamicum

<400> 2450

Met His Ile Val Asn Ile Arg Phe Lys Pro Lys Ala Lys Tyr Val Asp
 1 5 10 15

Thr Phe Arg Tyr Thr Val Asp Lys Phe Thr Glu Ser Thr Arg Thr Glu
 20 25 30

Glu Gly Cys Leu Tyr Phe Asp Trp Phe Arg Asn Thr Asp Tyr Pro Gly
 35 40 45

Glu Tyr Leu Val Ile Gly Val Trp Thr Asp Glu Gly Ala Thr Glu His
 50 55 60

Lys Lys Ser Glu His Phe Leu Arg Ala Gln Glu Thr Leu Pro Pro Leu
 65 70 75 80

Leu Gln Gln Thr Pro Met Ile Ile Gln Ser Glu Phe Ser Lys Lys Lys

85

90

95

Gly Trp Glu Arg Phe Ser Asp Phe Thr Val Tyr
100 105

<210> 2451

<211> 453

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(430)

<223> RXA01805

<400> 2451

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ttcccagcct agtctgaact ggctaaacaa gatcgggtaca gtg gtg gtc gtg att 115
Val Val Val Val Ile
1 5

ttg att aat gtg aaa ttc aag cca ttg cca gaa tat gta gac acc ttc 163
Leu Ile Asn Val Lys Phe Lys Pro Leu Pro Glu Tyr Val Asp Thr Phe
10 15 20

cgc gag cag gta gcg gag ttt aca gaa aag acc cgt gcg gaa gaa gga 211
Arg Glu Gln Val Ala Glu Phe Thr Glu Lys Thr Arg Ala Glu Glu Gly
25 30 35

aac atc ttc ttc gat tgg tca att aac acc gac aac cca aac gag ttc 259
Asn Ile Phe Phe Asp Trp Ser Ile Asn Thr Asp Asn Pro Asn Glu Phe
40 45 50

atc ctc atc gaa gca ttc cag gac gac gct gcc gaa gct cac gtc aac 307
Ile Leu Ile Glu Ala Phe Gln Asp Asp Ala Ala Glu Ala His Val Asn
55 60 65

agc gac cac ttc aag gcg gcc tgt gag ctg ttc cca acc atc ctg tct 355
Ser Asp His Phe Lys Ala Ala Cys Glu Leu Phe Pro Thr Ile Leu Ser
70 75 80 85

gag acc cca gag atc atc aac acc ctt atc gag ggc aag act gag tgg 403
Glu Thr Pro Glu Ile Ile Asn Thr Leu Ile Glu Gly Lys Thr Glu Trp
90 95 100

gac cgc atg gca gag ttc gca gtc aac taaaatatga cctttgctgg 450
Asp Arg Met Ala Glu Phe Ala Val Asn
105 110

ttg 453

<210> 2452

<211> 110

<212> PRT

<213> Corynebacterium glutamicum

<400> 2452

Val Val Val Val Ile Leu Ile Asn Val Lys Phe Lys Pro Leu Pro Glu

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      1             5             10             15
Tyr Val Asp Thr Phe Arg Glu Gln Val Ala Glu Phe Thr Glu Lys Thr
      20             25             30
Arg Ala Glu Glu Gly Asn Ile Phe Phe Asp Trp Ser Ile Asn Thr Asp
      35             40             45
Asn Pro Asn Glu Phe Ile Leu Ile Glu Ala Phe Gln Asp Asp Ala Ala
      50             55             60
Glu Ala His Val Asn Ser Asp His Phe Lys Ala Ala Cys Glu Leu Phe
      65             70             75             80
Pro Thr Ile Leu Ser Glu Thr Pro Glu Ile Ile Asn Thr Leu Ile Glu
      85             90             95
Gly Lys Thr Glu Trp Asp Arg Met Ala Glu Phe Ala Val Asn
      100             105             110

<210> 2453
<211> 603
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(580)
<223> RXA01806

<400> 2453
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accagtgacc ccgcacacat ttcatgaagg gagttaaac atg agt tcg ctc gac 115
                                     Met Ser Ser Leu Asp
                                     1             5

aat gcc ccg ctg ctg gaa ttg gat gtt cag gaa tgg gta aac cac gaa 163
Asn Ala Pro Leu Leu Glu Leu Asp Val Gln Glu Trp Val Asn His Glu
      10             15             20

ggc ttg agc aat gag gac ctg cgc ggc aag gtt gtg gtg gtg gag gtg 211
Gly Leu Ser Asn Glu Asp Leu Arg Gly Lys Val Val Val Val Glu Val
      25             30             35

ttt cag atg cta tgc cct gga tgc gtg aat cac ggt gtc cct cag gct 259
Phe Gln Met Leu Cys Pro Gly Cys Val Asn His Gly Val Pro Gln Ala
      40             45             50

caa aaa atc cac cgc atg att gat gaa tcc caa gtg caa gtc atc ggg 307
Gln Lys Ile His Arg Met Ile Asp Glu Ser Gln Val Gln Val Ile Gly
      55             60             65

ctg cac agc gtg ttt gag cac cat gat gtg atg aca cct gag gct ttg 355
Leu His Ser Val Phe Glu His His Asp Val Met Thr Pro Glu Ala Leu
      70             75             80             85

aaa gtg ttc atc gat gag ttt ggg atc aag ttc ccc gtg gca gtg gat 403
Lys Val Phe Ile Asp Glu Phe Gly Ile Lys Phe Pro Val Ala Val Asp
      90             95             100

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atg ccg agg gaa ggc cag cgg att cct tcg acg atg aaa aag tat cgt 451
Met Pro Arg Glu Gly Gln Arg Ile Pro Ser Thr Met Lys Lys Tyr Arg
      105      110      115

ttg gaa gga acg ccc agc atc att ttg gct gat cga aaa gga cgg att 499
Leu Glu Gly Thr Pro Ser Ile Ile Leu Ala Asp Arg Lys Gly Arg Ile
      120      125      130

cgt cag gtg cag ttc ggg cag gtt gat gat ttc gtg ctg gga ttg ctg 547
Arg Gln Val Gln Phe Gly Gln Val Asp Asp Phe Val Leu Gly Leu Leu
      135      140      145

ctc ggc agt ttg ctg tca gag acg gac gaa acc taaagcgctt tggctctgcag 600
Leu Gly Ser Leu Leu Ser Glu Thr Asp Glu Thr
      150      155      160

gcc 603

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<210> 2454

<211> 160

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2454

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Met Ser Ser Leu Asp Asn Ala Pro Leu Leu Glu Leu Asp Val Gln Glu
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Trp Val Asn His Glu Gly Leu Ser Asn Glu Asp Leu Arg Gly Lys Val
      20      25      30

Val Val Val Glu Val Phe Gln Met Leu Cys Pro Gly Cys Val Asn His
      35      40      45

Gly Val Pro Gln Ala Gln Lys Ile His Arg Met Ile Asp Glu Ser Gln
      50      55      60

Val Gln Val Ile Gly Leu His Ser Val Phe Glu His His Asp Val Met
      65      70      75      80

Thr Pro Glu Ala Leu Lys Val Phe Ile Asp Glu Phe Gly Ile Lys Phe
      85      90      95

Pro Val Ala Val Asp Met Pro Arg Glu Gly Gln Arg Ile Pro Ser Thr
      100      105      110

Met Lys Lys Tyr Arg Leu Glu Gly Thr Pro Ser Ile Ile Leu Ala Asp
      115      120      125

Arg Lys Gly Arg Ile Arg Gln Val Gln Phe Gly Gln Val Asp Asp Phe
      130      135      140

Val Leu Gly Leu Leu Leu Gly Ser Leu Leu Ser Glu Thr Asp Glu Thr
      145      150      155      160

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<210> 2455

<211> 855
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(832)
 <223> RXA01816

<400> 2455
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 gttagagtcc ttcttccct gccagaaagg cacctcacag gtg caa tta tta cac 115
 Val Gln Leu Leu His
 1 5
 acc ccc gca gcc ata tcc att tcc ttc gac gac ccc aac ctc atc tct 163
 Thr Pro Ala Ala Ile Ser Ile Ser Phe Asp Asp Pro Asn Leu Ile Ser
 10 15 20
 acc gca ggg ctg gtc ccg acc atg gcc ctg gcc gag gac cgg tta aca 211
 Thr Ala Gly Leu Val Pro Thr Met Ala Leu Ala Glu Asp Arg Leu Thr
 25 30 35
 gta cca acc gac aaa ggt gct aac cca ggt gcc aaa atc acg acc ctc 259
 Val Pro Thr Asp Lys Gly Ala Asn Pro Gly Ala Lys Ile Thr Thr Leu
 40 45 50
 att gcg ggg atg gtc gcc ggt gcc gac tcc atc gac gat atc gat gca 307
 Ile Ala Gly Met Val Ala Gly Ala Asp Ser Ile Asp Asp Ile Asp Ala
 55 60 65
 ctc cgc cac ggc ggt atg cac cga ctc ttt gac tgg atc tac gcc ccc 355
 Leu Arg His Gly Gly Met His Arg Leu Phe Asp Trp Ile Tyr Ala Pro
 70 75 80 85
 tcc acg ttg ggg tcg ttc ctc cgg gcc ttt acc ttc ggg cat gtc cgc 403
 Ser Thr Leu Gly Ser Phe Leu Arg Ala Phe Thr Phe Gly His Val Arg
 90 95 100
 caa ctc gac gct gtg gcc tcc cgg ttc ctg gtg ggt ctg gca aca cag 451
 Gln Leu Asp Ala Val Ala Ser Arg Phe Leu Val Gly Leu Ala Thr Gln
 105 110 115
 gcc ccg gcc ctg gtc ccg gtt gat gct tct acc agt gat tac gtc ttc 499
 Ala Pro Ala Leu Val Pro Val Asp Ala Ser Thr Ser Asp Tyr Val Phe
 120 125 130
 atc gat gtt gat gac acc atc att aag gtc cac gga cat cag aaa caa 547
 Ile Asp Val Asp Asp Thr Ile Ile Lys Val His Gly His Gln Lys Gln
 135 140 145
 ggc gct ggt ttt ggt tac tcc ggt atc cgt gga ctc aac gcc ctg ctg 595
 Gly Ala Gly Phe Gly Tyr Ser Gly Ile Arg Gly Leu Asn Ala Leu Leu
 150 155 160 165
 gcc aca gtg acc aca cca gag tca gca cca gtg gtc gtg gcc caa cga 643
 Ala Thr Val Thr Thr Pro Glu Ser Ala Pro Val Val Val Ala Gln Arg
 170 175 180
 tta cgg aaa gga tcg tgc ggt tcc ccg cgg ggt gca gcc cgg ttg att 691

Leu Arg Lys Gly Ser Cys Gly Ser Pro Arg Gly Ala Gly Arg Leu Ile
 185 190 195
 gct gat gcg gtg gct acc acc cgg cgt ttg ccg ggg atg gag gat gag 739
 Ala Asp Ala Val Ala Thr Thr Arg Arg Leu Pro Gly Met Glu Asp Glu
 200 205 210
 aag atc ctt tta cgc gcg gat tct gcc ttt tat ggc cat ccc agt atc 787
 Lys Ile Leu Leu Arg Ala Asp Ser Ala Phe Tyr Gly His Pro Ser Ile
 215 220 225
 agt gct gcg atc aag gca ggg gcg gat gtg tct tca cgg tgc gga 832
 Ser Ala Ala Ile Lys Ala Gly Ala Asp Val Ser Arg Cys Gly
 230 235 240
 tgacccccaa tgtcaagaaa gcg 855

<210> 2456

<211> 244

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2456

Val Gln Leu Leu His Thr Pro Ala Ala Ile Ser Ile Ser Phe Asp Asp
 1 5 10 15
 Pro Asn Leu Ile Ser Thr Ala Gly Leu Val Pro Thr Met Ala Leu Ala
 20 25 30
 Glu Asp Arg Leu Thr Val Pro Thr Asp Lys Gly Ala Asn Pro Gly Ala
 35 40 45
 Lys Ile Thr Thr Leu Ile Ala Gly Met Val Ala Gly Ala Asp Ser Ile
 50 55 60
 Asp Asp Ile Asp Ala Leu Arg His Gly Gly Met His Arg Leu Phe Asp
 65 70 75 80
 Trp Ile Tyr Ala Pro Ser Thr Leu Gly Ser Phe Leu Arg Ala Phe Thr
 85 90 95
 Phe Gly His Val Arg Gln Leu Asp Ala Val Ala Ser Arg Phe Leu Val
 100 105 110
 Gly Leu Ala Thr Gln Ala Pro Ala Leu Val Pro Val Asp Ala Ser Thr
 115 120 125
 Ser Asp Tyr Val Phe Ile Asp Val Asp Asp Thr Ile Ile Lys Val His
 130 135 140
 Gly His Gln Lys Gln Gly Ala Gly Phe Gly Tyr Ser Gly Ile Arg Gly
 145 150 155 160
 Leu Asn Ala Leu Leu Ala Thr Val Thr Thr Pro Glu Ser Ala Pro Val
 165 170 175
 Val Val Ala Gln Arg Leu Arg Lys Gly Ser Cys Gly Ser Pro Arg Gly
 180 185 190
 Ala Gly Arg Leu Ile Ala Asp Ala Val Ala Thr Thr Arg Arg Leu Pro

195	200	205
Gly Met Glu Asp Glu Lys Ile Leu Leu Arg Ala Asp Ser Ala Phe Tyr		
210	215	220
Gly His Pro Ser Ile Ser Ala Ala Ile Lys Ala Gly Ala Asp Val Ser		
225	230	240
Ser Arg Cys Gly		

<210> 2457

<211> 756

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(733)

<223> RXA01817

<400> 2457

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ctgcgatcaa ggcagggg	cg	gatgtgtctt	cacggtgcgg	atg acc ccc aat gtc	115
				Met Thr Pro Asn Val	
				1 5	

aag aaa gcg atc gcc cag gtt cct gat gat gcg tgg cag aca att aag	163
Lys Lys Ala Ile Ala Gln Val Pro Asp Asp Ala Trp Gln Thr Ile Lys	
	10 15 20

tac acc aac gcg atc ttc gac gag gac acc ggg cgc tgg atc tcg gtg	211
Tyr Thr Asn Ala Ile Phe Asp Glu Asp Thr Gly Arg Trp Ile Ser Val	
	25 30 35

gcc gag gtc gcc gag ata cgc ttc acc gca ttt acc tcc cgg aag aaa	259
Ala Glu Val Ala Glu Ile Pro Phe Thr Ala Phe Thr Ser Arg Lys Lys	
	40 45 50

acc gac cac atc ccc gga ctg ctg gtg gta cgc cgg ata cgc gag ctg	307
Thr Asp His Ile Pro Gly Leu Leu Val Val Arg Arg Ile Pro Glu Leu	
	55 60 65

aat aac aag gat gtg gat cag cgc ggg ttg ttt gat cta cac cgc ttc	355
Asn Asn Lys Asp Val Asp Gln Pro Gly Leu Phe Asp Leu His Arg Phe	
	70 75 80 85

cat gcg gtg ttc acc acc gcc gac cca ggc atc ctc gat act gtt gct	403
His Ala Val Phe Thr Thr Ala Asp Pro Gly Ile Leu Asp Thr Val Ala	
	90 95 100

gcg gat aaa acc cac cgt caa cac gca atc atc gaa caa gtc aac gcg	451
Ala Asp Lys Thr His Arg Gln His Ala Ile Ile Glu Gln Val Asn Ala	
	105 110 115

gac gta aag gcc agt gcg ttg gcg cat atg cca tca ggt gta ttc acc	499
Asp Val Lys Ala Ser Ala Leu Ala His Met Pro Ser Gly Val Phe Thr	
	120 125 130

gcc aac agc gcc tgg ttg gtg tgt gcg gtc atg gcg ttc aac ctc acc 547
 Ala Asn Ser Ala Trp Leu Val Cys Ala Val Met Ala Phe Asn Leu Thr
 135 140 145

cgc aca gcc ggt gtg atc gct gca gcc gcg atg gcc agg gcc acc acc 595
 Arg Thr Ala Gly Val Ile Ala Ala Gly Ala Met Ala Arg Ala Thr Thr
 150 155 160 165

gca acg atc cgg cgg aaa ctt gtg gcc gtt ccg gcc agg att gca cgc 643
 Ala Thr Ile Arg Arg Lys Leu Val Ala Val Pro Ala Arg Ile Ala Arg
 170 175 180

agc gcc cgg aga ttg att ctt cac ttg cca cgg aac tgg cgg tgg gaa 691
 Ser Ala Arg Arg Leu Ile Leu His Leu Pro Arg Asn Trp Arg Trp Glu
 185 190 195

acc cag tgg tca aga ttg tgt gat cac ggc cgt tta cca ccg 733
 Thr Gln Trp Ser Arg Leu Cys Asp His Gly Arg Leu Pro Pro
 200 205 210

taaccggtag ctccctgact acc 756

<210> 2458

<211> 211

<212> PRT

<213> Corynebacterium glutamicum

<400> 2458

Met Thr Pro Asn Val Lys Lys Ala Ile Ala Gln Val Pro Asp Asp Ala
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Trp Gln Thr Ile Lys Tyr Thr Asn Ala Ile Phe Asp Glu Asp Thr Gly
 20 25 30

Arg Trp Ile Ser Val Ala Glu Val Ala Glu Ile Pro Phe Thr Ala Phe
 35 40 45

Thr Ser Arg Lys Lys Thr Asp Val His Ile Pro Gly Leu Val Val Arg
 50 55 60

Arg Ile Pro Glu Leu Asn Asn Lys Asp Val Asp Gln Pro Gly Leu Phe
 65 70 75 80

Asp Leu His Arg Phe His Ala Val Phe Thr Thr Ala Asp Pro Gly Ile
 85 90 95

Leu Asp Thr Val Ala Ala Asp Lys Thr His Arg Gln His Ala Ile Ile
 100 105 110

Glu Gln Val Asn Ala Asp Val Lys Ala Ser Ala Leu Ala His Met Pro
 115 120 125

Ser Gly Val Phe Thr Ala Asn Ser Ala Trp Leu Val Cys Ala Val Met
 130 135 140

Ala Phe Asn Leu Thr Arg Thr Ala Gly Val Ile Ala Ala Gly Ala Met
 145 150 155 160

Ala Arg Ala Thr Thr Ala Thr Ile Arg Arg Lys Leu Val Ala Val Pro
 165 170 175

Ala Arg Ile Ala Arg Ser Ala Arg Arg Leu Ile Leu His Leu Pro Arg
 180 185 190

Asn Trp Arg Trp Glu Thr Gln Trp Ser Arg Leu Cys Asp His Gly Arg
 195 200 205

Leu Pro Pro
 210

<210> 2459

<211> 1497

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1474)

<223> RXA01820

<400> 2459

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aggcacctca caggtgcaat tattacacaa cccacacagcg atg tcc gca tcc ttt 115
 Met Ser Ala Ser Phe
 1 5

gat gac ccc aac ctc atc tcg ctt gct gga ctg gtt cca acc atg cac 163
 Asp Asp Pro Asn Leu Ile Ser Leu Ala Gly Leu Val Pro Thr Met His
 10 15 20

tta gcc gat gct gcc agc ctg tcc acc ttg gcc cag gac cgg ttg agc 211
 Leu Ala Asp Ala Ala Ser Leu Ser Thr Leu Ala Gln Asp Arg Leu Ser
 25 30 35

atc acc ggt gat aaa ggt gcc aat gct ggt gcg aag atc gcc tcc cta 259
 Ile Thr Gly Asp Lys Gly Ala Asn Ala Gly Ala Lys Ile Ala Ser Leu
 40 45 50

gtc gcg ggc atg gtc gcc ggt gct gat tcc atc gat gac atg gat gta 307
 Val Ala Gly Met Val Ala Gly Ala Asp Ser Ile Asp Asp Met Asp Val
 55 60 65

ctc cgc cac gga ggt atg cgc cga ctt ttc gac cgg atc tac gcc cca 355
 Leu Arg His Gly Gly Met Arg Arg Leu Phe Asp Arg Ile Tyr Ala Pro
 70 75 80 85

tcc aca ttg ggg tct ttt ctg cgg gcc ttc act ttc ggc cac gta cgc 403
 Ser Thr Leu Gly Ser Phe Leu Arg Ala Phe Thr Phe Gly His Val Arg
 90 95 100

caa ctc gat gct gtg gcc tcc cga ttc ctg gtc aac ctg gcc agg cag 451
 Gln Leu Asp Ala Val Ala Ser Arg Phe Leu Val Asn Leu Ala Arg Gln
 105 110 115

gca cca cac ctg gtg cca cca cca cgg gca ggc agt gcc ggt aac ggg 499
 Ala Pro His Leu Val Pro Pro Pro Ala Gly Ser Gly Gly Asn Gly
 120 125 130

tat gtg ttc gtt gat gtt gat gac acc atc att gaa gtc cac ggc cac 547

Tyr Val Phe Val Asp Val Asp Asp Thr Ile Ile Glu Val His Gly His	
135 140 145	
acc aaa caa ggt gcc ggc ttt ggt tac tcc ggt atc cgt gga ctc aac	595
Thr Lys Gln Gly Ala Gly Phe Gly Tyr Ser Gly Ile Arg Gly Leu Asn	
150 155 160 165	
gcc ttg ctg gcc acg gtc acc acc gca cag tcc gcc ccc atc att gtg	643
Ala Leu Leu Ala Thr Val Thr Thr Ala Gln Ser Ala Pro Ile Ile Val	
170 175 180	
ggc caa cga ttg cgg aaa gga tcg tgt ggt tcc cca cga ggg gcc cac	691
Gly Gln Arg Leu Arg Lys Gly Ser Cys Gly Ser Pro Arg Gly Ala His	
185 190 195	
cgc ctg atc gcc gat gcg atg acc acc acc agg cgc ctg ccc ggg atg	739
Arg Leu Ile Ala Asp Ala Met Thr Thr Thr Arg Arg Leu Pro Gly Met	
200 205 210	
gag gat aag aaa atc ctc gtc cgg gca gat tcg gcg tat tat ggt cat	787
Glu Asp Lys Lys Ile Leu Val Arg Ala Asp Ser Ala Tyr Tyr Gly His	
215 220 225	
ccc agt gtc agt gtg gcc cta agg tcc ggt gcg gat gtg tcc gtc acg	835
Pro Ser Val Ser Val Ala Leu Arg Ser Gly Ala Asp Val Ser Val Thr	
230 235 240 245	
gtg cgg atg acc ccg aac gtc aag aaa gcg atc gtc gcg atc ccg gaa	883
Val Arg Met Thr Pro Asn Val Lys Lys Ala Ile Val Ala Ile Pro Glu	
250 255 260	
gat gcg tgg cag acg att cag tac acc gat gcg atc ttc gat gag gca	931
Asp Ala Trp Gln Thr Ile Gln Tyr Thr Asp Ala Ile Phe Asp Glu Ala	
265 270 275	
tca caa tcg tgg atc tcc tta gcc cag gtc gcc gaa gtg cct ttc acc	979
Ser Gln Ser Trp Ile Ser Leu Ala Gln Val Ala Glu Val Pro Phe Thr	
280 285 290	
gcg ttt acc tcc cgg aag aag gcc gac cat gtt ccc gga cgc ttg gtg	1027
Ala Phe Thr Ser Arg Lys Lys Ala Asp His Val Pro Gly Arg Leu Val	
295 300 305	
gta cgc cgg att cct gag ctg aat aag aag gat gtg tat cag ccg ggc	1075
Val Arg Arg Ile Pro Glu Leu Asn Lys Lys Asp Val Tyr Gln Pro Gly	
310 315 320 325	
ttg ttt gat ctt cac cgc ttc cat gcg gtc ttc acc acc gcc gac cca	1123
Leu Phe Asp Leu His Arg Phe His Ala Val Phe Thr Thr Ala Asp Pro	
330 335 340	
ggc gtg ctg gat act gtt gct gcg gat aaa acc cac cgt cag cac gcg	1171
Gly Val Leu Asp Thr Val Ala Ala Asp Lys Thr His Arg Gln His Ala	
345 350 355	
atc att gaa cag gtc aac gca gac ttg aag gca agc gcg ttg gcg cat	1219
Ile Ile Glu Gln Val Asn Ala Asp Leu Lys Ala Ser Ala Leu Ala His	
360 365 370	
ctg ccg tcg ggg acg ttc acc gcc aac agt gcc tgg ctc gta tgc gcg	1267
Leu Pro Ser Gly Thr Phe Thr Ala Asn Ser Ala Trp Leu Val Cys Ala	

375	380	385	
gtc atg gcg ttt aat ctc acc cgt gcc acc ggg gtt atc gct gca ggc			1315
Val Met Ala Phe Asn Leu Thr Arg Ala Thr Gly Val Ile Ala Ala Gly			
390	395	400	405
ggg atg gcc aag gcc acc acc gcg acg atc cgg cgg aca ctg atg gcc			1363
Gly Met Ala Lys Ala Thr Thr Ala Thr Ile Arg Arg Thr Leu Met Ala			
	410	415	420
ggt cca gcc cgg gtc gcc cgc agg tcc cgc cga ctg gtg ctc cac ctt			1411
Val Pro Ala Arg Val Ala Arg Arg Ser Arg Arg Leu Val Leu His Leu			
	425	430	435
ccc gag ggg tgg acg tgg caa cca cag tgg cag aaa ctg ttt gat cac			1459
Pro Glu Gly Trp Thr Trp Gln Pro Gln Trp Gln Lys Leu Phe Asp His			
	440	445	450
ggc cat tca cca cag taaccggtag ctccctgacc acc			1497
Gly His Ser Pro Pro			
	455		

<210> 2460

<211> 458

<212> PRT

<213> Corynebacterium glutamicum

<400> 2460

Met	Ser	Ala	Ser	Phe	Asp	Asp	Pro	Asn	Leu	Ile	Ser	Leu	Ala	Gly	Leu
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Val	Pro	Thr	Met	His	Leu	Ala	Asp	Ala	Ala	Ser	Leu	Ser	Thr	Leu	Ala
			20					25					30		

Gln	Asp	Arg	Leu	Ser	Ile	Thr	Gly	Asp	Lys	Gly	Ala	Asn	Ala	Gly	Ala
	35						40				45				

Lys	Ile	Ala	Ser	Leu	Val	Ala	Gly	Met	Val	Ala	Gly	Ala	Asp	Ser	Ile
	50					55					60				

Asp	Asp	Met	Asp	Val	Leu	Arg	His	Gly	Gly	Met	Arg	Arg	Leu	Phe	Asp
	65				70					75					80

Arg	Ile	Tyr	Ala	Pro	Ser	Thr	Leu	Gly	Ser	Phe	Leu	Arg	Ala	Phe	Thr
			85						90					95	

Phe	Gly	His	Val	Arg	Gln	Leu	Asp	Ala	Val	Ala	Ser	Arg	Phe	Leu	Val
			100				105						110		

Asn	Leu	Ala	Arg	Gln	Ala	Pro	His	Leu	Val	Pro	Pro	Pro	Pro	Ala	Gly
		115					120					125			

Ser	Gly	Gly	Asn	Gly	Tyr	Val	Phe	Val	Asp	Val	Asp	Asp	Thr	Ile	Ile
	130					135					140				

Glu	Val	His	Gly	His	Thr	Lys	Gln	Gly	Ala	Gly	Phe	Gly	Tyr	Ser	Gly
	145					150				155					160

Ile	Arg	Gly	Leu	Asn	Ala	Leu	Leu	Ala	Thr	Val	Thr	Thr	Ala	Gln	Ser
				165						170					175

Ala Pro Ile Ile Val Gly Gln Arg Leu Arg Lys Gly Ser Cys Gly Ser
 180 185 190
 Pro Arg Gly Ala His Arg Leu Ile Ala Asp Ala Met Thr Thr Thr Arg
 195 200 205
 Arg Leu Pro Gly Met Glu Asp Lys Lys Ile Leu Val Arg Ala Asp Ser
 210 215 220
 Ala Tyr Tyr Gly His Pro Ser Val Ser Val Ala Leu Arg Ser Gly Ala
 225 230 235 240
 Asp Val Ser Val Thr Val Arg Met Thr Pro Asn Val Lys Lys Ala Ile
 245 250 255
 Val Ala Ile Pro Glu Asp Ala Trp Gln Thr Ile Gln Tyr Thr Asp Ala
 260 265 270
 Ile Phe Asp Glu Ala Ser Gln Ser Trp Ile Ser Leu Ala Gln Val Ala
 275 280 285
 Glu Val Pro Phe Thr Ala Phe Thr Ser Arg Lys Lys Ala Asp His Val
 290 295 300
 Pro Gly Arg Leu Val Val Arg Arg Ile Pro Glu Leu Asn Lys Lys Asp
 305 310 315 320
 Val Tyr Gln Pro Gly Leu Phe Asp Leu His Arg Phe His Ala Val Phe
 325 330 335
 Thr Thr Ala Asp Pro Gly Val Leu Asp Thr Val Ala Ala Asp Lys Thr
 340 345 350
 His Arg Gln His Ala Ile Ile Glu Gln Val Asn Ala Asp Leu Lys Ala
 355 360 365
 Ser Ala Leu Ala His Leu Pro Ser Gly Thr Phe Thr Ala Asn Ser Ala
 370 375 380
 Trp Leu Val Cys Ala Val Met Ala Phe Asn Leu Thr Arg Ala Thr Gly
 385 390 395 400
 Val Ile Ala Ala Gly Gly Met Ala Lys Ala Thr Thr Ala Thr Ile Arg
 405 410 415
 Arg Thr Leu Met Ala Val Pro Ala Arg Val Ala Arg Arg Ser Arg Arg
 420 425 430
 Leu Val Leu His Leu Pro Glu Gly Trp Thr Trp Gln Pro Gln Trp Gln
 435 440 445
 Lys Leu Phe Asp His Gly His Ser Pro Pro
 450 455

<210> 2461

<211> 1041

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1018)

<223> RXA01842

<400> 2461

cacgtcatgg tctcgcggtg atcatcttcc taccgtagaca ggcaaggccg caaacggccg 60

tgaccacag	g	aa	gaa	aatc	acg	agg	agag	ga	agcac	acg	atg	tcg	aag	gta	tac	115
											Met	Ser	Lys	Val	Tyr	
											1				5	

gtg	tcc	aac	gag	tac	ggc	ggc	ccg	gaa	aac	cag	gaa	ctg	atc	acc	cgc	163
Val	Ser	Asn	Glu	Tyr	Gly	Gly	Pro	Glu	Asn	Gln	Glu	Leu	Ile	Thr	Arg	
				10						15				20		

aac	acc	ccc	cag	cca	ggc	ccg	gga	gaa	ctc	ggg	gtc	aag	gtc	cac	gcg	211
Asn	Thr	Pro	Gln	Pro	Gly	Pro	Gly	Glu	Leu	Gly	Val	Lys	Val	His	Ala	
			25					30					35			

gcc	ggg	gtc	aac	ccg	ctt	gat	tgg	aag	gtc	cgt	tcc	ggg	gtt	gcc	gga	259
Ala	Gly	Val	Asn	Pro	Leu	Asp	Trp	Lys	Val	Arg	Ser	Gly	Val	Ala	Gly	
		40					45					50				

acc	ccg	cga	gag	ctt	ccg	gca	ccc	ctg	ggc	gag	gag	gcc	tcc	ggg	atc	307
Thr	Pro	Arg	Glu	Leu	Pro	Ala	Pro	Leu	Gly	Glu	Ala	Ala	Ser	Gly	Ile	
		55				60					65					

gtc	acc	gcc	gtt	gga	gac	ggg	gtg	gag	ggc	ttc	gcg	gtc	ggc	gat	ccg	355
Val	Thr	Ala	Val	Gly	Asp	Gly	Val	Glu	Gly	Phe	Ala	Val	Gly	Asp	Pro	
		70			75					80					85	

gtg	ctc	ggc	ctg	gtg	gcc	ccc	ggc	gtc	ggc	gga	tat	gcc	gag	gac	acc	403
Val	Leu	Gly	Leu	Val	Ala	Pro	Gly	Val	Gly	Gly	Tyr	Ala	Glu	Asp	Thr	
			90					95						100		

ctg	ctg	gtg	gca	gag	agt	acc	gtg	cta	aag	ccg	gag	gag	atc	tcg	ttc	451
Leu	Leu	Val	Ala	Glu	Ser	Thr	Val	Leu	Lys	Pro	Glu	Glu	Ile	Ser	Phe	
			105					110					115			

acc	gac	gcc	gcc	gcg	atc	ccg	gtc	gct	ggg	gcg	agc	gcc	tac	gcc	ggc	499
Thr	Asp	Ala	Ala	Ala	Ile	Pro	Val	Ala	Gly	Ala	Ser	Ala	Tyr	Ala	Gly	
		120					125					130				

act	cac	cag	gtc	gag	ctt	gaa	cca	ggc	cag	tcg	ttg	ctg	atc	aat	ggg	547
Thr	His	Gln	Val	Glu	Leu	Glu	Pro	Gly	Gln	Ser	Leu	Leu	Ile	Asn	Gly	
		135				140					145					

gcc	ggg	ggg	gtc	ggg	ctg	atg	gcc	gcg	cag	atc	gga	ccg	gtc	cac	595	
Ala	Gly	Gly	Gly	Val	Gly	Leu	Met	Ala	Ala	Gln	Ile	Gly	Arg	Val	His	
		150			155				160					165		

aag	ttc	cag	gtc	gtc	ggc	gtt	gac	cac	gag	gac	aag	cgc	gag	ctc	atc	643
Lys	Phe	Gln	Val	Val	Gly	Val	Asp	His	Glu	Asp	Lys	Arg	Glu	Leu	Ile	
			170						175					180		

gaa	tcc	acc	ggg	gct	atc	ttc	gtc	gcc	acc	ggc	gac	gcc	gtc	gcg	gag	691
Glu	Ser	Thr	Gly	Ala	Ile	Phe	Val	Ala	Thr	Gly	Asp	Ala	Val	Ala	Glu	
			185					190					195			

cag	gtg	cgt	gcg	ctg	ctc	cct	gac	ggg	gtg	gac	gta	gtc	ttc	gac	cta	739
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Gln Val Arg Ala Leu Leu Pro Asp Gly Val Asp Val Val Phe Asp Leu
 200 205 210
 gtc ggc ggg gag gcg ttg cgg gtg gtt gct ccc tta gcg aag aat ccg 787
 Val Gly Gly Glu Ala Leu Arg Val Val Ala Pro Leu Ala Lys Asn Pro
 215 220 225
 gcg cac gtg atc tgc gcg gct gat gct gcc acc gtg gga gaa ctc ggt 835
 Ala His Val Ile Ser Ala Ala Asp Ala Ala Thr Val Gly Glu Leu Gly
 230 235 240 245
 gga cag gtg ctg cgc cgc acc ccg gaa atg gtc gga cag atc acc ggg 883
 Gly Gln Val Leu Arg Arg Thr Pro Glu Met Val Gly Gln Ile Thr Gly
 250 255 260
 gtg gtc cag tac ggg ctg gtc gac ccg aag gtc gat acg acc tac ccg 931
 Val Val Gln Tyr Gly Leu Val Asp Pro Lys Val Asp Thr Tyr Pro
 265 270 275
 ctg gaa cag gcc ggt aag gcc ctg gcc cac gtt gag cag ggc cac gcc 979
 Leu Glu Gln Ala Gly Lys Ala Leu Ala His Val Glu Gln Gly His Ala
 280 285 290
 cgc ggc aag atc gtc ctc gag ctc atc acc tcc cag gac taaccagaca 1028
 Arg Gly Lys Ile Val Leu Glu Leu Ile Thr Ser Gln Asp
 295 300 305
 acgcggtgac ctc 1041
 <210> 2462
 <211> 306
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 2462
 Met Ser Lys Val Tyr Val Ser Asn Glu Tyr Gly Gly Pro Glu Asn Gln
 1 5 10 15
 Glu Leu Ile Thr Arg Asn Thr Pro Gln Pro Gly Pro Gly Glu Leu Gly
 20 25 30
 Val Lys Val His Ala Ala Gly Val Asn Pro Leu Asp Trp Lys Val Arg
 35 40 45
 Ser Gly Val Ala Gly Thr Pro Arg Glu Leu Pro Ala Pro Leu Gly Glu
 50 55 60
 Glu Ala Ser Gly Ile Val Thr Ala Val Gly Asp Gly Val Glu Gly Phe
 65 70 75 80
 Ala Val Gly Asp Pro Val Leu Gly Leu Val Ala Pro Gly Val Gly Gly
 85 90 95
 Tyr Ala Glu Asp Thr Leu Leu Val Ala Glu Ser Thr Val Leu Lys Pro
 100 105 110
 Glu Glu Ile Ser Phe Thr Asp Ala Ala Ala Ile Pro Val Ala Gly Ala
 115 120 125
 Ser Ala Tyr Ala Gly Thr His Gln Val Glu Leu Glu Pro Gly Gln Ser

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130                      135                      140
Leu Leu Ile Asn Gly Ala Gly Gly Gly Val Gly Leu Met Ala Ala Gln
145                      150                      155                      160
Ile Gly Arg Val His Lys Phe Gln Val Val Gly Val Asp His Glu Asp
165                      170                      175
Lys Arg Glu Leu Ile Glu Ser Thr Gly Ala Ile Phe Val Ala Thr Gly
180                      185                      190
Asp Ala Val Ala Glu Gln Val Arg Ala Leu Leu Pro Asp Gly Val Asp
195                      200                      205
Val Val Phe Asp Leu Val Gly Gly Glu Ala Leu Arg Val Val Ala Pro
210                      215                      220
Leu Ala Lys Asn Pro Ala His Val Ile Ser Ala Ala Asp Ala Ala Thr
225                      230                      235                      240
Val Gly Glu Leu Gly Gly Gln Val Leu Arg Arg Thr Pro Glu Met Val
245                      250                      255
Gly Gln Ile Thr Gly Val Val Gln Tyr Gly Leu Val Asp Pro Lys Val
260                      265                      270
Asp Thr Thr Tyr Pro Leu Glu Gln Ala Gly Lys Ala Leu Ala His Val
275                      280                      285
Glu Gln Gly His Ala Arg Gly Lys Ile Val Leu Glu Leu Ile Thr Ser
290                      295                      300
Gln Asp
305
<210> 2463
<211> 303
<212> DNA
<213> Corynebacterium glutamicum
<220>
<221> CDS
<222> {101}..(280)
<223> RXA01844
<400> 2463
gaccaattgg tctgctgca tccgcatgat cgccaacgcc agttgcgggt aggcgtccac 60
gacctgcgcc agggcctcga cgggcaggta gagcgcgcag gtg gtc tca atc gcc 115
Val Val Ser Ile Ala
1 5
cag gag ttg gag atc att gag gac ggc acg ggt gcg gtg etc gtc tcg 163
Gln Glu Leu Glu Ile Ile Glu Asp Gly Thr Gly Ala Val Leu Val Ser
10 15 20
gag cag gca acc acc ttc gac aac ggg ttc atc ggc tac tcc tac ttc 211
Glu Gln Ala Thr Thr Phe Asp Asn Gly Phe Ile Gly Tyr Ser Tyr Phe
25 30 35

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gcc tcc cca ctg ccg cag gtt taaccggtac tagccggttt ttc 303
Ala Ser Pro Leu Pro Gln Val
55 60

<213> *Corynebacterium glutamicum*

<213> Corynebacterium glutamicum

<223> RXA01845

acc acc tgc act gtc gag cag cgc gtg gcc gcc gcc ctc caa cac ctg 307
Thr Thr Ser Thr Val Glu Gln Arg Val Ala Ala Ala Leu Gln His Leu
55 60 65

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gac gcc aag ctc ggg caa atc cga caa gac gga tcc agc ctg ctg cag 355
Asp Ala Lys Leu Gly Gln Ile Arg Gln Asp Gly Ser Ser Leu Leu Gln
70 75 80 85

gtc cgc ctg cgc cgc gac gac gtg gcc ggc acc acc gtc gag tcc gcc 403
Val Arg Leu Arg Arg Asp Asp Val Ala Gly Thr Thr Val Glu Ser Ala
90 95 100

tcc cgg gca atg gcg cgg atg aag aaa acc ggt gtc atc gac tcc gcc 451
Ser Arg Ala Met Ala Arg Met Lys Lys Thr Gly Val Ile Asp Ser Gly
105 110 115

cgc gaa tgg atc gcc att acc aac cac cag gcc ctg gcc gac ctg gtc 499
Arg Glu Trp Ile Ala Ile Thr Asn His Gln Ala Leu Ala Asp Leu Val
120 125 130

gcc ggc ctc taaacgccca catccctctc tct 531
Ala Gly Leu
135

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<210> 2466

<211> 136

<212> PRT

<213> Corynebacterium glutamicum

<400> 2466

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Met Ile Ser Asn Ser Trp Ala Ile Glu Thr Thr Cys Ala Leu Tyr Leu
1 5 10 15

Pro Val Glu Ala Leu Ala Glu Val Val Asp Ala Tyr Pro Gln Leu Ala
20 25 30

Leu Ala Ile Met Arg Met Gln Gln Asp Gln Leu Val Arg Ser Arg Glu
35 40 45

Arg Glu Thr Ala Gln Thr Thr Ser Thr Val Glu Gln Arg Val Ala Ala
50 55 60

Ala Leu Gln His Leu Asp Ala Lys Leu Gly Gln Ile Arg Gln Asp Gly
65 70 75 80

Ser Ser Leu Leu Gln Val Arg Leu Arg Arg Asp Asp Val Ala Gly Thr
85 90 95

Thr Val Glu Ser Ala Ser Arg Ala Met Ala Arg Met Lys Lys Thr Gly
100 105 110

Val Ile Asp Ser Gly Arg Glu Trp Ile Ala Ile Thr Asn His Gln Ala
115 120 125

Leu Ala Asp Leu Val Ala Gly Leu
130 135

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<210> 2467

<211> 669

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(646)

<223> RXA01856

<400> 2467

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gttgtagctg cttctgcgtg gctagtaaaa taattggcta atg aat cct ttt ctt 115
                                     Met Asn Pro Phe Leu
                                     1 5

tcg gac acg ttg att gtc cag cag acc tct tcc ttc ctg tct aac aac 163
Ser Asp Thr Leu Ile Val Gln Gln Thr Ser Phe Leu Ser Asn Asn
                10                15                20

ttt gag atc tac aat cca gac ggc gaa gtt gtt atc aga atc aaa act 211
Phe Glu Ile Tyr Asn Pro Asp Gly Glu Val Val Ile Arg Ile Lys Thr
                25                30                35

gaa ggg tcg ttg ggc tct cgg ctg gtc aag ggc gac cgc aga ttc aca 259
Glu Gly Ser Leu Gly Ser Arg Leu Val Lys Gly Asp Arg Arg Phe Thr
                40                45                50

ctg gaa gac gcc ttc ggc acc cca ttg atg cag gtg cgc gat ccc atg 307
Leu Glu Asp Ala Phe Gly Thr Pro Leu Met Gln Val Arg Asp Pro Met
                55                60                65

aac ttt gtt cgc gac acc tat gaa att gat gat cca aat ggc aat ccc 355
Asn Phe Val Arg Asp Thr Tyr Glu Ile Asp Asp Pro Asn Gly Asn Pro
                70                75                80                85

att gct cat gtg cgg aag cgt ttc acc ttc ttc aac aag cgg atg gac 403
Ile Ala His Val Arg Lys Arg Phe Thr Phe Phe Asn Lys Arg Met Asp
                90                95                100

atc gaa cta cca ggt gac cgc gtt att gaa atg cac ggt aac ttc ctt 451
Ile Glu Leu Pro Gly Asp Arg Val Ile Glu Met His Gly Asn Phe Leu
                105                110                115

gga ttt gaa ttt gag ttc cgc atg ggc gat cgg att cct gcg aaa gta 499
Gly Phe Glu Phe Glu Phe Arg Met Gly Asp Arg Ile Pro Ala Lys Val
                120                125                130

acc cga aaa tgg tcc ggc gct ggc aac gga tac cta ggc cga agc acc 547
Thr Arg Lys Trp Ser Gly Ala Gly Asn Gly Tyr Leu Gly Arg Ser Thr
                135                140                145

tac gcc ctt att ttc gat gaa gaa gcc cct gat gaa atc aga aaa gtc 595
Tyr Ala Leu Ile Phe Asp Glu Glu Ala Pro Asp Glu Ile Arg Lys Val
                150                155                160                165

atc att gga ggc atg gtc gcg cta gat ctg atc cgg gag aag gaa cgt 643
Ile Ile Gly Gly Met Val Ala Leu Asp Leu Ile Arg Glu Lys Glu Arg
                170                175                180

aat taagccaccc cggtttcattg tct 667
Asn

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<210> 2468

<211> 182

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2468

Met Asn Pro Phe Leu Ser Asp Thr Leu Ile Val Gln Gln Thr Ser Ser
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Phe Leu Ser Asn Asn Phe Glu Ile Tyr Asn Pro Asp Gly Glu Val Val
 20 25 30

Ile Arg Ile Lys Thr Glu Gly Ser Leu Gly Ser Arg Leu Val Lys Gly
 35 40 45

Asp Arg Arg Phe Thr Leu Glu Asp Ala Phe Gly Thr Pro Leu Met Gln
 50 55 60

Val Arg Asp Pro Met Asn Phe Val Arg Asp Thr Tyr Glu Ile Asp Asp
 65 70 75 80

Pro Asn Gly Asn Pro Ile Ala His Val Arg Lys Arg Phe Thr Phe Phe
 85 90 95

Asn Lys Arg Met Asp Ile Glu Leu Pro Gly Asp Arg Val Ile Glu Met
 100 105 110

His Gly Asn Phe Leu Gly Phe Glu Phe Glu Phe Arg Met Gly Asp Arg
 115 120 125

Ile Pro Ala Lys Val Thr Arg Lys Trp Ser Gly Ala Gly Asn Gly Tyr
 130 135 140

Leu Gly Arg Ser Thr Tyr Ala Leu Ile Phe Asp Glu Glu Ala Pro Asp
 145 150 155 160

Glu Ile Arg Lys Val Ile Ile Gly Gly Met Val Ala Leu Asp Leu Ile
 165 170 175

Arg Glu Lys Glu Arg Asn
 180

<210> 2469

<211> 774

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(751)

<223> RXA01857

<400> 2469

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tcgtactaat ctaacttaat ctctccctag gagttctccc atg gct tca cgc cgt 115
 Met Ala Ser Arg Arg
 1 5

ttc cgt atg atg ctc acc gca agc atc acc gca gct tcc ctt ggt ttt 163
 Phe Arg Met Met Leu Thr Ala Ser Ile Thr Ala Ala Ser Leu Gly Phe

	10	15	20	
tcg ctc acc cca gca atc gcc gat gaa gct gta acc gtt gct acg gca				211
Ser Leu Thr Pro Ala Ile Ala Asp Glu Ala Val Thr Val Ala Thr Ala	25	30	35	
ccc tcc gtc gga ttc gat tcc ggc gtc gaa cgc gat gca cca ttc acc				259
Pro Ser Val Gly Phe Asp Ser Gly Val Glu Arg Asp Ala Pro Phe Thr	40	45	50	
gca gtt cca cac gac gta gtt ctc ggc gtt gga gcg acc cag tcc gag				307
Ala Val Pro His Asp Val Val Leu Gly Val Gly Ala Thr Gln Ser Glu	55	60	65	
ctc att ttc aac tgg atc acc gcg cag ggc cta acc ggc cag gtt gca				355
Leu Ile Phe Asn Trp Ile Thr Ala Gln Gly Leu Thr Gly Gln Val Ala	70	75	80	85
cag atc tcc ctg gac gat acc ttc gca tcc cca atc acc gtt gat gca				403
Gln Ile Ser Leu Asp Thr Phe Ala Ser Pro Ile Thr Val Asp Ala	90	95	100	
gtt tct gaa aac gtc agc atc gtg aac acc gaa ggc gat tcc cgc gac				451
Val Ser Glu Asn Val Ser Ile Val Asn Thr Glu Gly Asp Ser Arg Asp	105	110	115	
cga gct gaa ggt gaa tac gtt gaa tac cgc gat ggc gca gtc aac cgc				499
Arg Ala Glu Gly Glu Tyr Val Glu Tyr Arg Asp Gly Ala Val Asn Arg	120	125	130	
gca acc gta gat agc ctc gca gaa aac acc acc tac tcc tac cgc gtc				547
Ala Thr Val Asp Ser Leu Ala Glu Asn Thr Thr Tyr Ser Tyr Arg Val	135	140	145	
ggc tcc gaa gct gac ggc tgg tcc gaa gtg caa acc ttc aac acc ggc				595
Gly Ser Glu Ala Asp Gly Trp Ser Glu Val Gln Thr Phe Asn Thr Gly	150	155	160	165
acc tac ggt gac aac tgg aac ttc ctc ttc ttc ggc gac acc cag ctg				643
Thr Tyr Gly Asp Asn Trp Asn Phe Leu Phe Phe Gly Asp Thr Gln Leu	170	175	180	
tac aac acc cac tcc aac cgt gca gaa gaa gtc cag aac tgg gca aac				691
Tyr Asn Thr His Ser Asn Arg Ala Glu Glu Val Gln Asn Trp Ala Asn	185	190	195	
aac ctg gaa cgg cgg ccc acc aat cga aaa ccc agg aac ctc ctt cat				739
Asn Leu Glu Arg Arg Pro Thr Asn Arg Lys Pro Arg Asn Leu Leu His	200	205	210	
cct ctc cgc ggg tgatcaggca aacctcca gct				774
Pro Leu Arg Gly	215			

<210> 2470

<211> 217

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2470

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Met Ala Ser Arg Arg Phe Arg Met Met Leu Thr Ala Ser Ile Thr Ala
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Ala Ser Leu Gly Phe Ser Leu Thr Pro Ala Ile Ala Asp Glu Ala Val
              20              25              30
Thr Val Ala Thr Ala Pro Ser Val Gly Phe Asp Ser Gly Val Glu Arg
 35              40              45
Asp Ala Pro Phe Thr Ala Val Pro His Asp Val Val Leu Gly Val Gly
 50              55              60
Ala Thr Gln Ser Glu Leu Ile Phe Asn Trp Ile Thr Ala Gln Gly Leu
 65              70              75              80
Thr Gly Gln Val Ala Gln Ile Ser Leu Asp Asp Thr Phe Ala Ser Pro
 85              90              95
Ile Thr Val Asp Ala Val Ser Glu Asn Val Ser Ile Val Asn Thr Glu
100              105              110
Gly Asp Ser Arg Asp Arg Ala Glu Gly Glu Tyr Val Glu Tyr Arg Asp
115              120              125
Gly Ala Val Asn Arg Ala Thr Val Asp Ser Leu Ala Glu Asn Thr Thr
130              135              140
Tyr Ser Tyr Arg Val Gly Ser Glu Ala Asp Gly Trp Ser Glu Val Gln
145              150              155              160
Thr Phe Asn Thr Gly Thr Tyr Gly Asp Asn Trp Asn Phe Leu Phe Phe
165              170              175
Gly Asp Thr Gln Leu Tyr Asn Thr His Ser Asn Arg Ala Glu Glu Val
180              185              190
Gln Asn Trp Ala Asn Asn Leu Glu Arg Arg Pro Thr Asn Arg Lys Pro
195              200              205
Arg Asn Leu Leu His Pro Leu Arg Gly
210              215

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<210> 2471

<211> 673

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(673)

<223> RXA01858

<400> 2471

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cgtgtgtttg ttttgactgg aacagcgctg gcttttcggc cagcggcct gcggacagta 60
gcggaatcac gcgggacatt gatccccgga cgtaaagccg atg ttt atg aca cgg 115
                               Met Phe Met Thr Pro
                               1              5
cgg gcg ttg acc gaa gat aat gag ttg acc ctg gct ttg aaa tca ctc 163

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Arg Ala Leu Thr Glu Asp Asn Glu Leu Thr Leu Ala Leu Lys Ser Leu
 10 15 20
 gga ggg ctt atg gtg tca ccc aat gag tgc tca gta gtg aca gaa gtg 211
 Gly Gly Leu Met Val Ser Pro Asn Glu Cys Ser Val Val Thr Glu Val
 25 30 35
 atg ccg act tgg aga gaa tta tgg cat caa agg ctt cga tgg caa cgc 259
 Met Pro Thr Trp Arg Glu Leu Trp His Gln Arg Leu Arg Trp Gln Arg
 40 45 50
 ggt gcg ctg gaa aac ctc ggt gct tat ggc atc aca cca caa acg aca 307
 Gly Ala Leu Glu Asn Leu Gly Ala Tyr Gly Ile Thr Pro Gln Thr Thr
 55 60 65
 cgg tat tgg ttc cag cag ctg gga atc ggt tac ggc gca tta gcc ttg 355
 Arg Tyr Trp Phe Gln Glu Leu Gly Ile Gly Tyr Gly Ala Leu Ala Leu
 70 75 80 85
 gtc gcc tat ttc gca gtc att atc att acg ttt ctc gcc cgc gat caa 403
 Val Ala Tyr Phe Ala Val Ile Ile Ile Thr Phe Leu Ala Arg Asp Gln
 90 95 100
 tgg atc tgg tat cca ttc tgg atg ctg ctg gga ctg ttg ttc atg att 451
 Trp Ile Trp Tyr Pro Phe Trp Met Leu Leu Gly Leu Leu Phe Met Ile
 105 110 115
 gaa cgc gtg cta acg gtg tgg aga tcc aca tgg ttt gcc agg ttt gtt 499
 Glu Arg Val Leu Thr Val Trp Arg Ser Thr Trp Phe Ala Arg Phe Val
 120 125 130
 gct gcg tta tta atc cca gag ctc atc tac gcc agc tat ctc aac ctg 547
 Ala Ala Leu Leu Ile Pro Glu Leu Ile Tyr Ala Ser Tyr Leu Asn Leu
 135 140 145
 gta ttt ctc aaa ggc gtt gtg gat att cta ttg gcc aag caa gct cac 595
 Val Phe Leu Lys Gly Val Val Asp Ile Leu Leu Ala Lys Gln Ala His
 150 155 160 165
 tgg ggt gag cat ggt gac aag aca atg cag gta gcc gat gca gct gcc 643
 Trp Gly Glu His Gly Asp Lys Thr Met Gln Val Ala Asp Ala Ala Ala
 170 175 180
 gaa att aac gat gaa ggg gag gaa cgc cga 673
 Glu Ile Asn Asp Glu Gly Glu Glu Arg Arg
 185 190

<210> 2472

<211> 191

<212> PRT

<213> Corynebacterium glutamicum

<400> 2472

Met Phe Met Thr Pro Arg Ala Leu Thr Glu Asp Asn Glu Leu Thr Leu
 1 5 10 15

Ala Leu Lys Ser Leu Gly Gly Leu Met Val Ser Pro Asn Glu Cys Ser
 20 25 30

Val Val Thr Glu Val Met Pro Thr Trp Arg Glu Leu Trp His Gln Arg

	35					40						45							
Leu Arg Trp Gln Arg Gly Ala Leu Glu Asn Leu Gly Ala Tyr Gly Ile 50 55 60																			
Thr Pro Gln Thr Thr Arg Tyr Trp Phe Gln Gln Leu Gly Ile Gly Tyr 65 70 75 80																			
Gly Ala Leu Ala Leu Val Ala Tyr Phe Ala Val Ile Ile Ile Thr Phe 85 90 95																			
Leu Ala Arg Asp Gln Trp Ile Trp Tyr Pro Phe Trp Met Leu Leu Gly 100 105 110																			
Leu Leu Phe Met Ile Glu Arg Val Leu Thr Val Trp Arg Ser Thr Trp 115 120 125																			
Phe Ala Arg Phe Val Ala Ala Leu Leu Ile Pro Glu Leu Ile Tyr Ala 130 135 140																			
Ser Tyr Leu Asn Leu Val Phe Leu Lys Gly Val Val Asp Ile Leu Leu 145 150 155 160																			
Ala Lys Gln Ala His Trp Gly Glu His Gly Asp Lys Thr Met Gln Val 165 170 175																			
Ala Asp Ala Ala Glu Ile Asn Asp Glu Gly Glu Glu Arg Arg 180 185 190																			
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<211>	798																		
<212>	DNA																		
<213>	Corynebacterium glutamicum																		
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<222>	(101)..(775)																		
<223>	RXA01870																		
<400>	2473																		
ggatcatgtc cacc ccagaa ggtagccctg cagtgtgagc gtaatcgagg gcaagtacca	60																		
gctgaaacot caaggccgag gtggcctgtg gtggtcaatc	115																		
Val Gly Val Ala Val	5																		
gtt ttg ttg ctg ctt cca acg ttg atc aac ctg gtg gtt ccg gat aaa	163																		
Val Leu Leu Leu Leu Pro Thr Leu Ile Asn Leu Val Val Pro Asp Lys	20																		
gcc aat gac tac aag cag cta gaa atc gat ctt ctg ggt gtg gat tgg	211																		
Ala Asn Asp Tyr Lys Gln Leu Glu Ile Asp Leu Leu Gly Val Asp Trp	35																		
tca gtg cca atc acc acg gag gaa tcc gct gcg gtg ctg tgt gag gaa	259																		
Ser Val Pro Ile Thr Thr Glu Glu Ser Ala Ala Val Leu Cys Glu Glu	40																		
aca tct gat gaa atc aca cag aag tat tgg gac tgc aac ggg gac acc	307																		
Thr Ser Asp Glu Ile Thr Gln Lys Tyr Trp Asp Cys Asn Gly Asp Thr																			

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55              60              65
acg gtg gtg acc atg atc gtc gag ggc gtg aaa gat ccg tcc aat acg 355
Thr Val Val Thr Met Ile Val Glu Gly Val Lys Asp Pro Ser Asn Thr
70              75              80              85

ttg cgt cgc atg gtg ggt tca tcg ctg ata acc agt gtg gat gac agc 403
Leu Arg Arg Met Val Gly Ser Ser Leu Ile Thr Ser Val Asp Asp Ser
90              95              100

cta gag gca gta tct agc gaa gat ggc cgt gcg cat gcg ttg tat gtg 451
Leu Glu Ala Val Ser Ser Glu Asp Gly Arg Ala His Ala Leu Tyr Val
105              110              115

cca ggt cag caa gaa gga tct ttg tgg acg ctg cct atc gtg gca ctg 499
Pro Gly Gln Gln Glu Gly Ser Leu Trp Thr Leu Pro Ile Val Ala Leu
120              125              130

agc gtg cag ggt tcg ggt gat tat gaa gac ctg aca gcg atc gca att 547
Ser Val Gln Gly Ser Gly Asp Tyr Glu Asp Leu Thr Ala Ile Ala Ile
135              140              145

atc aac ggc acc tcg ttg gat tat tac agc acc cac att tgg tcc agc 595
Ile Asn Gly Thr Ser Leu Asp Tyr Tyr Ser Thr His Ile Trp Ser Ser
150              155              160

atg gcc gct gac cgc ggg ttg ccg tac cag cag gac ttc ccc ctg atg 643
Met Ala Ala Asp Arg Gly Leu Pro Tyr Gln Gln Asp Phe Pro Leu Met
170              175              180

ctg gaa gag gag cca tgg caa gac acc ccc ggc ggg gat cgt ccc ttc 691
Leu Glu Glu Glu Pro Trp Gln Asp Thr Pro Gly Gly Asp Arg Pro Phe
185              190              195

gag ctg ccc aat gat ttc ttt gat cag tac ccc gat ctt ttt ggc cca 739
Glu Leu Pro Asn Asp Phe Phe Asp Gln Tyr Pro Asp Leu Phe Gly Pro
200              205              210

ggc tcc gtc att ccc aac ctt gaa gga gaa tcc cta tgagtcgcat 785
Gly Ser Val Ile Pro Asn Leu Glu Gly Glu Ser Leu
215              220              225

gtttagcatc acc 798

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<210> 2474

<211> 225

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2474

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Val Gly Val Ala Val Val Leu Leu Leu Pro Thr Leu Ile Asn Leu
1              5              10              15

Val Val Pro Asp Lys Ala Asn Asp Tyr Lys Gln Leu Glu Ile Asp Leu
20              25              30

Leu Gly Val Asp Trp Ser Val Pro Ile Thr Thr Glu Glu Ser Ala Ala
35              40              45

Val Leu Cys Glu Glu Thr Ser Asp Glu Ile Thr Gln Lys Tyr Trp Asp

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      50              55              60
Cys Asn Gly Asp Thr Thr Val Val Thr Met Ile Val Glu Gly Val Lys
65              70              75              80
Asp Pro Ser Asn Thr Leu Arg Arg Met Val Gly Ser Ser Leu Ile Thr
      85              90              95
Ser Val Asp Asp Ser Leu Glu Ala Val Ser Ser Glu Asp Gly Arg Ala
      100             105             110
His Ala Leu Tyr Val Pro Gly Gln Gln Glu Gly Ser Leu Trp Thr Leu
      115             120             125
Pro Ile Val Ala Leu Ser Val Gln Gly Ser Gly Asp Tyr Glu Asp Leu
      130             135             140
Thr Ala Ile Ala Ile Ile Asn Gly Thr Ser Leu Asp Tyr Tyr Ser Thr
      145             150             155             160
His Ile Trp Ser Ser Met Ala Ala Asp Arg Gly Leu Pro Tyr Gln Gln
      165             170             175
Asp Phe Pro Leu Met Leu Glu Glu Glu Pro Trp Gln Asp Thr Pro Gly
      180             185             190
Gly Asp Arg Pro Phe Glu Leu Pro Asn Asp Phe Phe Asp Gln Tyr Pro
      195             200             205
Asp Leu Phe Gly Pro Gly Ser Val Ile Pro Asn Leu Glu Gly Glu Ser
      210             215             220
Leu
      225
<210> 2475
<211> 1086
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1063)
<223> RXA01871

<400> 2475
gcggggatcg tcccttcgag ctgcccaatg atttctttga tcagtacccc gatctttttg 60
gccagggtc cgctattccc aaccttgaag gagaatccct atg agt cgc atg ttt 115
                                         Met Ser Arg Met Phe
                                         1               5

agc atc acc ttg tgg gtt gcc atc ctc ctc tca acc ccg gcg ctg ttt 163
Ser Ile Thr Leu Trp Val Ala Ile Leu Leu Ser Thr Pro Ala Leu Phe
      10              15              20

ttg agc ttg gcc acg ttc atc ttc gtg gat ggc atc tct gtc ctc gtg 211
Leu Ser Leu Ala Thr Phe Ile Phe Val Asp Gly Ile Ser Val Leu Val
      25              30              35

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aat ata gtg ttc gcg gtg ctc tac ttg gta gtc att gtt ttc ctg tta 259
 Asn Ile Val Phe Ala Val Leu Tyr Leu Val Val Ile Val Phe Leu Leu
 40 45 50

agt cgc acc ccg ctg tgg cca cgt ttt aaa ggc tcc ggc agc aag aag 307
 Ser Arg Thr Pro Leu Trp Pro Arg Phe Lys Gly Ser Gly Ser Lys Lys
 55 60 65

gga ggc gga ttc gcg tgg gcg gcg tca tca ttg ttg tgg ggc gcg ttc 355
 Gly Gly Gly Phe Ala Trp Ala Ala Ser Ser Leu Leu Trp Gly Ala Phe
 70 75 80 85

gtt ggt ttc ggc atc gtc atg ttg ttt gcc ggt cgc gtc atg gat ctc 403
 Val Gly Phe Gly Ile Val Met Leu Phe Ala Gly Pro Val Met Asp Leu
 90 95 100

acg gac aaa ctc ggc tgg gat ttc gtt gcc atg agt ttc acc gga ggc 451
 Thr Asp Lys Leu Gly Trp Asp Phe Val Ala Met Ser Phe Thr Gly Ala
 105 110 115

tat cca gaa gaa atc gcc aaa gcg tta ggc gtt gcc atc atc ttg ttg 499
 Tyr Pro Glu Glu Ile Ala Lys Ala Leu Gly Val Ala Ile Ile Leu Leu
 120 125 130

agc ttc cgc caa ctc aac cgt cgc tgg cat gga ttt atc acc ggc gcg 547
 Ser Phe Arg Gln Leu Asn Arg Pro Trp His Gly Phe Ile Thr Gly Ala
 135 140 145

cta gtg ggc tta ggt ttt gag gtc aac gaa aac ctc ctc tat ggc gcc 595
 Leu Val Gly Leu Gly Phe Glu Val Asn Glu Asn Leu Leu Tyr Gly Ala
 150 155 160 165

acc ggt gca atc atg gac ccc aac gct gac ctc gac ggc gtc ott atg 643
 Thr Gly Ala Ile Met Asp Pro Asn Ala Asp Leu Asp Gly Val Leu Met
 170 175 180

atg tgg caa tac cgc acc atg ttg ggc cca ctc atc cat acg ttg ctc 691
 Met Trp Gln Tyr Arg Thr Met Leu Gly Pro Leu Ile His Thr Leu Leu
 185 190 195

acc gga ttc gca ggt tac ggc atc gcg ttg gca ttc ttc cgc gca cga 739
 Thr Gly Phe Ala Gly Tyr Gly Ile Ala Leu Ala Phe Phe Arg Ala Arg
 200 205 210

aaa aca gtc gcc tgg cgc tgg ggc gtg gcg atc ggt tgg act ctc atc 787
 Lys Thr Val Ala Trp Arg Trp Gly Val Ala Ile Gly Trp Thr Leu Ile
 215 220 225

gcc ttc gca ctg cat ttt tca tgg aac ctg atg tgg gaa aac gta atc 835
 Ala Phe Ala Leu His Phe Ser Trp Asn Leu Met Trp Glu Asn Val Ile
 230 235 240 245

ggt tcc tat gtc acc atc atc gtg gtc agc gtt gtc atg tac ggt ctg 883
 Gly Ser Tyr Val Thr Ile Ile Val Val Ser Val Val Met Tyr Gly Leu
 250 255 260

gct atc tac atc ctc tgg agt aat tgg gcc gaa gcc cgc aac gac tcc 931
 Ala Ile Tyr Ile Leu Trp Ser Asn Trp Ala Glu Ala Arg Asn Asp Ser
 265 270 275

agc tac gct ttc gtc cgc gga atc atc aca aac acc aaa gat tta tcg 979

Ser Tyr Ala Phe Val Pro Gly Ile Ile Thr Asn Thr Lys Asp Leu Ser
 280 285 290
 ctt ctt gac gcc ccc att cca gta ggc gct gag gtt ccc gag tcg cgc 1027
 Leu Leu Asp Ala Pro Ile Pro Val Gly Ala Glu Val Pro Glu Ser Arg
 295 300 305
 att ccc caa cag ata gag gaa ccc aag gcg gag aac tagctttcac 1073
 Ile Pro Gln Gln Ile Glu Glu Pro Lys Ala Glu Asn
 310 315 320
 tcgctctcca tcc 1086

<210> 2476

<211> 321

<212> PRT

<213> Corynebacterium glutamicum

<400> 2476

Met Ser Arg Met Phe Ser Ile Thr Leu Trp Val Ala Ile Leu Leu Ser
 1 5 10 15
 Thr Pro Ala Leu Phe Leu Ser Leu Ala Thr Phe Ile Phe Val Asp Gly
 20 25 30
 Ile Ser Val Leu Val Asn Ile Val Phe Ala Val Leu Tyr Leu Val Val
 35 40 45
 Ile Val Phe Leu Leu Ser Arg Thr Pro Leu Trp Pro Arg Phe Lys Gly
 50 55 60
 Ser Gly Ser Lys Lys Gly Gly Gly Phe Ala Trp Ala Ala Ser Ser Leu
 65 70 75 80
 Leu Trp Gly Ala Phe Val Gly Phe Gly Ile Val Met Leu Phe Ala Gly
 85 90 95
 Pro Val Met Asp Leu Thr Asp Lys Leu Gly Trp Asp Phe Val Ala Met
 100 105 110
 Ser Phe Thr Gly Ala Tyr Pro Glu Glu Ile Ala Lys Ala Leu Gly Val
 115 120 125
 Ala Ile Ile Leu Leu Ser Phe Arg Gln Leu Asn Arg Pro Trp His Gly
 130 135 140
 Phe Ile Thr Gly Ala Leu Val Gly Leu Gly Phe Glu Val Asn Glu Asn
 145 150 155 160
 Leu Leu Tyr Gly Ala Thr Gly Ala Ile Met Asp Pro Asn Ala Asp Leu
 165 170 175
 Asp Gly Val Leu Met Met Trp Gln Tyr Arg Thr Met Leu Gly Pro Leu
 180 185 190
 Ile His Thr Leu Leu Thr Gly Phe Ala Gly Tyr Gly Ile Ala Leu Ala
 195 200 205
 Phe Phe Arg Ala Arg Lys Thr Val Ala Trp Arg Trp Gly Val Ala Ile
 210 215 220

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Gly Trp Thr Leu Ile Ala Phe Ala Leu His Phe Ser Trp Asn Leu Met
225                230                235                240

Trp Glu Asn Val Ile Gly Ser Tyr Val Thr Ile Ile Val Val Ser Val
245                250                255

Val Met Tyr Gly Leu Ala Ile Tyr Ile Leu Trp Ser Asn Trp Ala Glu
260                265                270

Ala Arg Asn Asp Ser Ser Tyr Ala Phe Val Pro Gly Ile Ile Thr Asn
275                280                285

Thr Lys Asp Leu Ser Leu Leu Asp Ala Pro Ile Pro Val Gly Ala Glu
290                295                300

Val Pro Glu Ser Arg Ile Pro Gln Gln Ile Glu Glu Pro Lys Ala Glu
305                310                315                320

Asn

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<210> 2477
<211> 302
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(279)
<223> RXA01903

<400> 2477
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Ala His Leu Asp Asp Arg Gly Ile Tyr Ile Ile Pro Ala Gln Tyr Pro
1 5 10 15

tgg gga tac gag gaa atc att aac cta cgg gca cgc gct acc tct aca 96
Trp Gly Tyr Glu Glu Ile Ile Asn Leu Pro Ala Arg Ala Thr Ser Thr
20 25 30

cct gct gtt gct cct cgc act gag gct gct cca gct aca gta tct gat 144
Pro Ala Val Ala Pro Arg Thr Glu Ala Ala Pro Ala Thr Val Ser Asp
35 40 45

gct gag gtc cag agc ctg ctt gag tac ttg cgt act aat gct ttc gta 192
Ala Glu Val Gln Ser Leu Leu Glu Tyr Leu Arg Thr Asn Ala Phe Val
50 55 60

agt cgt cac gac ggc gac acc acg aag gcc gac atc ttc aac aag cac 240
Ser Arg His Asp Gly Asp Thr Thr Lys Ala Asp Ile Phe Asn Lys His
65 70 75 80

gcg gat act gtc aac aag ctt gca gca cta cgt gca ccc taaaccacaca 289
Ala Asp Thr Val Asn Lys Leu Ala Ala Leu Arg Ala Pro
85 90

ccgcataacc ccc 302

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<400> 2478

Trp Gly Tyr Glu Glu Ile Ile Asn Leu Pro Ala Arg Ala Thr Ser Thr
20 25 30

Pro Ala Val Ala Pro Arg Thr Glu Ala Ala Pro Ala Thr Val Ser Asp
35 40 45

Ala Glu Val Gln Ser Leu Leu Glu Tyr Leu Arg Thr Asn Ala Phe Val
50 55 60

Ser Arg His Asp Gly Asp Thr Thr Lys Ala Asp Ile Phe Asn Lys His
65 70 75 80

Ala Asp Thr Val Asn Lys Leu Ala Ala Leu Arg Ala Pro
85 90

<211> 546

<212> DNA

<213> Corynebacterium glutamicum

 $\langle 220 \rangle$

<221> CDS

<222> (101) .. (523)

<223> RXA01904

<400> 2479

attagttttt attcgaagg gtggtctaaa ttttttacta ctgcgtcgtg tccaccggat 60

acacttgagg taatacagtt acgaggctaa ggagtatgta atg agc att tgc cgc 115
Met Ser Ile Ser Pro
1 5

aag aat tcc ggt aca cca aac gag aac gcc gca gca gcg cag gtg gca 163
Lys Asn Ser Gly Thr Pro Asn Glu Asn Ala Ala Ala Ala Gln Val Ala
10 15 20

gca aat ctg gct aat tta acg tcg cag gct aca ggg tcc atg gac gaa 211
Ala Asn Leu Ala Asn Leu Thr Ser Gln Ala Thr Gly Ser Met Asp Glu
25 30 35

act aat gag caa gtc att aaa agt aac gag cat ggc tct gat gct tat 259
Thr Asn Glu Gln Val Ile Lys Ser Asn Glu His Gly Ser Asp Ala Tyr
40 45 50

ttg gcg gat att aaa gcc agt cga gag atg tgg gca aaa att gcg ctc 307
Leu Ala Asp Ile Lys Ala Ser Arg Glu Met Trp Ala Lys Ile Ala Leu
55 60 65

gat ccg aat caa tct gaa gaa act agg aaa gaa gct cgg gag aat atg 355
Asp Pro Asn Gln Ser Glu Glu Thr Arg Lys Glu Ala Arg Glu Asn Met
70 75 80 85

gcg cgg ata gat gag tac gct cgt gag cac gat aaa gac aac aag ggt 403
Ala Arg Ile Asp Glu Tyr Ala Arg Glu His Asp Lys Asp Asn Lys Gly
90 95 100

ttg ttg cag aag tta gcg aaa aac aaa gca gag ctc atc ggg act gtt 451
Leu Leu Gln Lys Leu Ala Lys Asn Lys Ala Glu Leu Ile Gly Thr Val
105 110 115

gcg gtt gca acc tta ggt gta gtg gca gcc att gct aac aat ggc aag 499
Ala Val Ala Thr Leu Gly Val Val Ala Ala Ile Ala Asn Asn Gly Lys
120 125 130

ata ccg atg att cag ttg aaa aaa taacccccgc acaggctgga cat 546
Ile Pro Met Ile Gln Leu Lys Lys
135 140

<210> 2480

<211> 141

<212> PRT

<213> Corynebacterium glutamicum

<400> 2480

Met Ser Ile Ser Pro Lys Asn Ser Gly Thr Pro Asn Glu Asn Ala Ala
1 5 10 15

Ala Ala Gln Val Ala Ala Asn Leu Ala Asn Leu Thr Ser Gln Ala Thr
20 25 30

Gly Ser Met Asp Glu Thr Asn Glu Gln Val Ile Lys Ser Asn Glu His
35 40 45

Gly Ser Asp Ala Tyr Leu Ala Asp Ile Lys Ala Ser Arg Glu Met Trp
50 55 60

Ala Lys Ile Ala Leu Asp Pro Asn Gln Ser Glu Glu Thr Arg Lys Glu
65 70 75 80

Ala Arg Glu Asn Met Ala Arg Ile Asp Glu Tyr Ala Arg Glu His Asp
85 90 95

Lys Asp Asn Lys Gly Leu Leu Gln Lys Leu Ala Lys Asn Lys Ala Glu
100 105 110

Leu Ile Gly Thr Val Ala Val Ala Thr Leu Gly Val Val Ala Ala Ile
115 120 125

Ala Asn Asn Gly Lys Ile Pro Met Ile Gln Leu Lys Lys
130 135 140

<210> 2481

<211> 654

<212> DNA

<213> Corynebacterium glutamicum

 $\langle 220 \rangle$

<221> CDS

<222> (101) .. (631)

<223> RXA01905

<400> 2481
 aaatgaaagt cacaaacttt gttgggggttt ctttaaagta aaatacagaa gtttctctgg 60
 caaaaaacct cactactttc tacagaaagg cgtcttctc atg aag gct tct cag 115
 Met Lys Ala Ser Gln
 1 5
 acc ctc acc cgc aac act cgt gca cgc aag ctc ggc atg ggt att ctc 163
 Thr Leu Thr Arg Asn Thr Arg Ala Arg Lys Leu Gly Met Gly Ile Leu
 10 15 20
 gca gca act att atg gct acc ggt gca ctt gct ggc act gct cca cag 211
 Ala Ala Thr Ile Met Ala Thr Gly Ala Leu Ala Gly Thr Ala Pro Gln
 25 30 35
 gcg aca gca gca gta gat acc act gcg cca tac gtg tcc tat gtc gtt 259
 Ala Thr Ala Ala Val Asp Thr Thr Ala Pro Tyr Val Ser Tyr Val Val
 40 45 50
 gac att cct ggc aag gtt ggt gaa cca atc aag cct cag tac ctc acc 307
 Asp Ile Pro Gly Lys Val Gly Glu Pro Ile Lys Pro Gln Tyr Leu Thr
 55 60 65
 atc tcc gat cag tcc gcc tac acc gtg acc ttc aag tac atg cca tcc 355
 Ile Ser Asp Gln Ser Ala Tyr Thr Val Thr Phe Lys Tyr Met Pro Ser
 70 75 80 85
 tgg ttg aag tac gac gca aac aag aag atg ctg tac ggt acc cca acc 403
 Trp Leu Lys Tyr Asp Ala Asn Lys Lys Met Leu Tyr Gly Thr Pro Thr
 90 95 100
 gag gtt gat gtc tgg act cct gag gta cat gtt gtt gat gct cat ggc 451
 Glu Val Asp Val Trp Thr Pro Glu Val His Val Val Asp Ala His Gly
 105 110 115
 aac aag act gtc cgt tac ttc acc gtt gta gca gtc cca gca aac act 499
 Asn Lys Thr Val Arg Tyr Phe Thr Val Val Ala Val Pro Ala Asn Thr
 120 125 130
 gga cca acc acc acc acg cca tct act tca aag cca tct acc ccg cag 547
 Gly Pro Thr Thr Thr Thr Pro Ser Thr Ser Lys Pro Ser Thr Pro Gln
 135 140 145
 gtg acc acc cca act act ccg aag gcg cct acc ttg cca aag tcc acc 595
 Val Thr Thr Pro Thr Thr Pro Lys Ala Pro Thr Leu Pro Lys Ser Thr
 150 155 160 165
 ttc gac tgg acc ttg tgg ggc tcc atc ttt ggt ttc tagttctcac 641
 Phe Asp Trp Thr Leu Trp Gly Ser Ile Phe Gly Phe
 170 175
 tagcacctca aaa 654

<210> 2482

<211> 177

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2482

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Met Lys Ala Ser Gln Thr Leu Thr Arg Asn Thr Arg Ala Arg Lys Leu
 1             5             10             15
Gly Met Gly Ile Leu Ala Ala Thr Ile Met Ala Thr Gly Ala Leu Ala
          20             25             30
Gly Thr Ala Pro Gln Ala Thr Ala Ala Val Asp Thr Thr Ala Pro Tyr
          35             40             45
Val Ser Tyr Val Val Asp Ile Pro Gly Lys Val Gly Glu Pro Ile Lys
          50             55             60
Pro Gln Tyr Leu Thr Ile Ser Asp Gln Ser Ala Tyr Thr Val Thr Phe
          65             70             75             80
Lys Tyr Met Pro Ser Trp Leu Lys Tyr Asp Ala Asn Lys Lys Met Leu
          85             90             95
Tyr Gly Thr Pro Thr Glu Val Asp Val Trp Thr Pro Glu Val His Val
          100            105            110
Val Asp Ala His Gly Asn Lys Thr Val Arg Tyr Phe Thr Val Val Ala
          115            120            125
Val Pro Ala Asn Thr Gly Pro Thr Thr Thr Thr Pro Ser Thr Ser Lys
          130            135            140
Pro Ser Thr Pro Gln Val Thr Thr Pro Thr Thr Pro Lys Ala Pro Thr
          145            150            155            160
Leu Pro Lys Ser Thr Phe Asp Trp Thr Leu Trp Gly Ser Ile Phe Gly
          165            170            175
Phe

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<210> 2483
<211> 588
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(565)
<223> RXA01906

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<400> 2483
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gcaccacaac aaccacacct aaagaaaggt tttccacccc atg tcc gaa ttc cct 115
Met Ser Glu Phe Pro
1 5
aca cct acg act ttt cac gtc gaa cca gaa acg ctt agc tcc gcc acc 163
Thr Pro Thr Thr Phe His Val Glu Pro Glu Thr Leu Ser Ser Ala Thr
10 15 20
gat ctc act gtt gat gca cat aaa atc gca gaa ctg ctg ctc agc acc 211
Asp Leu Thr Val Asp Ala His Lys Ile Ala Glu Leu Leu Leu Ser Thr
25 30 35

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act gat tac cgt gtg ttc tac atg ccg cgt ctc gcc ggt gtg act cct 259
 Thr Asp Tyr Arg Val Phe Tyr Met Pro Arg Leu Ala Gly Val Thr Pro
 40 45 50

atc gtg tcc tac ctc tat gtc tac gat ggt gaa aac ttc ctc att gtt 307
 Ile Val Ser Tyr Leu Tyr Val Tyr Asp Gly Glu Asn Phe Leu Ile Val
 55 60 65

ggt cgc tcc act cat gtg ccg tgg gag tac tac gtt cac tac ccc atc 355
 Gly Arg Ser Thr His Val Pro Trp Glu Tyr Tyr Val His Tyr Pro Ile
 70 75 80 85

aag cca tca cgt gaa ttt ggc tct gct att gct gtg cct ctc gat gat 403
 Lys Pro Ser Arg Glu Phe Gly Ser Ala Ile Ala Val Pro Leu Asp Asp
 90 95 100

tct gat gac cct tat gat gca gca gaa gtt gtt gct cta gta aag cag 451
 Ser Asp Asp Pro Tyr Asp Ala Ala Glu Val Val Ala Leu Val Lys Gln
 105 110 115

tac atg acg ccc acg ctc act cct ggt gag ggt tat atg cag gcc ttt 499
 Tyr Met Thr Pro Thr Leu Thr Pro Gly Glu Gly Tyr Met Gln Gly Phe
 120 125 130

tac aag ggt ctc acc ttc acc aac cac ctc gat ata cat cga cca ctg 547
 Tyr Lys Gly Leu Thr Phe Thr Asn His Leu Asp Ile His Arg Pro Leu
 135 140 145

acc cag att atc tca gac taacagctat attcaccac cta 588
 Thr Gln Ile Ile Ser Asp
 150 155

<210> 2484
 <211> 155
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 2484
 Met Ser Glu Phe Pro Thr Pro Thr Thr Phe His Val Glu Pro Glu Thr
 1 5 10 15
 Leu Ser Ser Ala Thr Asp Leu Thr Val Asp Ala His Lys Ile Ala Glu
 20 25 30
 Leu Leu Leu Ser Thr Thr Asp Tyr Arg Val Phe Tyr Met Pro Arg Leu
 35 40 45
 Ala Gly Val Thr Pro Ile Val Ser Tyr Leu Tyr Val Tyr Asp Gly Glu
 50 55 60
 Asn Phe Leu Ile Val Gly Arg Ser Thr His Val Pro Trp Glu Tyr Tyr
 65 70 75 80
 Val His Tyr Pro Ile Lys Pro Ser Arg Glu Phe Gly Ser Ala Ile Ala
 85 90 95
 Val Pro Leu Asp Asp Ser Asp Asp Pro Tyr Asp Ala Ala Glu Val Val
 100 105 110

Ala Leu Val Lys Gln Tyr Met Thr Pro Thr Leu Thr Pro Gly Glu Gly
 115 120 125

Tyr Met Gln Gly Phe Tyr Lys Gly Leu Thr Phe Thr Asn His Leu Asp
 130 135 140

Ile His Arg Pro Leu Thr Gln Ile Ile Ser Asp
 145 150 155

<210> 2485
 <211> 735
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(712)
 <223> RXA01907

<400> 2485
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ttttcttact tttcctcata actacagaag ggacgccctc atg tct gct ttt gat 115
 Met Ser Ala Phe Asp
 1 5

gaa ctc cgc aag aac tac cgc tac aag ttc act gac acc tgg ccg gcc 163
 Glu Leu Arg Lys Asn Tyr Arg Tyr Lys Phe Thr Asp Thr Trp Pro Ala
 10 15 20

aac gct gtt acc ggc acc ggc tac tac gcc aac cca gct ttt atc atc 211
 Asn Ala Val Thr Gly Thr Gly Tyr Tyr Ala Asn Pro Ala Phe Ile Ile
 25 30 35

atc tcc gct gat gcc atg acg cag aac acc cat gcc gat tcc aat ctc 259
 Ile Ser Ala Asp Ala Met Thr Gln Asn Thr His Ala Asp Ser Asn Leu
 40 45 50

atc acg gtt aaa gag cac ctt aac acc ctg ttt ccg tac agc gta caa 307
 Ile Thr Val Lys Glu His Leu Asn Thr Leu Phe Pro Tyr Ser Val Gln
 55 60 65

cgc aag gat cgt gcc ttt gtc tct gag atc tac acc cct att aac ctg 355
 Arg Lys Asp Arg Ala Phe Val Ser Glu Ile Tyr Thr Pro Ile Asn Leu
 70 75 80 85

ctc gaa gat aat cca gaa cta gct caa gaa ata ctc gat gtg ctc gac 403
 Leu Glu Asp Asn Pro Glu Leu Ala Gln Glu Ile Leu Asp Val Leu Asp
 90 95 100

acc ctg agc aac aac gct gtt ttt aac gat gcg cac tac agc gag ctt 451
 Thr Leu Ser Asn Asn Ala Val Phe Asn Asp Ala His Tyr Ser Glu Leu
 105 110 115

gaa cta gag cgc ctc aat gaa tat gtc atc gac acc ttg gcc tat gac 499
 Glu Leu Glu Arg Leu Asn Glu Tyr Val Ile Asp Thr Leu Ala Tyr Asp
 120 125 130

atg aag tcc gac atg atg cgc gcc ctc gtt aag gcc cga cca gag gcc 547
 Met Lys Ser Asp Met Met Arg Ala Leu Val Lys Ala Arg Pro Glu Ala

135 140 145

gat ctt gag gcg atg gaa gaa ctc gac att gcc aat atc cag agc tgg 595
 Asp Leu Glu Ala Met Glu Glu Leu Asp Ile Ala Asn Ile Gln Ser Trp
 150 155 160 165

att aat ctc cac tcc tcc act gtg agc gaa cac aac gat ggc agc gtt 643
 Ile Asn Leu His Ser Ser Thr Val Ser Glu His Asn Asp Gly Ser Val
 170 175 180

gat gat gca ccg ttt aat tct ctc gca tta gct gag att tat ttg caa 691
 Asp Asp Ala Pro Phe Asn Ser Leu Ala Leu Ala Glu Ile Tyr Leu Gln
 185 190 195

cag ctt gca gac cac act gtc taagcacgct gtgtaactac cac 735
 Gln Leu Ala Asp His Thr Val
 200

<210> 2486
 <211> 204
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2486
 Met Ser Ala Phe Asp Glu Leu Arg Lys Asn Tyr Arg Tyr Lys Phe Thr
 1 5 10 15
 Asp Thr Trp Pro Ala Asn Ala Val Thr Gly Thr Gly Tyr Tyr Ala Asn
 20 25 30
 Pro Ala Phe Ile Ile Ile Ser Ala Asp Ala Met Thr Gln Asn Thr His
 35 40 45
 Ala Asp Ser Asn Leu Ile Thr Val Lys Glu His Leu Asn Thr Leu Phe
 50 55 60
 Pro Tyr Ser Val Gln Arg Lys Asp Arg Ala Phe Val Ser Glu Ile Tyr
 65 70 75 80
 Thr Pro Ile Asn Leu Leu Glu Asp Asn Pro Glu Leu Ala Gln Glu Ile
 85 90 95
 Leu Asp Val Leu Asp Thr Leu Ser Asn Asn Ala Val Phe Asn Asp Ala
 100 105 110
 His Tyr Ser Glu Leu Glu Leu Glu Arg Leu Asn Glu Tyr Val Ile Asp
 115 120 125
 Thr Leu Ala Tyr Asp Met Lys Ser Asp Met Met Arg Ala Leu Val Lys
 130 135 140
 Ala Arg Pro Glu Ala Asp Leu Glu Ala Met Glu Glu Leu Asp Ile Ala
 145 150 155 160
 Asn Ile Gln Ser Trp Ile Asn Leu His Ser Ser Thr Val Ser Glu His
 165 170 175
 Asn Asp Gly Ser Val Asp Asp Ala Pro Phe Asn Ser Leu Ala Leu Ala
 180 185 190

Glu Ile Tyr Leu Gln Gln Leu Ala Asp His Thr Val
195 200

<210> 2487

<211> 529

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(529)

<223> RXA01923

<400> 2487

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agtgcacgt cccatgtttc tcacactctc aggagctgac atg tct gca ctt att 115
Met Ser Ala Leu Ile
1 5

aaa ggt tca gga cct cat cat gtg gtt gtc tta aat ggt tgg ttt ggt 163
Lys Gly Ser Gly Pro His His Val Val Leu Asn Gly Trp Phe Gly
10 15 20

cat gct gcg ggc tgg gga gct ttc gct gac tat ctt gac ctc ggc aac 211
His Ala Ala Gly Trp Gly Ala Phe Ala Asp Tyr Leu Asp Leu Gly Asn
25 30 35

tac acc tgg cac ttt tgg gat tac cga ggt tac ggc aac aga aaa gac 259
Tyr Thr Trp His Phe Trp Asp Tyr Arg Gly Tyr Gly Asn Arg Lys Asp
40 45 50

gac gca gga gaa ttt act ctg gag gaa att tca gcg gat atc gtt gca 307
Asp Ala Gly Glu Phe Thr Leu Glu Glu Ile Ser Ala Asp Ile Val Ala
55 60 65

tac atc gac tcg att gag gca gaa aag gtt tcc atc ctg ggc cat tcc 355
Tyr Ile Asp Ser Ile Glu Ala Glu Lys Val Ser Ile Leu Gly His Ser
70 75 80 85

atg ggt gga gtg ttc atg cag aaa gtc ctt gca gac agc gcc acc ccc 403
Met Gly Gly Val Phe Met Gln Lys Val Leu Ala Asp Ser Ala Thr Pro
90 95 100

atc gct tca ctg gtt gga att tct gcc gtt gct gca gct gga aca cca 451
Ile Ala Ser Leu Val Gly Ile Ser Ala Val Ala Ala Gly Thr Pro
105 110 115

ttc gat gag gat tct cgg aag ctt ttc acc tca gca ggg cac aac ccg 499
Phe Asp Glu Asp Ser Arg Lys Leu Phe Thr Ser Ala Gly His Asn Pro
120 125 130

gac tcg agg cga gcc atc atc gat ttc acc 529
Asp Ser Arg Arg Ala Ile Ile Asp Phe Thr
135 140

<210> 2488

<211> 143

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2488

Met Ser Ala Leu Ile Lys Gly Ser Gly Pro His His Val Val Val Leu
 1 5 10 15

Asn Gly Trp Phe Gly His Ala Ala Gly Trp Gly Ala Phe Ala Asp Tyr
 20 25 30

Leu Asp Leu Gly Asn Tyr Thr Trp His Phe Trp Asp Tyr Arg Gly Tyr
 35 40 45

Gly Asn Arg Lys Asp Asp Ala Gly Glu Phe Thr Leu Glu Glu Ile Ser
 50 55 60

Ala Asp Ile Val Ala Tyr Ile Asp Ser Ile Glu Ala Glu Lys Val Ser
 65 70 75 80

Ile Leu Gly His Ser Met Gly Gly Val Phe Met Gln Lys Val Leu Ala
 85 90 95

Asp Ser Ala Thr Pro Ile Ala Ser Leu Val Gly Ile Ser Ala Val Ala
 100 105 110

Ala Ala Gly Thr Pro Phe Asp Glu Asp Ser Arg Lys Leu Phe Thr Ser
 115 120 125

Ala Gly His Asn Pro Asp Ser Arg Arg Ala Ile Asp Phe Thr
 130 135 140

<210> 2489

<211> 777

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> {101}..(754)

<223> RXA01931

<400> 2489

tcgataggca tggcgccgat tctaggtcga actgatctaa agtcccacca cgcaaaagta 60

accaaggcgt acatctaccc ggcactttaa gatcagtgcc atg agc act tct ttt 115
 Met Ser Thr Ser Phe
 1 5

gag tcc att ccc gga gtt act atc tcc gct cga aaa gcc ttg agc act 163
 Glu Ser Ile Pro Gly Val Thr Ile Ser Ala Arg Lys Ala Leu Ser Thr
 10 15 20

gcg ggg ttt aaa gat ctg gaa tcg ott gca ggt acc aat tac gaa gaa 211
 Ala Gly Phe Lys Asp Leu Glu Ser Leu Ala Gly Thr Asn Tyr Glu Glu
 25 30 35

gtg gct ggt ctg tca gga att ggc gca cgt act ttg gag cga ttg caa 259
 Val Ala Gly Leu Ser Gly Ile Gly Ala Arg Thr Leu Glu Arg Leu Gln
 40 45 50

gca gcg ctg gtg gag aag aga atg agc ttt ggc ggt aaa gtg cca gag 307

Ala Ala Leu Val Glu Lys Arg Met Ser Phe Gly Gly Lys Val Pro Glu
55 60 65

gca gaa cag cgc acc gcg acg tgg aca acg cta gat tct gca gca cca 355
Ala Glu Gln Arg Thr Ala Thr Trp Thr Thr Leu Asp Ser Ala Ala Pro
70 75 80 85

gag gca aca gaa acc tca gaa tcc cca gag tac ttc att caa aac cta 403
Glu Ala Thr Glu Thr Ser Glu Ser Pro Glu Tyr Phe Ile Gln Asn Leu
90 95 100

gac att cct cgc aga att acc cac gcc cgg ttg ttg ttg gaa att ttc 451
Asp Ile Pro Arg Arg Ile Thr His Gly Arg Leu Leu Leu Ile Phe
105 110 115

aac aga gcg aca gcc cag aaa cct tat gta gca ggg tct tcg att gtt 499
Asn Arg Ala Thr Gly Gln Lys Pro Tyr Val Ala Gly Ser Ser Ile Val
120 125 130

ggt tat ggg cga gtt cat tat cgc tat gcc acg ggt agg gaa ggg atc 547
Gly Tyr Gly Arg Val His Tyr Arg Tyr Ala Thr Gly Arg Glu Gly Ile
135 140 145

act att cgt gtg ggt ttc agt ccg cga aag gca aag att tca ctt tat 595
Thr Ile Arg Val Gly Phe Ser Pro Arg Lys Ala Lys Ile Ser Leu Tyr
150 155 160 165

gga cta acc agt gcg cct gcg tct cga gaa ctt ctg aag aaa cca gag gat 643
Gly Leu Thr Ser Ala Pro Ala Ser Arg Glu Leu Lys Lys Leu Gly
170 175 180

aag cat tct gtt ggt gtg tcc tgc cta tat atc aac aaa cca gag gat 691
Lys His Ser Val Gly Val Ser Cys Leu Tyr Ile Asn Lys Pro Glu Asp
185 190 195

ggt gat ctt gag gtg ctt gag gaa atg atc cgt att tct tgg gaa gcg 739
Val Asp Leu Glu Val Leu Glu Glu Met Ile Arg Ile Ser Trp Glu Ala
200 205 210

gaa cct gcc gaa tgt taaatctcaa cctttaacaa agt 777
Glu Pro Gly Glu Cys
215

<210> 2490

<211> 218

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2490

Met Ser Thr Ser Phe Glu Ser Ile Pro Gly Val Thr Ile Ser Ala Arg
1 5 10 15

Lys Ala Leu Ser Thr Ala Gly Phe Lys Asp Leu Glu Ser Leu Ala Gly
20 25 30

Thr Asn Tyr Glu Glu Val Ala Gly Leu Ser Gly Ile Gly Ala Arg Thr
35 40 45

Leu Glu Arg Leu Gln Ala Ala Leu Val Glu Lys Arg Met Ser Phe Gly
50 55 60

Gly Lys Val Pro Glu Ala Glu Gln Arg Thr Ala Thr Trp Thr Thr Leu
 65 70 75 80
 Asp Ser Ala Ala Pro Glu Ala Thr Glu Thr Ser Glu Ser Pro Glu Tyr
 85 90 95
 Phe Ile Gln Asn Leu Asp Ile Pro Arg Arg Ile Thr His Gly Arg Leu
 100 105 110
 Leu Leu Glu Ile Phe Asn Arg Ala Thr Gly Gln Lys Pro Tyr Val Ala
 115 120 125
 Gly Ser Ser Ile Val Gly Tyr Gly Arg Val His Tyr Arg Tyr Ala Thr
 130 135 140
 Gly Arg Glu Gly Ile Thr Ile Arg Val Gly Phe Ser Pro Arg Lys Ala
 145 150 155 160
 Lys Ile Ser Leu Tyr Gly Leu Thr Ser Ala Pro Ala Ser Arg Glu Leu
 165 170 175
 Leu Lys Lys Leu Gly Lys His Ser Val Gly Val Ser Cys Leu Tyr Ile
 180 185 190
 Asn Lys Pro Glu Asp Val Asp Leu Glu Val Leu Glu Glu Met Ile Arg
 195 200 205
 Ile Ser Trp Glu Ala Glu Pro Gly Glu Cys
 210 215
 <210> 2491
 <211> 558
 <212> DNA
 <213> Corynebacterium glutamicum
 <220>
 <221> CDS
 <222> (101)..(535)
 <223> RXA01941
 <400> 2491
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 ccagcgcagc gttgaaaaac gttgggcgcc agtcaccac atg gcc ttg act tca 115
 Met Ala Leu Thr Ser
 1 5
 ctt ttg cac cag ctt gca gat aaa aaa cac agt gac ctc agc cgg gaa 163
 Leu Leu His Gln Leu Ala Asp Lys Lys His Ser Asp Leu Ser Arg Glu
 10 15 20
 gac atc gta ccg cgg gcc ttt act gtc ccg acc tct act gac gcc cac 211
 Asp Ile Val Pro Arg Ala Phe Thr Val Pro Thr Ser Thr Asp Ala His
 25 30 35
 gct att cat caa gac ttg gaa aaa ctc cga aac tcc gta ctc aaa gag 259
 Ala Ile His Gln Asp Leu Glu Lys Leu Arg Asn Ser Val Leu Lys Glu
 40 45 50

caa aat cac cta acc act gtg ttg gga act tgg tca gaa ttc ctc acc 307
 Gln Asn His Leu Thr Thr Val Leu Gly Thr Trp Ser Glu Phe Leu Thr
 55 60 65

tcc aac agc gat aac tcc gac att ttg cgt tcc tcc gct gaa ctt ggg 355
 Ser Asn Ser Asp Asn Ser Asp Ile Leu Arg Ser Ser Ala Glu Leu Gly
 70 75 80 85

ctc caa ttg gag cag gtc cgc gat aaa gca ctc gaa gtg gaa cag cgt 403
 Leu Gln Leu Glu Gln Val Arg Asp Lys Ala Leu Glu Val Glu Gln Arg
 90 95 100

atc aaa gcc tct gct cag gtg gat ctt acg gac ctg gct cat gag att 451
 Ile Lys Ala Ser Ala Gln Val Asp Leu Thr Asp Leu Ala His Glu Ile
 105 110 115

gag atc tgc aat caa cac cac gca acc ctc atc agt gcg att cag gta 499
 Glu Ile Cys Asn Gln His His Ala Thr Leu Ile Ser Ala Ile Gln Val
 120 125 130

aga ctg caa tcg cat act gct gag ctt cgg gct ggg tgattttctta 545
 Arg Leu Gln Ser His Thr Ala Glu Leu Arg Ala Gly
 135 140 145

agactgacct agt 558

<210> 2492
 <211> 145
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2492
 Met Ala Leu Thr Ser Leu Leu His Gln Leu Ala Asp Lys Lys His Ser
 1 5 10 15

Asp Leu Ser Arg Glu Asp Ile Val Pro Arg Ala Phe Thr Val Pro Thr
 20 25 30

Ser Thr Asp Ala His Ala Ile His Gln Asp Leu Glu Lys Leu Arg Asn
 35 40 45

Ser Val Leu Lys Glu Gln Asn His Leu Thr Thr Val Leu Gly Thr Trp
 50 55 60

Ser Glu Phe Leu Thr Ser Asn Ser Asp Asn Ser Asp Ile Leu Arg Ser
 65 70 75 80

Ser Ala Glu Leu Gly Leu Gln Leu Glu Gln Val Arg Asp Lys Ala Leu
 85 90 95

Glu Val Glu Gln Arg Ile Lys Ala Ser Ala Gln Val Asp Leu Thr Asp
 100 105 110

Leu Ala His Glu Ile Glu Ile Cys Asn Gln His His Ala Thr Leu Ile
 115 120 125

Ser Ala Ile Gln Val Arg Leu Gln Ser His Thr Ala Glu Leu Arg Ala
 130 135 140

Gly

145

<210> 2493
 <211> 723
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(700)
 <223> RXA01942

<400> 2493
 gccgcgaaat tcgggtgaaat tgaaggtatt cctgcagatc aggcacaaatc ttccacgact 60

gtgatcaagg tcaacggcaa gaacgagtaa cctgggatcc atg ttg cgc att gga 115
 Met Leu Arg Ile Gly
 1 5

cta aca gga ggg atc ggc agc ggt aaa tct acc gtt gcc gat ctt ttg 163
 Leu Thr Gly Gly Ile Gly Ser Gly Lys Ser Thr Val Ala Asp Leu Leu
 10 15 20

tca tct gaa gga ttt ctc atc gtc gac gcg gac caa gtt gcc cgc gat 211
 Ser Ser Glu Gly Phe Leu Ile Val Asp Ala Asp Gln Val Ala Arg Asp
 25 30 35

atc gtc gaa ccc gga caa cgc gca tta gca gag cta gct gaa gct ttt 259
 Ile Val Glu Pro Gly Gln Pro Ala Leu Ala Glu Leu Ala Glu Phe
 40 45 50

ggc caa gac atc tta aaa ccc gac ggc act cta gac cgc gcg gga tta 307
 Gly Gln Asp Ile Leu Lys Pro Asp Gly Thr Leu Asp Arg Ala Gly Leu
 55 60 65

gca gcc aaa gca ttt gtc agc gaa gaa caa aca gcg ctg ctc aat gcc 355
 Ala Ala Lys Ala Phe Val Ser Glu Glu Gln Thr Ala Leu Leu Asn Ala
 70 75 80 85

att acc cac cct cgt atc gcc gaa gag tca gct cgt cga ttc aac gaa 403
 Ile Thr His Pro Arg Ile Ala Glu Glu Ser Ala Arg Arg Phe Asn Glu
 90 95 100

gcc gaa gat caa ggc gcc aaa gtt gcg gtt tat gac atg cct ttg ctt 451
 Ala Glu Asp Gln Gly Ala Lys Val Ala Val Tyr Asp Met Pro Leu Leu
 105 110 115

gta gaa aaa ggc ctt gac cgc aag atg gac ctt gtc gtc gta gtt gat 499
 Val Glu Lys Gly Leu Asp Arg Lys Met Asp Leu Val Val Val Val Asp
 120 125 130

gtt gac gta gag gaa cgc gtc cgc aga ctt gtg gaa aaa cgt gcc ctc 547
 Val Asp Val Glu Glu Arg Val Arg Arg Leu Val Glu Lys Arg Gly Leu
 135 140 145

aca gag gac gac gtg cgg cgt cga atc gct tct caa gtg ccc gac gac 595
 Thr Glu Asp Asp Val Arg Arg Arg Ile Ala Ser Gln Val Pro Asp Asp
 150 155 160 165

gtc aga ctt aaa gcc gct gac atc gtt gtg gac aat aac gcc acg cta 643

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Val Arg Leu Lys Ala Ala Asp Ile Val Val Asp Asn Asn Gly Thr Leu
      170                      175                      180

gag gac ctt cat gct gaa gca agc aag ctg att gct gag att ctt agt    691
Glu Asp Leu His Ala Glu Ala Ser Lys Leu Ile Ala Glu Ile Leu Ser
      185                      190                      195

cgc gtg aat tagcactaaa acatcgtaa agt                                723
Arg Val Asn
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<210> 2494

<211> 200

<212> PRT

<213> Corynebacterium glutamicum

<400> 2494

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Met Leu Arg Ile Gly Leu Thr Gly Gly Ile Gly Ser Gly Lys Ser Thr
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Val Ala Asp Leu Leu Ser Ser Glu Gly Phe Leu Ile Val Asp Ala Asp
      20          25          30

Gln Val Ala Arg Asp Ile Val Glu Pro Gly Gln Pro Ala Leu Ala Glu
      35          40          45

Leu Ala Glu Ala Phe Gly Gln Asp Ile Leu Lys Pro Asp Gly Thr Leu
      50          55          60

Asp Arg Ala Gly Leu Ala Ala Lys Ala Phe Val Ser Glu Glu Gln Thr
      65          70          75          80

Ala Leu Leu Asn Ala Ile Thr His Pro Arg Ile Ala Glu Glu Ser Ala
      85          90          95

Arg Arg Phe Asn Glu Ala Glu Asp Gln Gly Ala Lys Val Ala Val Tyr
      100         105         110

Asp Met Pro Leu Leu Val Glu Lys Gly Leu Asp Arg Lys Met Asp Leu
      115         120         125

Val Val Val Val Asp Val Asp Val Glu Glu Arg Val Arg Arg Leu Val
      130         135         140

Glu Lys Arg Gly Leu Thr Glu Asp Asp Val Arg Arg Arg Ile Ala Ser
      145         150         155         160

Gln Val Pro Asp Asp Val Arg Leu Lys Ala Ala Asp Ile Val Val Asp
      165         170         175

Asn Asn Gly Thr Leu Glu Asp Leu His Ala Glu Ala Ser Lys Leu Ile
      180         185         190

Ala Glu Ile Leu Ser Arg Val Asn
      195         200

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<210> 2495

<211> 585

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(562)

<223> RXA01957

<400> 2495

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gaccgcacaaa cactaaaacc tccacaacaa ggacatcacc atg act act cgc acc 115
 Met Thr Thr Arg Thr
 1 5

gta tct act tct gca ccc cat gtc act gtc aac atc aat acc gcg cac 163
 Val Ser Thr Ser Ala Pro His Val Thr Val Asn Ile Asn Thr Ala His
 10 15 20

aac aaa aca cgc act gtt acc aat ggc gcc aga aaa act aat gca gag 211
 Asn Lys Thr Arg Thr Val Thr Asn Gly Ala Arg Lys Thr Asn Ala Glu
 25 30 35

cgt ggc aag agc tgc atc tca ttt cgt gta ggg cca gaa ttg ttt gat 259
 Arg Gly Lys Ser Cys Ile Ser Phe Arg Val Gly Pro Glu Leu Phe Asp
 40 45 50

gaa ttc aaa gcg acc tgc atc gac aac gat att tcc atg acc aag gcg 307
 Glu Phe Lys Ala Thr Cys Ile Asp Asn Asp Ile Ser Met Thr Lys Ala
 55 60 65

ttt gag aaa gag ctt cgc acc tgg gtt gat gag cac aac gct ggt gca 355
 Phe Glu Lys Glu Leu Arg Thr Trp Val Asp Glu His Asn Ala Gly Ala
 70 75 80 85

aca aag aaa aga aac acc cat cgc acc tac gta caa gca ccc gtt ggt 403
 Thr Lys Lys Arg Asn Thr His Arg Thr Tyr Val Gln Ala Pro Val Gly
 90 95 100

act gtc gcc acc agc tct att cca ggt ctt ggg tta ttt act gtg ttc 451
 Thr Val Ala Thr Ser Ser Ile Pro Gly Leu Gly Leu Phe Thr Val Phe
 105 110 115

aag aag agc tct gat cag atg tgg tac gac ctg gaa agc agc ccg ctg 499
 Lys Lys Ser Ser Asp Gln Met Trp Tyr Asp Leu Glu Ser Ser Pro Leu
 120 125 130

atc gca caa gag ccc atg tgc aat atg gac atg cat cgt aac ggc tct 547
 Ile Ala Gln Glu Pro Met Ser Asn Met Asp Met His Arg Asn Gly Ser
 135 140 145

ttt gag ctg cac ctg tagatctctc tctcgaccac aca 585
 Phe Glu Leu His Leu
 150

<210> 2496

<211> 154

<212> PRT

<213> Corynebacterium glutamicum

<400> 2496

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Met Thr Thr Arg Thr Val Ser Thr Ser Ala Pro His Val Thr Val Asn
 1          5          10          15

Ile Asn Thr Ala His Asn Lys Thr Arg Thr Val Thr Asn Gly Ala Arg
          20          25          30

Lys Thr Asn Ala Glu Arg Gly Lys Ser Cys Ile Ser Phe Arg Val Gly
          35          40          45

Pro Glu Leu Phe Asp Glu Phe Lys Ala Thr Cys Ile Asp Asn Asp Ile
 50          55          60

Ser Met Thr Lys Ala Phe Glu Lys Glu Leu Arg Thr Trp Val Asp Glu
 65          70          75          80

His Asn Ala Gly Ala Thr Lys Lys Arg Asn Thr His Arg Thr Tyr Val
          85          90          95

Gln Ala Pro Val Gly Thr Val Ala Thr Ser Ser Ile Pro Gly Leu Gly
          100          105          110

Leu Phe Thr Val Phe Lys Lys Ser Ser Asp Gln Met Trp Tyr Asp Leu
          115          120          125

Glu Ser Ser Pro Leu Ile Ala Gln Glu Pro Met Ser Asn Met Asp Met
          130          135          140

His Arg Asn Gly Ser Phe Glu Leu His Leu
145          150

<210> 2497
<211> 630
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(607)
<223> RXA01958

<400> 2497
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cacacagctc tcaccacctc ctagaaagga cggtttcacc atg tct aaa aaa cgc 115
Met Ser Lys Lys Arg
1

gac cac ctc acc gtc att cct gac ctt gag tca cgc acc cat cac agc 163
Asp His Leu Thr Val Ile Pro Asp Leu Glu Ser Arg Thr His His Ser
10          15          20

cgc agt aca caa ccg cca act acg ctg ccc gca cca cag ctg act att 211
Arg Ser Thr Gln Pro Pro Thr Thr Leu Pro Ala Pro Gln Leu Thr Ile
25          30          35

atc acc gca cca gac aag cat caa cca cag ctt cgg gtt gtt aaa aac 259
Ile Thr Ala Pro Asp Lys His Gln Pro Gln Leu Arg Val Val Lys Asn
40          45          50

acc acc acc cca tct tct gtg cag ccc tcg ccg atc aac tac agc ttt 307

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Thr Thr Thr Pro Ser Ser Val Gln Pro Ser Pro Ile Asn Tyr Ser Phe
  55                                60                                65

act gat cct gta ctt cgc gag gct cac tat gca ttc cag cac agc gaa 355
Thr Asp Pro Val Leu Arg Glu Ala His Tyr Ala Phe Gln His Ser Glu
  70                                75                                80                                85

ctt gcc agg cca aca gtc ctg gac tca cac tgg gtt cgt cgc gca caa 403
Leu Ala Arg Pro Thr Val Leu Asp Ser His Trp Val Arg Arg Ala Gln
                                90                                95                                100

gaa gaa ttc gac act gag cat aat gct gcc tat gtc cgt gcc gct gac 451
Glu Glu Phe Asp Thr Glu His Asn Ala Ala Tyr Val Arg Ala Ala Asp
                                105                                110                                115

cag ctc tta tcc cct ttt gat gcc tac atc ctc gac aac ggc gat gtt 499
Gln Leu Leu Ser Pro Phe Asp Ala Tyr Ile Leu Asp Asn Gly Asp Val
                                120                                125                                130

tac acc aag acc cca cgt gcc atc agt gct gct gaa caa gaa gaa ata 547
Tyr Thr Lys Thr Pro Arg Ala Ile Ser Ala Ala Glu Gln Glu Glu Ile
                                135                                140                                145

ctt gag cac ttg cac gaa cac cat atc tgc tgg gac gaa gaa gct gaa 595
Leu Glu His Leu His Glu His His Ile Cys Trp Asp Glu Glu Ala Glu
                                150                                155                                160                                165

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Phe Leu Leu Arg

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<210> 2498

<211> 169

<212> PRT

<213> Corynebacterium glutamicum

<400> 2498

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Met Ser Lys Lys Arg Asp His Leu Thr Val Ile Pro Asp Leu Glu Ser
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Arg Thr His His Ser Arg Ser Thr Gln Pro Pro Thr Thr Leu Pro Ala
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Pro Gln Leu Thr Ile Ile Thr Ala Pro Asp Lys His Gln Pro Gln Leu
                                35                                40                                45

Arg Val Val Lys Asn Thr Thr Thr Pro Ser Ser Val Gln Pro Ser Pro
                                50                                55                                60

Ile Asn Tyr Ser Phe Thr Asp Pro Val Leu Arg Glu Ala His Tyr Ala
                                65                                70                                75                                80

Phe Gln His Ser Glu Leu Ala Arg Pro Thr Val Leu Asp Ser His Trp
                                85                                90                                95

Val Arg Arg Ala Gln Glu Glu Phe Asp Thr Glu His Asn Ala Ala Tyr
                                100                                105                                110

Val Arg Ala Ala Asp Gln Leu Leu Ser Pro Phe Asp Ala Tyr Ile Leu
                                115                                120                                125

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Asp Asn Gly Asp Val Tyr Thr Lys Thr Pro Arg Ala Ile Ser Ala Ala
130 135 140

Glu Gln Glu Glu Ile Leu Glu His Leu His Glu His His Ile Cys Trp
145 150 155 160

Asp Glu Glu Ala Glu Phe Leu Leu Arg
165

<210> 2499

<211> 481

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(481)

<223> RXA01959

<400> 2499

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cactgcctat ttgaccattc ttgtgcaaga aagtacacct atg ccc cac gac gtt 115
Met Pro His Asp Val
1 5

tac gat gtc gaa cac atc att tcc aag caa cct ttc tgc tcc atc ttt 163
Tyr Asp Val Glu His Ile Ile Ser Lys Gln Pro Phe Cys Ser Ile Phe
10 15 20

ttc cag ctc ccc gct gca gcg ctg aaa cct act att caa aaa gct gcc 211
Phe Gln Leu Pro Ala Ala Ala Leu Lys Pro Thr Ile Gln Lys Ala Ala
25 30 35

acc aac cgc gac ctt act aag ctc aac acc gaa cag atc gct gag aac 259
Thr Asn Arg Asp Leu Thr Lys Leu Asn Thr Glu Gln Ile Ala Glu Asn
40 45 50

cta cag cgc tac ctc gac acc tac agt gtc atg tct cac cag cgt gtc 307
Leu Gln Arg Tyr Leu Asp Thr Tyr Ser Val Met Ser His Gln Arg Val
55 60 65

acc att gaa gag gtc act cat gtg cgc aac cct cat gag cct gat tat 355
Thr Ile Glu Glu Val Thr His Val Arg Asn Pro His Glu Pro Asp Tyr
70 75 80 85

gag ttt tca cca cag tac ggt gca cat atc tcg ctc atc ggt gag tct 403
Glu Phe Ser Pro Gln Tyr Gly Ala His Ile Ser Leu Ile Gly Glu Ser
90 95 100

tat gct gtg aac acg gcc acc aac gag cct tat gcc acc gac tcc gag 451
Tyr Ala Val Asn Thr Ala Thr Asn Glu Pro Tyr Ala Thr Asp Ser Glu
105 110 115

ggc cat cct ctc gca ctg tat ttt gaa atg 481
Gly His Pro Leu Ala Leu Tyr Phe Glu Met
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<210> 2500
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<212> PRT
<213> Corynebacterium glutamicum
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<400> 2500
Met Pro His Asp Val Tyr Asp Val Glu His Ile Ile Ser Lys Gln Pro
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Phe Cys Ser Ile Phe Phe Gln Leu Pro Ala Ala Ala Leu Lys Pro Thr
20 25 30

Ile Gln Lys Ala Ala Thr Asn Arg Asp Leu Thr Lys Leu Asn Thr Glu
35 40 45

Gln Ile Ala Glu Asn Leu Gln Arg Tyr Leu Asp Thr Tyr Ser Val Met
50 55 60

Ser His Gln Arg Val Thr Ile Glu Glu Val Thr His Val Arg Asn Pro
65 70 75 80

His Glu Pro Asp Tyr Glu Phe Ser Pro Gln Tyr Gly Ala His Ile Ser
85 90 95

Leu Ile Gly Glu Ser Tyr Ala Val Asn Thr Ala Thr Asn Glu Pro Tyr
100 105 110

Ala Thr Asp Ser Glu Gly His Pro Leu Ala Leu Tyr Phe Glu Met
115 120 125

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<211> 603
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(580)  
<223> RXA01961
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atccaccttg aagccgcca caactaagaa agcatccttc atg act gac aac gct 115
Met Thr Asp Asn Ala
1 5

gac aac acc aca gat aac gta acc aat aac tca gac acc aat ctc gat 163
Asp Asn Thr Thr Asp Asn Val Thr Asn Asn Ser Asp Thr Asn Leu Asp
10 15 20

tac agc ttc gac cgc ctg cct gac gag ccg tat gcc tac ggc ttg gaa 211
Tyr Ser Phe Asp Pro Leu Pro Asp Glu Pro Tyr Ala Tyr Gly Phe Glu

 25 30 35

ctg gtc gct gct gat gca cac tct gac tca aca aca acc agc acc gat 259
Leu Val Ala Ala Asp Ala His Ser Asp Ser Thr Thr Thr Ser Thr Asp
40 45 50

acc cca gag act gtc gct gtg gca ctt aaa acc cgc gag gac act atc 307

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Thr Pro Glu Thr Val Ala Val Ala Leu Lys Thr Arg Glu Asp Thr Ile
  55                      60                      65

aac tgg gtc aac acc cag cgt gcc gaa ggt aaa ccc gat gaa att cgt   355
Asn Trp Val Asn Thr Gln Arg Ala Glu Gly Lys Pro Asp Glu Ile Arg
  70                      75                      80                      85

atc aat aac cca att cga tca gag cgt att gct gag ttt gtc cac gaa   403
Ile Asn Asn Pro Ile Arg Ser Glu Arg Ile Ala Glu Phe Val His Glu
  90                      95                      100

atg atc atg cat cac ggc ctc gta gcc tgc atg gaa gat ctc gca ata   451
Met Ile Met His His Gly Leu Val Ala Cys Met Glu Asp Leu Ala Ile
  105                      110                      115

ctt atc aag cgc gac aag ctc acc cag ctg gaa gcc gaa aac gct atc   499
Leu Ile Lys Arg Asp Lys Leu Thr Gln Leu Glu Ala Glu Asn Ala Ile
  120                      125                      130

aca gcc tgg cac aac ctc acc aaa gaa tcc ctt ggt cag atc atg ggg   547
Thr Ala Trp His Asn Leu Thr Lys Glu Ser Leu Gly Gln Ile Met Gly
  135                      140                      145

ctc ttc tat cag tac gtc gaa aac aac aca aaa taggaagaa gaaacaccat 600
Leu Phe Tyr Gln Tyr Val Glu Asn Asn Thr Lys
  150                      155                      160

cat                                                                    603

<210> 2502
<211> 160
<212> FRT
<213> Corynebacterium glutamicum

<400> 2502
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Asp Thr Asn Leu Asp Tyr Ser Phe Asp Pro Leu Pro Asp Glu Pro Tyr
  20                      25                      30

Ala Tyr Gly Phe Glu Leu Val Ala Ala Asp Ala His Ser Asp Ser Thr
  35                      40                      45

Thr Thr Ser Thr Asp Thr Pro Glu Thr Val Ala Val Ala Leu Lys Thr
  50                      55                      60

Arg Glu Asp Thr Ile Asn Trp Val Asn Thr Gln Arg Ala Glu Gly Lys
  65                      70                      75                      80

Pro Asp Glu Ile Arg Ile Asn Asn Pro Ile Arg Ser Glu Arg Ile Ala
  85                      90                      95

Glu Phe Val His Glu Met Ile Met His His Gly Leu Val Ala Cys Met
  100                      105                      110

Glu Asp Leu Ala Ile Leu Ile Lys Arg Asp Lys Leu Thr Gln Leu Glu
  115                      120                      125

Ala Glu Asn Ala Ile Thr Ala Trp His Asn Leu Thr Lys Glu Ser Leu

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Gly Gln Ile Met Gly Leu Phe Tyr Gln Tyr Val Glu Asn Asn Thr Lys			
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cgctgaaaac aacacaaaat aggaagaag aaacaccatc	atg tct gac aac act	115	
	Met Ser Asp Asn Thr		
	1 5		
cag gac aac cct ttc tcc atc cgc tac gca cac cct gac cac cag ctc		163	
Gln Asp Asn Pro Phe Ser Ile Arg Tyr Ala His Pro Asp His Gln Leu			
	10 15 20		
gct ctt aat gag ctt gtt gat act gcc gat cta cct gca cca aca agc		211	
Ala Leu Asn Glu Leu Val Asp Thr Ala Asp Leu Pro Ala Pro Thr Ser			
	25 30 35		
tat atg aaa aat ccc tgg tcc ggg gac aac acg cct atc gcc gag tgg		259	
Tyr Met Lys Asn Pro Trp Ser Gly Asp Asn Thr Pro Ile Ala Glu Trp			
	40 45 50		
cga cgc gag cgc atc acc cag tgg cag cgc acc gag atc att gtc aat		307	
Arg Arg Glu Arg Ile Thr Gln Trp Gln Arg Thr Glu Ile Ile Val Asn			
	55 60 65		
caa cgc gat gat gac gat ctc att cac gtc agc ttc cgg aag ctc ggc		355	
Gln Arg Asp Asp Asp Leu Ile His Val Ser Phe Pro Lys Leu Gly			
	70 75 80 85		
cag cac att cag ctc aac acc gac gat att ctc gca ttg gtc gca gcc		403	
Gln His Ile Gln Leu Asn Thr Asp Asp Ile Leu Ala Leu Val Ala Ala			
	90 95 100		
tgc gtc aca ccc act gct aac gac att gag gca act atc gaa gaa aat		451	
Cys Val Thr Pro Thr Ala Asn Asp Ile Glu Ala Thr Ile Glu Glu Asn			
	105 110 115		
ctc cac tca tat cgg cac gat acg gtc atc atg ttt aac gca gat gat		499	
Leu His Ser Tyr Pro His Asp Thr Val Ile Met Phe Asn Ala Asp Asp			
	120 125 130		
cta gat gat gcc ctt ggt ctc gtt gtt gcc gtc aaa gac gcg agc ggg		547	
Leu Asp Asp Ala Leu Gly Leu Val Val Ala Val Lys Asp Ala Ser Gly			
	135 140 145		

gaa cac tca ccg cgc gct gtc tgg cgc acc aac acc gat cat gga gct 595
 Glu His Ser Pro Arg Ala Val Trp Arg Thr Asn Thr Asp His Gly Ala
 150 155 160 165

ctt gac gag act gaa ctc gcg cgg ctc att ctc aaa ttc ggt gcc agc 643
 Leu Asp Glu Thr Glu Leu Ala Arg Leu Ile Leu Lys Phe Gly Gly Ser
 170 175 180

ttc gat gac tac gcc gtg ctg caa cat taaaccgact cactaagcac 690
 Phe Asp Asp Tyr Gly Val Leu Gln His
 185 190

cgc 693

<210> 2504

<211> 190

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2504

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Pro Asp His Gln Leu Ala Leu Asn Glu Leu Val Asp Thr Ala Asp Leu
 20 25 30

Pro Ala Pro Thr Ser Tyr Met Lys Asn Pro Trp Ser Gly Asp Asn Thr
 35 40 45

Pro Ile Ala Glu Trp Arg Arg Glu Arg Ile Thr Gln Trp Gln Arg Thr
 50 55 60

Glu Ile Ile Val Asn Gln Arg Asp Asp Asp Asp Leu Ile His Val Ser
 65 70 75 80

Phe Pro Lys Leu Gly Gln His Ile Gln Leu Asn Thr Asp Asp Ile Leu
 85 90 95

Ala Leu Val Ala Ala Cys Val Thr Pro Thr Ala Asn Asp Ile Glu Ala
 100 105 110

Thr Ile Glu Glu Asn Leu His Ser Tyr Pro His Asp Thr Val Ile Met
 115 120 125

Phe Asn Ala Asp Asp Leu Asp Asp Ala Leu Gly Leu Val Val Ala Val
 130 135 140

Lys Asp Ala Ser Gly Glu His Ser Pro Arg Ala Val Trp Arg Thr Asn
 145 150 155 160

Thr Asp His Gly Ala Leu Asp Glu Thr Glu Leu Ala Arg Leu Ile Leu
 165 170 175

Lys Phe Gly Gly Ser Phe Asp Asp Tyr Gly Val Leu Gln His
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<210> 2505

<211> 784

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> {101}..(784)

<223> RXA01963

<400> 2505

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 Met Lys Asn Arg Lys
 1 5

aaa atc atg tct acc ctc acc act gtc tgc gcc gta ctg ggt ata gtt 163
 Lys Ile Met Ser Thr Leu Thr Thr Val Cys Ala Val Leu Gly Ile Val
 10 15 20

gca gct cat cca ttc cac gcc tct gct gtc atc ggc gcc tct gtc cca 211
 Ala Ala His Pro Phe His Ala Ser Ala Val Ile Gly Gly Ser Val Pro
 25 30 35

tca act gat tcc gtt gcc aac gct gtc gca aaa atc gga cca gcc gca 259
 Ser Thr Asp Ser Val Ala Asn Ala Val Ala Lys Ile Gly Pro Gly Ala
 40 45 50

ttg aac tgc agc ggt gtc atg atc tca cca tgg tgg gca ctc acc gca 307
 Leu Asn Cys Ser Gly Val Met Ile Ser Pro Ser Trp Ala Leu Thr Ala
 55 60 65

cgc cac tgt gtc gat gac atc aac ata ctc ggc gac atc gac acc atc 355
 Arg His Cys Val Asp Asp Ile Asn Ile Leu Gly Asp Ile Asp Thr Ile
 70 75 80 85

acg cct att act cca ggt att cat cgc aat gaa ggt aac tat atg ggt 403
 Thr Pro Ile Thr Pro Gly Ile His Arg Asn Glu Gly Asn Tyr Met Gly
 90 95 100

gag gtt tac cgc gca ccg tcc ggt gat cta gcg ctc att aat atc aac 451
 Glu Val Tyr Arg Ala Pro Ser Gly Asp Leu Ala Leu Ile Asn Ile Asn
 105 110 115

ggc gtg cac aag gcc acc att gcg cag ctc ccc aca caa gaa tat cca 499
 Gly Val His Lys Gly Thr Ile Ala Gln Leu Pro Thr Gln Glu Tyr Pro
 120 125 130

ctg gga acc gct gca cag tca gtc ggt ttt ggt ggc ggt ggt gtc aat 547
 Leu Gly Thr Ala Ala Gln Ser Val Gly Phe Gly Gly Gly Val Asn
 135 140 145

atc cgc acc gct gaa tcg gtc aac atg att ctc acc gac ata tat agc 595
 Ile Arg Thr Ala Glu Ser Val Asn Met Ile Leu Thr Asp Ile Tyr Ser
 150 155 160 165

gtg agg tca ggg aaa ttc cat cac ggt gtc ggt cga tca cac tat ctc 643
 Val Arg Ser Gly Lys Phe His His Gly Val Gly Arg Ser His Tyr Leu
 170 175 180

ctc ttt gat tat gac agt gct gaa act ggt cga atc cac aaa ggt gat 691
 Leu Phe Asp Tyr Asp Ser Ala Glu Thr Gly Arg Ile His Lys Gly Asp

185

190

195

tct ggg ggc ccc atc ttc att ggt gac gag gtt gtg ggc att atg tct 739
 Ser Gly Gly Pro Ile Phe Ile Gly Asp Glu Val Val Gly Ile Met Ser
 200 205 210

cac ggc aca ata aat aag aac gac ggg tct ttt gat gac gaa tcc 784
 His Gly Thr Ile Asn Lys Asn Asp Gly Ser Phe Asp Asp Glu Ser
 215 220 225

<210> 2506

<211> 228

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2506

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Val Leu Gly Ile Val Ala Ala His Pro Phe His Ala Ser Ala Val Ile
 20 25 30

Gly Gly Ser Val Pro Ser Thr Asp Ser Val Ala Asn Ala Val Ala Lys
 35 40 45

Ile Gly Pro Gly Ala Leu Asn Cys Ser Gly Val Met Ile Ser Pro Ser
 50 55 60

Trp Ala Leu Thr Ala Arg His Cys Val Asp Asp Ile Asn Ile Leu Gly
 65 70 75 80

Asp Ile Asp Thr Ile Thr Pro Ile Thr Pro Gly Ile His Arg Asn Glu
 85 90 95

Gly Asn Tyr Met Gly Glu Val Tyr Arg Ala Pro Ser Gly Asp Leu Ala
 100 105 110

Leu Ile Asn Ile Asn Gly Val His Lys Gly Thr Ile Ala Gln Leu Pro
 115 120 125

Thr Gln Glu Tyr Pro Leu Gly Thr Ala Ala Gln Ser Val Gly Phe Gly
 130 135 140

Gly Gly Gly Val Asn Ile Arg Thr Ala Glu Ser Val Asn Met Ile Leu
 145 150 155 160

Thr Asp Ile Tyr Ser Val Arg Ser Gly Lys Phe His His Gly Val Gly
 165 170 175

Arg Ser His Tyr Leu Leu Phe Asp Tyr Asp Ser Ala Glu Thr Gly Arg
 180 185 190

Ile His Lys Gly Asp Ser Gly Gly Pro Ile Phe Ile Gly Asp Glu Val
 195 200 205

Val Gly Ile Met Ser His Gly Thr Ile Asn Lys Asn Asp Gly Ser Phe
 210 215 220

Asp Asp Glu Ser
 225

<210> 2507
 <211> 1426
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1426)
 <223> RXA01964

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 Met Thr Ser Ala Val
 1 5
 aat gtg cag aag aag acc aca cag aaa gta ctt aag ccc att aat acg 163
 Asn Val Gln Lys Lys Thr Thr Gln Lys Val Leu Lys Pro Ile Asn Thr
 10 15 20
 aag aat tac tct gcg aca gat gca gta cag aca ggc cag cac gga tct 211
 Lys Asn Tyr Ser Ala Thr Asp Ala Val Gln Thr Gly Gln His Gly Ser
 25 30 35
 gct tta ggc tcg aat atc ggt gtc tac acc tat acc gct gga ctc gat 259
 Ala Leu Gly Ser Asn Ile Gly Val Tyr Thr Tyr Thr Ala Gly Leu Asp
 40 45 50
 att gga aac ggt tat gtc aag ggc att atc gag gca acc ggt gat acg 307
 Ile Gly Asn Gly Tyr Val Lys Gly Ile Ile Glu Ala Thr Gly Asp Thr
 55 60 65
 act ggc acg tct gtt gat gtt att gat atg ccc tct gca gca acg cgc 355
 Thr Gly Thr Ser Val Asp Val Ile Asp Met Pro Ser Ala Ala Thr Arg
 70 75 80 85
 atg agc cgg cca acg gaa gtt ccc gaa cca gat gac acc gct gtt gct 403
 Met Ser Arg Pro Thr Glu Val Pro Glu Pro Asp Asp Thr Ala Val Ala
 90 95 100
 gtc acc ggt gcg gat ttc ttc aac cac att gat acc aat ttc aat tcg 451
 Val Thr Gly Ala Asp Phe Phe Asn His Ile Asp Thr Asn Phe Asn Ser
 105 110 115
 cct atg gtg aaa ggt aat tat cgt tac ctt tgt ggc acg cgc agc ttg 499
 Pro Met Val Lys Gly Asn Tyr Arg Tyr Leu Cys Gly Thr Arg Ser Leu
 120 125 130
 tct gca cga ggt agc ttg gag gaa ttt gat ctg gtg ggt aac cgc tcc 547
 Ser Ala Arg Gly Ser Leu Glu Glu Phe Asp Leu Val Gly Asn Arg Ser
 135 140 145
 aag gcg gaa caa gaa ctg agc aag gtg ctg gtc atg gca gta ctt gcg 595
 Lys Ala Glu Gln Glu Leu Ser Lys Val Leu Val Met Ala Val Leu Ala
 150 155 160 165
 gcc aag gct gtg aaa gac ttt gtg gca gca cat ggt cga atc cca cag 643
 Ala Lys Ala Val Lys Asp Phe Val Ala Ala His Gly Arg Ile Pro Gln

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ggt	gct	ggt	gag	ggt	gat	ccc	ggt	gtg	ctg	cgt	gtg	cat	acg	tat	ctt	691							
Val	Ala	Val	Glu	Gly	Asp	Pro	Gly	Val	Leu	Arg	Val	His	Thr	Tyr	Leu								
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gca	ctt	gcg	tta	ccg	att	aat	gaa	tat	gtg	ggt	cac	cgt	cat	ggg	tat	739							
Ala	Leu	Ala	Leu	Pro	Ile	Asn	Glu	Tyr	Val	Gly	His	Arg	His	Gly	Tyr								
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Lys	Ala	Gln	Phe	Met	Gly	Asp	Gly	Ala	Ala	Asn	Pro	Ala	Val	His	Val								
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gtg	acg	ggt	aac	aac	ttt	gaa	acc	cca	gca	acg	gtg	cag	ctc	atc	ttt	835							
Val	Thr	Val	Asn	Asn	Phe	Glu	Thr	Pro	Ala	Thr	Val	Gln	Leu	Ile	Phe								
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Glu	Arg	Val	Glu	Val	Ile	Ala	Glu	Gly	Ala	Ser	Ala	Gln	Tyr	Ala	Ile								
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acc	gca	ggt	ggc	gaa	gta	ctt	atg	aac	gga	atg	ctc	gcc	gat	gta	cgc	931							
Thr	Ala	Gly	Gly	Glu	Val	Leu	Met	Asn	Gly	Met	Leu	Ala	Asp	Val	Arg								
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tcc	aaa	ggg	ctt	gct	cta	gag	ggc	gtg	aca	gca	ggt	gat	gtg	cta	caa	979							
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Pro	Val	Phe	Thr	Asp	Gly	Arg	Phe	Asn	His	Asp	Ala	Ser	Arg	Ala	Tyr								
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gac	aag	ggt	tat	ggc	acc	gtc	ttg	gag	tcg	gcg	att	cag	gct	atg	gac	1123							
Asp	Lys	Gly	Tyr	Gly	Thr	Val	Leu	Glu	Ser	Ala	Ile	Gln	Ala	Met	Asp								
																330							
gat	gct	ggg	ttg	gca	cac	aac	ttt	aac	tcg	cgt	aag	cag	ttg	gct	gat	1171							
Asp	Ala	Gly	Leu	Ala	His	Asn	Phe	Asn	Ser	Arg	Lys	Gln	Leu	Ala	Asp								
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Tyr	Leu	Gln	Arg	Pro	Pro	Ser	Ala	Leu	Lys	Arg	Asn	Phe	Tyr	Thr	Arg								
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gtg	gaa	cag	cat	ggt	gat	cag	gag	gca	gtg	ttc	ttt	gtt	cag	gat	gtg	1267							
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Ala	Ala	Glu	Phe	Ala	Arg	Val	Leu	Ser	Asp	Val	Gly	Ala	Leu	Thr	Glu								
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Val	Ala	Phe	Val	Tyr	Gly	Gly	Gly	Ser	Gly	Pro	Leu	Arg	Asp	Arg	Leu								
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cat gaa gcg ttg ctg att aag gca gcg gag atg ggt tcg gaa gat acg 1411
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ttc ccg gtg ctg tat 1426
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 440

<210> 2508

<211> 442

<212> PRT

<213> Corynebacterium glutamicum

<400> 2508

Met Thr Ser Ala Val Asn Val Gln Lys Lys Thr Thr Gln Lys Val Leu
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 20 25 30

Gly Gln His Gly Ser Ala Leu Gly Ser Asn Ile Gly Val Tyr Thr Tyr
 35 40 45

Thr Ala Gly Leu Asp Ile Gly Asn Gly Tyr Val Lys Gly Ile Ile Glu
 50 55 60

Ala Thr Gly Asp Thr Thr Gly Thr Ser Val Asp Val Ile Asp Met Pro
 65 70 75 80

Ser Ala Ala Thr Arg Met Ser Arg Pro Thr Glu Val Pro Glu Pro Asp
 85 90 95

Asp Thr Ala Val Ala Val Thr Gly Ala Asp Phe Phe Asn His Ile Asp
 100 105 110

Thr Asn Phe Asn Ser Pro Met Val Lys Gly Asn Tyr Arg Tyr Leu Cys
 115 120 125

Gly Thr Arg Ser Leu Ser Ala Arg Gly Ser Leu Glu Glu Phe Asp Leu
 130 135 140

Val Gly Asn Arg Ser Lys Ala Glu Gln Glu Leu Ser Lys Val Leu Val
 145 150 155 160

Met Ala Val Leu Ala Ala Lys Ala Val Lys Asp Phe Val Ala Ala His
 165 170 175

Gly Arg Ile Pro Gln Val Ala Val Glu Gly Asp Pro Gly Val Leu Arg
 180 185 190

Val His Thr Tyr Leu Ala Leu Ala Leu Pro Ile Asn Glu Tyr Val Gly
 195 200 205

His Arg His Gly Tyr Lys Ala Gln Phe Met Gly Asp Gly Ala Ala Asn
 210 215 220

Pro Ala Val His Val Val Thr Val Asn Asn Phe Glu Thr Pro Ala Thr
 225 230 235 240

Val Gln Leu Ile Phe Glu Arg Val Glu Val Ile Ala Glu Gly Ala Ser
 245 250 255
 Ala Gln Tyr Ala Ile Thr Ala Gly Gly Glu Val Leu Met Asn Gly Met
 260 265 270
 Leu Ala Asp Val Arg Ser Lys Gly Leu Ala Leu Glu Gly Val Thr Ala
 275 280 285
 Gly Asp Val Leu Gln Ala Arg His Thr Ile Gly Val Asp Val Gly Glu
 290 295 300
 Gly Thr Val Asn Phe Pro Val Phe Thr Asp Gly Arg Phe Asn His Asp
 305 310 315 320
 Ala Ser Arg Ala Tyr Asp Lys Gly Tyr Gly Thr Val Leu Glu Ser Ala
 325 330 335
 Ile Gln Ala Met Asp Asp Ala Gly Leu Ala His Asn Phe Asn Ser Arg
 340 345 350
 Lys Gln Leu Ala Asp Tyr Leu Gln Arg Pro Pro Ser Ala Leu Lys Arg
 355 360 365
 Asn Phe Tyr Thr Arg Val Glu Gln His Val Asp Gln Glu Ala Val Phe
 370 375 380
 Phe Val Gln Asp Val Ala Ala Glu Phe Ala Arg Val Leu Ser Asp Val
 385 390 395 400
 Gly Ala Leu Thr Glu Val Ala Phe Val Tyr Gly Gly Gly Ser Gly Pro
 405 410 415
 Leu Arg Asp Arg Leu His Glu Ala Leu Leu Ile Lys Ala Ala Glu Met
 420 425 430
 Gly Ser Glu Asp Thr Phe Pro Val Leu Tyr
 435 440

<210> 2509

<211> 684

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(661)

<223> RXA01965

<400> 2509

acttctatgt tactattaaa ttagtcaata acgtagtgca taaacaatgc agttattgaa 60

gagaaacttc ccgacacaat gtacgaaatg ggggtcacac atg gct caa aaa cag 115
 Met Ala Gln Lys Gln
 1 5

gac acg aca cat gta tca gag gac gat gcc ccg tgg cgt aat gtg cgt 163
 Asp Thr Thr His Val Ser Glu Asp Asp Ala Pro Trp Arg Asn Val Arg
 10 15 20

atg cgc ttc cca gaa aca gac gct atc gtt gag cgg ttt ttg gaa aca 211
 Met Arg Phe Pro Glu Thr Asp Ala Ile Val Glu Arg Phe Leu Glu Thr
 25 30 35

cag ggt gct cgt ggc atc tcg ctt gcg atg cga cag ctg atc tat ttg 259
 Gln Gly Ala Arg Gly Ile Ser Leu Ala Met Arg Gln Leu Ile Tyr Leu
 40 45 50

ttt gtc gct gaa tac ggt gat gta gag gtt gct acc gtt att ggc ctc 307
 Phe Val Ala Glu Tyr Gly Asp Val Glu Val Ala Thr Val Ile Gly Leu
 55 60 65

aag ctg gtg gaa agc ctg cag gca ggg gct gag ggt agt gat ctt ttt 355
 Lys Leu Val Glu Ser Leu Gln Ala Gly Ala Glu Gly Ser Asp Leu Phe
 70 75 80 85

gct cag ctc gcg gcc ggt gct gac gta gac gct gtg act aca cgc 403
 Ala Gln Leu Ala Ala Gly Val Ala Asp Val Asp Ala Val Thr Thr Arg
 90 95 100

aag aag gca ccg cag cag ata gca ccg cca tcg acc aca acc cgt gca 451
 Lys Lys Ala Pro Gln Gln Ile Ala Pro Pro Ser Thr Thr Arg Ala
 105 110 115

cct gat cag gta aat gag ttt gtt gcc gag gcg gag agt cag ccg gtt 499
 Pro Asp Gln Val Asn Glu Phe Val Ala Glu Ala Glu Ser Gln Pro Val
 120 125 130

gag gag tca gtt gtt gag gcc aaa gta ccc aag cag cag gta gca cca 547
 Glu Glu Ser Val Val Glu Ala Lys Val Pro Lys Gln Gln Val Ala Pro
 135 140 145

cag ccg gca cag aag ccg gag caa aaa cca gaa caa aag tcg gcg caa 595
 Gln Pro Ala Gln Lys Pro Glu Gln Lys Pro Glu Gln Lys Ser Ala Gln
 150 155 160 165

cca gca cag tca gag cca gat gat ggc ttt gat atg gat gat gtc atg 643
 Pro Ala Gln Ser Glu Pro Asp Asp Gly Phe Asp Met Asp Asp Val Met
 170 175 180

ggc caa gcg ttc ggt cgc tagctcatcac cttgttacaa cga 684
 Gly Gln Ala Phe Gly Arg
 185

<210> 2510

<211> 187

<212> PRT

<213> Corynebacterium glutamicum

<400> 2510

Met Ala Gln Lys Gln Asp Thr Thr His Val Ser Glu Asp Asp Ala Pro
 1 5 10 15

Trp Arg Asn Val Arg Met Arg Phe Pro Glu Thr Asp Ala Ile Val Glu
 20 25 30

Arg Phe Leu Glu Thr Gln Gly Ala Arg Gly Ile Ser Leu Ala Met Arg
 35 40 45

Gln Leu Ile Tyr Leu Phe Val Ala Glu Tyr Gly Asp Val Glu Val Ala

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50              55              60
Thr Val Ile Gly Leu Lys Leu Val Glu Ser Leu Gln Ala Gly Ala Glu
65              70              75
Gly Ser Asp Leu Phe Ala Gln Leu Ala Ala Gly Val Ala Asp Val Asp
85              90              95
Ala Val Thr Thr Arg Lys Lys Ala Pro Gln Gln Ile Ala Pro Pro Ser
100             105             110
Thr Thr Thr Arg Ala Pro Asp Gln Val Asn Glu Phe Val Ala Glu Ala
115             120             125
Glu Ser Gln Pro Val Glu Glu Ser Val Val Glu Ala Lys Val Pro Lys
130             135             140
Gln Gln Val Ala Pro Gln Pro Ala Gln Lys Pro Glu Gln Lys Pro Glu
145             150             155             160
Gln Lys Ser Ala Gln Pro Ala Gln Ser Glu Pro Asp Asp Gly Phe Asp
165             170             175
Met Asp Asp Val Met Gly Gln Ala Phe Gly Arg
180             185

<210> 2511
<211> 726
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (47)..(703)
<223> RXA01966

<400> 2511
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Val Ser Glu Ser
1
gaa aac aac aca aca cca gca gtc gca gct cgc gat gac cgt ctg gtc 106
Glu Asn Asn Thr Thr Pro Ala Val Ala Ala Arg Asp Asp Arg Leu Val 20
5              10              15
tgg gtc gat ctg gaa atg act ggt cta gat ttg aag cgc cac gtg atc 154
Trp Val Asp Leu Glu Met Thr Gly Leu Asp Leu Lys Arg His Val Ile 35
25              30              35
gtg gag gtt gcg gcg ttg gtc act gac gct aac ctc aac gtt ttg ggc 202
Val Glu Val Ala Ala Leu Val Thr Asp Ala Asn Leu Asn Val Leu Gly 50
40              45              50
gag ggc gtg gac ttg gtt gtt cac gca act gaa gaa gag ctc gcg cag 250
Glu Gly Val Asp Leu Val Val His Ala Thr Glu Glu Glu Leu Ala Gln 60
55              60              65
atg gat gat ttt gtc acc aac atg cac gaa tcc tct ggg ctg act gag 298
Met Asp Asp Phe Val Thr Asn Met His Glu Ser Ser Gly Leu Thr Glu 70
70              75              80

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cag atc cgg gaa tcc gcg gtc acg ttg aag gaa gcc gaa gat gct gtg 346
 Gln Ile Arg Glu Ser Ala Val Thr Leu Lys Glu Ala Glu Asp Ala Val
 85 90 95 100

ctc gca ttg att gaa aag cac tgc gat cca gcc cat cct gca ccg cta 394
 Leu Ala Leu Ile Glu Lys His Cys Asp Pro Ala His Pro Ala Pro Leu
 105 110 115

gct ggt aac tcc att gcc act gac cgc gcg ttt atc cgc gaa cat atg 442
 Ala Gly Asn Ser Ile Ala Thr Asp Arg Ala Phe Ile Arg Glu His Met
 120 125 130

cca cgt ctt gat gag gcc ctg cat tac cgc atg gtg gat gtg tcc tcg 490
 Pro Arg Leu Asp Glu Ala Leu His Tyr Arg Met Val Asp Val Ser Ser
 135 140 145

gtg aag gaa ttg gcg cgt cgc tgg tac cca cgc gtg tac tac aag cag 538
 Val Lys Glu Leu Ala Arg Arg Trp Tyr Pro Arg Val Tyr Tyr Lys Gln
 150 155 160

ccg gag aag ggt ttg gcg cac cgc gcg ttg gcg gac att gtg gag tcg 586
 Pro Glu Lys Gly Leu Ala His Arg Ala Leu Ala Asp Ile Val Glu Ser
 165 170 175 180

att cgg gag ttg gat tac tac cgt cgc tca ttt ttt gtt gca gag cct 634
 Ile Arg Glu Leu Asp Tyr Tyr Arg Arg Ser Phe Phe Val Ala Glu Pro
 185 190 195

ggt cct acc tct gag cag tgc gca gat gat gcg cag gca gcg gtg gac 682
 Gly Pro Thr Ser Glu Gln Cys Ala Asp Asp Ala Gln Ala Ala Val Asp
 200 205 210

cgt ttt gca ccc tac ttt gat tagagggttt taagcagcct ggt 726
 Arg Phe Ala Pro Tyr Phe Asp
 215

<210> 2512
 <211> 219
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 2512
 Val Ser Glu Ser Glu Asn Asn Thr Thr Pro Ala Val Ala Ala Arg Asp
 1 5 10 15

Asp Arg Leu Val Trp Val Asp Leu Glu Met Thr Gly Leu Asp Leu Lys
 20 25 30

Arg His Val Ile Val Glu Val Ala Ala Leu Val Thr Asp Ala Asn Leu
 35 40 45

Asn Val Leu Gly Glu Gly Val Asp Leu Val Val His Ala Thr Glu Glu
 50 55 60

Glu Leu Ala Gln Met Asp Asp Phe Val Thr Asn Met His Glu Ser Ser
 65 70 75 80

Gly Leu Thr Glu Gln Ile Arg Glu Ser Ala Val Thr Leu Lys Glu Ala
 85 90 95

Glu Asp Ala Val Leu Ala Leu Ile Glu Lys His Cys Asp Pro Ala His
100 105 110

Pro Ala Pro Leu Ala Gly Asn Ser Ile Ala Thr Asp Arg Ala Phe Ile
115 120 125

Arg Glu His Met Pro Arg Leu Asp Glu Ala Leu His Tyr Arg Met Val
130 135 140

Asp Val Ser Ser Val Lys Glu Leu Ala Arg Arg Trp Tyr Pro Arg Val
145 150 155 160

Tyr Tyr Lys Gln Pro Glu Lys Gly Leu Ala His Arg Ala Leu Ala Asp
165 170 175

Ile Val Glu Ser Ile Arg Glu Leu Asp Tyr Tyr Arg Arg Ser Phe Phe
180 185 190

Val Ala Glu Pro Gly Pro Thr Ser Glu Gln Cys Ala Asp Asp Ala Gln
195 200 205

Ala Ala Val Asp Arg Phe Ala Pro Tyr Phe Asp
210 215

<210> 2513

<211> 1281

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1258)

<223> RXA01968

<400> 2513

gaaactggcgc tttttaagtt gtggcaattt tgccagaagg gcgtaacagg tgcgggtttt 60

tcgtggtagg cgcggagcag tagcaggatc ttttcttgca gtg ctg gca att ggt 115
Val Leu Ala Ile Gly
1 5

tca ctg gcg ctt acg ggt tgc aca att gaa cga agc gat gcg cag gag 163
Ser Leu Ala Leu Thr Gly Cys Thr Ile Glu Arg Ser Asp Ala Gln Glu
10 15 20

caa tcc tcg cag caa agt aca gaa gtt gaa gct gaa gaa gct caa gct 211
Gln Ser Ser Gln Gln Ser Thr Glu Val Glu Ala Glu Glu Ala Gln Ala
25 30 35

cct gtg att tct gtt gat gat ggt gat gag gat gtg gac cct tcg gaa 259
Pro Val Ile Ser Val Asp Asp Gly Asp Glu Asp Val Asp Pro Ser Glu
40 45 50

tct gtc atc gta aag tcg atg ggt gac ggt ctg agc aag gtc acc atg 307
Ser Val Ile Val Lys Ser Met Gly Asp Gly Leu Ser Lys Val Thr Met
55 60 65

act aat gaa gaa ggc tat gag gtt gag tca gag ctt tct gac gat ggc 355
Thr Asn Glu Glu Gly Tyr Glu Val Glu Ser Glu Leu Ser Asp Asp Gly

70	75	80	85
cgt agc tgg acc act gcg gaa acc ctt ggc tac aac cgc acg tac acc Arg Ser Trp Thr Thr Ala Glu Thr Leu Gly Tyr Asn Arg Thr Tyr Thr	90	95	100
att aag gca acc gat aag aac ggc gag acc gct act gcg tct ttt agt Ile Lys Ala Thr Asp Lys Asn Gly Glu Thr Ala Thr Ala Ser Phe Ser	105	110	115
act gca acc cct gca gct acc aca aac gtg gcg ctt tct ccg ctg gct Thr Ala Thr Pro Ala Ala Thr Thr Asn Val Ala Leu Ser Pro Leu Ala	120	125	130
gat tct gtc gtt ggt gtt ggc cag act atc ggt ttc cgt ttt ggt tcc Asp Ser Val Val Gly Val Gly Gln Thr Ile Gly Phe Arg Phe Gly Ser	135	140	145
cct gtg aag gat cgc aag gcg gct cag gat gct att act gtg aca act Pro Val Lys Asp Arg Lys Ala Ala Gln Asp Ala Ile Thr Val Thr Thr	150	155	160
tca cca aag gtg gag ggt ggc ttt tac tgg ttg aac aac agt gag ttg Ser Pro Lys Val Glu Gly Gly Phe Tyr Trp Leu Asn Asn Ser Glu Leu	170	175	180
cgc tgg cgt cca gcg gag tac tgg gag cca ggt act gaa gtt acg gtc Arg Trp Arg Pro Ala Glu Tyr Trp Glu Pro Gly Thr Glu Val Thr Val	185	190	195
gag gct gac att tac ggc aag gat ctc ggc ggc ggt gtc tgg ggc gaa Glu Ala Asp Ile Tyr Gly Lys Asp Leu Gly Gly Gly Val Trp Gly Glu	200	205	210
act gat aac gcc acc aac ttc acc att ggt gac aag gtt gag gct gtg Thr Asp Asn Ala Thr Asn Phe Thr Ile Gly Asp Lys Val Glu Ala Val	215	220	225
gca gat gat gcc acc aag acc atg agt gtg tac aag aac ggt gag ttg Ala Asp Asp Ala Thr Lys Thr Met Ser Val Tyr Lys Asn Gly Glu Leu	230	235	240
ctg cgc act atg ccg gta tcc ttt ggt cgt gac acc tct gag tgg gca Leu Arg Thr Met Pro Val Ser Phe Gly Arg Asp Thr Ser Glu Trp Ala	250	255	260
acg cca aac ggt acc tac atc att ggt gat cgc aat gag tgg atg atc Thr Pro Asn Gly Thr Tyr Ile Ile Gly Asp Arg Asn Glu Ser Met Ile	265	270	275
atg gac tcc acc acc ttc ggt ctg gga tat gag gag ggt ggc tac cgc Met Asp Ser Thr Thr Phe Gly Leu Gly Tyr Glu Glu Gly Gly Tyr Arg	280	285	290
act ccg gtg aag tac gcg acc cag atg tcc tat tct gga att tac gtg Thr Pro Val Lys Tyr Ala Thr Gln Met Ser Tyr Ser Gly Ile Tyr Val	295	300	305
cac gca gca ccg tgg tct gta ggt gcg caa ggt agc tac aac acc tca His Ala Ala Pro Trp Ser Val Gly Ala Gln Gly Ser Tyr Asn Thr Ser	310	315	320
			325

cat ggt tgc atc aat gta tcc acc gaa aat gct cag tgg ttc cag gag 1123
 His Gly Cys Ile Asn Val Ser Thr Glu Asn Ala Gln Trp Phe Gln Glu
 330 335 340

gcc gtg aag cgc ggt gac att gtg acc gtg aaa aac acc atc ggt gag 1171
 Ala Val Lys Arg Gly Asp Ile Val Thr Val Lys Asn Thr Ile Gly Glu
 345 350 355

act ttg agt ggc tac gac gga ctg ggg gac tgg aac att cca tgg tct 1219
 Thr Leu Ser Gly Tyr Asp Gly Leu Gly Asp Trp Asn Ile Pro Trp Ser
 360 365 370

gaa tgg agc aag ggg aac gcg gat caa act tcg gcg tgg taactgcgga 1268
 Glu Trp Ser Lys Gly Asn Ala Asp Gln Thr Ser Ala Trp
 375 380 385

agtcgcaggt aaa 1281

<210> 2514

<211> 386

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2514

Val Leu Ala Ile Gly Ser Leu Ala Leu Thr Gly Cys Thr Ile Glu Arg
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Ser Asp Ala Gln Glu Gln Ser Ser Gln Ser Thr Glu Val Glu Ala
 20 25 30

Glu Glu Ala Gln Ala Pro Val Ile Ser Val Asp Asp Gly Asp Glu Asp
 35 40 45

Val Asp Pro Ser Glu Ser Val Ile Val Lys Ser Met Gly Asp Gly Leu
 50 55 60

Ser Lys Val Thr Met Thr Asn Glu Glu Gly Tyr Glu Val Glu Ser Glu
 65 70 75 80

Leu Ser Asp Asp Gly Arg Ser Trp Thr Thr Ala Glu Thr Leu Gly Tyr
 85 90 95

Asn Arg Thr Tyr Thr Ile Lys Ala Thr Asp Lys Asn Gly Glu Thr Ala
 100 105 110

Thr Ala Ser Phe Ser Thr Ala Thr Pro Ala Ala Thr Thr Asn Val Ala
 115 120 125

Leu Ser Pro Leu Ala Asp Ser Val Val Gly Val Gly Gln Thr Ile Gly
 130 135 140

Phe Arg Phe Gly Ser Pro Val Lys Asp Arg Lys Ala Ala Gln Asp Ala
 145 150 155 160

Ile Thr Val Thr Thr Ser Pro Lys Val Glu Gly Gly Phe Tyr Trp Leu
 165 170 175

Asn Asn Ser Glu Leu Arg Trp Arg Pro Ala Glu Tyr Trp Glu Pro Gly
 180 185 190

Thr Glu Val Thr Val Glu Ala Asp Ile Tyr Gly Lys Asp Leu Gly Gly
195 200 205

Gly Val Trp Gly Glu Thr Asp Asn Ala Thr Asn Phe Thr Ile Gly Asp
210 215 220

Lys Val Glu Ala Val Ala Asp Asp Ala Thr Lys Thr Met Ser Val Tyr
225 230 235 240

Lys Asn Gly Glu Leu Leu Arg Thr Met Pro Val Ser Phe Gly Arg Asp
245 250 255

Thr Ser Glu Trp Ala Thr Pro Asn Gly Thr Tyr Ile Ile Gly Asp Arg
260 265 270

Asn Glu Ser Met Ile Met Asp Ser Thr Thr Phe Gly Leu Gly Tyr Glu
275 280 285

Glu Gly Gly Tyr Arg Thr Pro Val Lys Tyr Ala Thr Gln Met Ser Tyr
290 295 300

Ser Gly Ile Tyr Val His Ala Ala Pro Trp Ser Val Gly Ala Gln Gly
305 310 315 320

Ser Tyr Asn Thr Ser His Gly Cys Ile Asn Val Ser Thr Glu Asn Ala
325 330 335

Gln Trp Phe Gln Glu Ala Val Lys Arg Gly Asp Ile Val Thr Val Lys
340 345 350

Asn Thr Ile Gly Glu Thr Leu Ser Gly Tyr Asp Gly Leu Gly Asp Trp
355 360 365

Asn Ile Pro Trp Ser Glu Trp Ser Lys Gly Asn Ala Asp Gln Thr Ser
370 375 380

Ala Trp
385

<210> 2515

<211> 497

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(474)

<223> RXA01969

<400> 2515

aaa tgc cag cgt cgt ggt tta agc cag gat ccg ttg tat aaa aac cgg 48
Lys Cys Gln Arg Arg Gly Leu Ser Gln Asp Pro Leu Tyr Lys Asn Arg
1 5 10 15

aat tcc ttg ttg acc acg cag aag tgg ttt agt cct cgt cag caa gaa 96
Asn Ser Leu Leu Thr Thr Gln Lys Trp Phe Ser Pro Arg Gln Gln Glu
20 25 30

agc ttg gag cag ttg tgg gcg tat gac aaa gcc tac ggg gcg tta aag 144

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Ser Leu Glu Gln Leu Trp Ala Tyr Asp Lys Ala Tyr Gly Ala Leu Lys
      35              40              45

ctt gcg tgg ctt gcg tat cag gcg att att gat tgt tat cag atg ggt 192
Leu Ala Trp Leu Ala Tyr Gln Ala Ile Ile Asp Cys Tyr Gln Met Gly
      50              55              60

aat aag cgt gaa gcg aag aag aaa atg cgg acc att att gat cag ctt 240
Asn Lys Arg Glu Ala Lys Lys Lys Met Arg Thr Ile Ile Asp Gln Leu
      65              70              75              80

cgg gtg ttg aag ggg cgg aat aag gaa ctc gcg cag ttg ggt cgt agt 288
Arg Val Leu Lys Gly Pro Asn Lys Glu Leu Ala Gln Leu Gly Arg Ser
      85              90              95

ttg ttt aaa cga ctt ggt gat gtg ttg gcg tat ttc gat gtt ggt gtc 336
Leu Phe Lys Arg Leu Gly Asp Val Leu Ala Tyr Phe Asp Val Gly Val
      100             105             110

tcc aac ggt cgg gtc gaa gcg atc aac gga cgg ttg gag cat ttg cgt 384
Ser Asn Gly Pro Val Glu Ala Ile Asn Gly Arg Leu Glu His Leu Arg
      115             120             125

ggg att gct cta ggt ttc cgt aat ttg aac cac tac att ctg cgg tgc 432
Gly Ile Ala Leu Gly Phe Arg Asn Leu Asn His Tyr Ile Leu Arg Cys
      130             135             140

ctt atc cat tca ggg cag ttg gtc cat aag atc aat gca ctc 474
Leu Ile His Ser Glu Gln Leu Val His Lys Ile Asn Ala Leu
      145             150             155

taaaacagga agagccactt aag 497

<210> 2516
<211> 158
<212> PRT
<213> Corynebacterium glutamicum

<400> 2516
Lys Cys Gln Arg Arg Gly Leu Ser Gln Asp Pro Leu Tyr Lys Asn Arg
  1              5              10              15

Asn Ser Leu Leu Thr Thr Gln Lys Trp Phe Ser Pro Arg Gln Gln Glu
      20              25              30

Ser Leu Glu Gln Leu Trp Ala Tyr Asp Lys Ala Tyr Gly Ala Leu Lys
      35              40              45

Leu Ala Trp Leu Ala Tyr Gln Ala Ile Ile Asp Cys Tyr Gln Met Gly
      50              55              60

Asn Lys Arg Glu Ala Lys Lys Lys Met Arg Thr Ile Ile Asp Gln Leu
      65              70              75              80

Arg Val Leu Lys Gly Pro Asn Lys Glu Leu Ala Gln Leu Gly Arg Ser
      85              90              95

Leu Phe Lys Arg Leu Gly Asp Val Leu Ala Tyr Phe Asp Val Gly Val
      100             105             110

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Ser Asn Gly Pro Val Glu Ala Ile Asn Gly Arg Leu Glu His Leu Arg
 115 120 125

Gly Ile Ala Leu Gly Phe Arg Asn Leu Asn His Tyr Ile Leu Arg Cys
 130 135 140

Leu Ile His Ser Gly Gln Leu Val His Lys Ile Asn Ala Leu
 145 150 155

<210> 2517
 <211> 605
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (1)..(582)
 <223> RXA01973

<400> 2517
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 Ser Ala Met Ser Lys Ser Gln Asp Asp Arg Lys Ile Ala Glu Leu Glu
 1 5 10 15

gca cag ttt cat agt ctt ggt ctt aac aac act gaa cta gtt acc ctt 96
 Ala Gln Phe His Ser Leu Gly Leu Asn Asn Thr Glu Leu Val Thr Leu
 20 25 30

gat gat gca gcg tcg cta ttg ggt gtg cgg gca ggt att cat cag att 144
 Asp Asp Ala Ala Ser Leu Leu Gly Val Pro Ala Gly Ile His Gln Ile
 35 40 45

gag gcc gag gtg atg ttg gtg aat ttc ggt gat ggt gca gat gcc atg 192
 Glu Ala Glu Val Met Leu Val Asn Phe Gly Asp Gly Ala Asp Gly Met
 50 55 60

ggc ggt gac acg acg aag ttt ttg cat tat cag cca gat gag tcg cag 240
 Gly Gly Asp Thr Thr Lys Phe Leu His Tyr Gln Pro Asp Glu Ser Gln
 65 70 75 80

cct tac gtc tgg gtg atg aag cgg gtg tat tcc ttt gag gcg atg aaa 288
 Pro Tyr Val Trp Val Met Lys Arg Val Tyr Ser Phe Glu Ala Met Lys
 85 90 95

aag ctc atg gtc ggg ttg ttt att gcc ttg tgc ata ctc atc gtg ggt 336
 Lys Leu Met Val Gly Leu Phe Ile Gly Leu Cys Ile Leu Ile Val Gly
 100 105 110

ggg cca gct tta ggg ctt atg ctc ggt ggt ttt atc ggt gtg ctt att 384
 Gly Pro Ala Leu Gly Leu Met Leu Gly Gly Phe Ile Gly Val Leu Ile
 115 120 125

ggt cta tgt cta ggt act tcc gca gcc atg att gtt gcc cct ttt ggg 432
 Gly Leu Cys Leu Gly Thr Ser Ala Ala Met Ile Val Gly Pro Phe Gly
 130 135 140

ctt atg cgg atg aag gcg tat cca cca tgt atg gac agt cca tgg gtg 480
 Leu Met Arg Met Lys Ala Tyr Pro Pro Cys Met Asp Ser Pro Trp Val
 145 150 155 160

tat atg tca caa gag cag tgg cgc acc gct atg ggt gcg gca cag cag 528
 Tyr Met Ser Gln Glu Gln Trp Arg Thr Ala Met Gly Ala Ala Gln Gln
 165 170 175

acc gag gtg tct ttt gtt gag cac tgg gac aat att tac ggg gat aat 576
 Thr Glu Val Ser Phe Val Glu His Trp Asp Asn Ile Tyr Gly Asp Asn
 180 185 190

ctg cat taacaaatta gttaataaag tgt 605
 Leu His

<210> 2518

<211> 194

<212> PRT

<213> Corynebacterium glutamicum

<400> 2518

Ser Ala Met Ser Lys Ser Gln Asp Asp Arg Lys Ile Ala Glu Leu Glu
 1 5 10 15

Ala Gln Phe His Ser Leu Gly Leu Asn Asn Thr Glu Leu Val Thr Leu
 20 25 30

Asp Asp Ala Ala Ser Leu Leu Gly Val Pro Ala Gly Ile His Gln Ile
 35 40 45

Glu Ala Glu Val Met Leu Val Asn Phe Gly Asp Gly Ala Asp Gly Met
 50 55 60

Gly Gly Asp Thr Thr Lys Phe Leu His Tyr Gln Pro Asp Glu Ser Gln
 65 70 75 80

Pro Tyr Val Trp Val Met Lys Arg Val Tyr Ser Phe Glu Ala Met Lys
 85 90 95

Lys Leu Met Val Gly Leu Phe Ile Gly Leu Cys Ile Leu Ile Val Gly
 100 105 110

Gly Pro Ala Leu Gly Leu Met Leu Gly Gly Phe Ile Gly Val Leu Ile
 115 120 125

Gly Leu Cys Leu Gly Thr Ser Ala Ala Met Ile Val Gly Pro Phe Gly
 130 135 140

Leu Met Arg Met Lys Ala Tyr Pro Pro Cys Met Asp Ser Pro Trp Val
 145 150 155 160

Tyr Met Ser Gln Glu Gln Trp Arg Thr Ala Met Gly Ala Ala Gln Gln
 165 170 175

Thr Glu Val Ser Phe Val Glu His Trp Asp Asn Ile Tyr Gly Asp Asn
 180 185 190

Leu His

<210> 2519

<211> 1552

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1552)

<223> RXA01974

<400> 2519

acaatatttta cggggataat ctgcattaac aaattagtta ataaagtgtg gtatttaatt 60

aattattaaa ttcaattaac tttttgttaa aggtgggaag atg acc cag gtt gtg 115
 Met Thr Gln Val Val
 1 5

gcg ggt acg ttg gtg gga gag tgc att aat cgt gag att gat gaa gac 163
 Ala Gly Thr Leu Val Gly Glu Ser Ile Asn Arg Glu Ile Asp Glu Asp
 10 15 20

aag tac cct tat ttg agc tgc tat gca gcg cct gtt gct gta ccg gtg 211
 Lys Tyr Pro Tyr Leu Ser Ser Tyr Ala Ala Pro Val Ala Val Pro Val
 25 30 35

cgt gag att att ggg cgc gaa gaa gaa gtc aat aag att atg gcc gcg 259
 Arg Glu Ile Ile Gly Arg Glu Glu Glu Val Asn Lys Ile Met Ala Ala
 40 45 50

ctg atg cgt cca gag att tct aat gtc atg ctt gtg ggt cct gct ggt 307
 Leu Met Arg Pro Glu Ile Ser Asn Val Met Leu Val Gly Pro Ala Gly
 55 60 65

tgc ggt aaa act acg ttg gta cag caa gca ctg gtg aaa gat cca gag 355
 Ser Gly Lys Thr Thr Leu Val Gln Gln Ala Leu Val Lys Asp Pro Glu
 70 75 80 85

cgt aac tac atc gag gtc gat gta gcg aaa atg gtt gcg gat ttg agc 403
 Arg Asn Tyr Ile Glu Val Asp Val Ala Lys Met Val Ala Asp Leu Ser
 90 95 100

acc ccg gcg caa atg gct gcg cgt att aaa ggt gtg ttt gag gac gcc 451
 Thr Pro Ala Gln Met Ala Ala Arg Ile Lys Gly Val Phe Glu Asp Ala
 105 110 115

att gcc tat cgc aag cac gaa ggt cat gaa ttg gtg ctg ttc gtt gat 499
 Ile Ala Tyr Arg Lys His Glu Gly His Glu Leu Val Leu Phe Val Asp
 120 125 130

gag ttt cac caa att gtg cag ctg tct aat gct gcg gta gag gca atc 547
 Glu Phe His Gln Ile Val Gln Leu Ser Asn Ala Ala Val Glu Ala Ile
 135 140 145

aag ccg att ttg gcg atg tct ggt gtc ctt ggt gtg cgc gtt atc gct 595
 Lys Pro Ile Leu Ala Met Ser Gly Val Leu Gly Val Arg Val Ile Ala
 150 155 160 165

gcg aca act ctc gaa gaa ttt cac gaa cac atc agg ccg aac caa gca 643
 Ala Thr Thr Leu Glu Glu Phe His Glu His Ile Arg Pro Asn Gln Ala
 170 175 180

ttg acg gag cgt ttg cag gaa att cga cta acg ccg acc gat cag aag 691
 Leu Thr Glu Arg Leu Gln Glu Ile Arg Leu Thr Pro Thr Asp Gln Lys

			185					190					195					
acc	act	gtg	gcg	att	ttg	cgt	ggt	atg	gca	gat	cgt	tat	ggc	gta	agt	739		
Thr	Thr	Val	Ala	Ile	Leu	Arg	Gly	Met	Ala	Asp	Arg	Tyr	Gly	Val	Ser			
			200				205				210							
gat	cag	ttc	tat	gac	gac	cac	gtt	ttt	gag	cag	att	tac	tcc	acc	act	787		
Asp	Gln	Phe	Tyr	Asp	Asp	His	Val	Phe	Glu	Gln	Ile	Tyr	Ser	Thr	Thr			
			215				220				225							
gag	cgt	ttt	atg	ccg	agt	tct	gtc	cag	cct	cgt	aaa	tcc	att	cgt	gtc	835		
Glu	Arg	Phe	Met	Pro	Ser	Ser	Val	Gln	Pro	Arg	Lys	Ser	Ile	Arg	Val			
			230		235				240				245					
ctt	gat	gcg	atg	gtt	ggt	tgg	cat	cga	ctt	tcc	ggc	aag	ccg	atg	gat	883		
Leu	Asp	Ala	Met	Val	Gly	Trp	His	Arg	Leu	Ser	Gly	Lys	Pro	Met	Asp			
			250						255				260					
atg	gat	ctg	ctc	ggt	gat	gtg	ctc	cac	gat	gct	att	ggt	gtc	gat	att	931		
Met	Asp	Leu	Leu	Gly	Asp	Val	Leu	His	Asp	Ala	Ile	Gly	Val	Asp	Ile			
			265				270				275							
gca	ttc	aag	gtc	gat	ggt	acg	agc	att	aaa	gac	aag	ctt	gat	gag	aag	979		
Ala	Phe	Lys	Val	Asp	Gly	Thr	Ser	Ile	Lys	Asp	Lys	Leu	Asp	Glu	Lys			
			280				285				290							
gta	atg	gcg	caa	agt	ctt	gcc	acc	act	gtg	gta	gca	cgt	cgt	ttg	cag	1027		
Val	Met	Ala	Gln	Ser	Leu	Ala	Thr	Thr	Val	Val	Ala	Arg	Arg	Leu	Gln			
			295		300						305							
ctg	gtg	gtg	gcg	gat	ctt	cat	gat	aaa	tca	cgg	cca	ctg	tcg	aac	ttc	1075		
Leu	Val	Val	Ala	Asp	Leu	His	Asp	Lys	Ser	Arg	Pro	Leu	Ser	Asn	Phe			
			310		315				320				325					
ttg	ttc	acc	ggg	cct	act	ggt	gtc	ggt	aaa	aca	gag	ctg	gtc	aag	caa	1123		
Leu	Phe	Thr	Gly	Pro	Thr	Gly	Val	Gly	Lys	Thr	Glu	Leu	Val	Lys	Gln			
			330						335				340					
cta	gca	cgg	gtg	ctc	ttt	ggt	gat	gac	act	ggg	cga	ttg	att	cgt	ttt	1171		
Leu	Ala	Arg	Val	Leu	Phe	Gly	Asp	Asp	Thr	Gly	Arg	Leu	Ile	Arg	Phe			
			345				350				355							
gac	atg	tca	gag	ttc	gcc	tta	gaa	tca	agt	ctt	gac	ctt	ttc	agg	tct	1219		
Asp	Met	Ser	Glu	Phe	Ala	Leu	Glu	Ser	Ser	Leu	Asp	Leu	Phe	Arg	Ser			
			360		365						370							
gag	ctc	act	cgt	cgt	gtc	gct	gac	cag	ggt	aac	gct	att	gtc	ctg	ctc	1267		
Glu	Leu	Thr	Arg	Arg	Val	Ala	Asp	Gln	Gly	Asn	Ala	Ile	Val	Leu	Leu			
			375		380						385							
gat	gag	gtt	gag	aaa	gct	gat	cga	gct	att	gcg	cgg	ttg	tta	ctg	cag	1315		
Asp	Glu	Val	Glu	Lys	Ala	Asp	Arg	Ala	Ile	Ala	Arg	Leu	Leu	Leu	Gln			
			390		395				400				405					
gta	ctt	gat	gat	ggc	cga	cta	tct	gac	gat	tac	aac	cgt	gag	gtg	agt	1363		
Val	Leu	Asp	Asp	Gly	Arg	Leu	Ser	Asp	Asp	Tyr	Asn	Arg	Glu	Val	Ser			
			410				415				420							
ttt	ctt	aat	acc	tat	atc	gtc	atg	aca	act	aac	gct	ggt	tct	gag	att	1411		
Phe	Leu	Asn	Thr	Tyr	Ile	Val	Met	Thr	Thr	Asn	Ala	Gly	Ser	Glu	Ile			
			425				430				435							

ttc gag aca att tcg aac tat gcc act gat gac acg ggc gat ggt cgg 1459
Phe Glu Thr Ile Ser Asn Tyr Ala Thr Asp Asp Thr Gly Asp Gly Arg
440 445 450

gcg atc aaa gac ttt gtg aaa aac att cac acg tcg atc aag aat aag 1507
Ala Ile Lys Asp Phe Val Lys Asn Ile His Thr Ser Ile Lys Asn Lys
455 460 465

ggt ttt cca cct gag ctt ctt ggt cgt gta gat gaa att gtg cct 1552
Gly Phe Pro Pro Glu Leu Leu Gly Arg Val Asp Glu Ile Val Pro
470 475 480

<210> 2520

<211> 484

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2520

Met Thr Gln Val Val Ala Gly Thr Leu Val Gly Glu Ser Ile Asn Arg
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Glu Ile Asp Glu Asp Lys Tyr Pro Tyr Leu Ser Ser Tyr Ala Ala Pro
20 25 30

Val Ala Val Pro Val Arg Glu Ile Ile Gly Arg Glu Glu Glu Val Asn
35 40 45

Lys Ile Met Ala Ala Leu Met Arg Pro Glu Ile Ser Asn Val Met Leu
50 55 60

Val Gly Pro Ala Gly Ser Gly Lys Thr Thr Leu Val Gln Gln Ala Leu
65 70 75 80

Val Lys Asp Pro Glu Arg Asn Tyr Ile Glu Val Asp Val Ala Lys Met
85 90 95

Val Ala Asp Leu Ser Thr Pro Ala Gln Met Ala Ala Arg Ile Lys Gly
100 105 110

Val Phe Glu Asp Ala Ile Ala Tyr Arg Lys His Glu Gly His Glu Leu
115 120 125

Val Leu Phe Val Asp Glu Phe His Gln Ile Val Gln Leu Ser Asn Ala
130 135 140

Ala Val Glu Ala Ile Lys Pro Ile Leu Ala Met Ser Gly Val Leu Gly
145 150 155 160

Val Arg Val Ile Ala Ala Thr Thr Leu Glu Glu Phe His Glu His Ile
165 170 175

Arg Pro Asn Gln Ala Leu Thr Glu Arg Leu Gln Glu Ile Arg Leu Thr
180 185 190

Pro Thr Asp Gln Lys Thr Thr Val Ala Ile Leu Arg Gly Met Ala Asp
195 200 205

Arg Tyr Gly Val Ser Asp Gln Phe Tyr Asp Asp His Val Phe Glu Gln
210 215 220

Ile Tyr Ser Thr Thr Glu Arg Phe Met Pro Ser Ser Val Gln Pro Arg
 225 230 235 240
 Lys Ser Ile Arg Val Leu Asp Ala Met Val Gly Trp His Arg Leu Ser
 245 250 255
 Gly Lys Pro Met Asp Met Asp Leu Leu Gly Asp Val Leu His Asp Ala
 260 265 270
 Ile Gly Val Asp Ile Ala Phe Lys Val Asp Gly Thr Ser Ile Lys Asp
 275 280 285
 Lys Leu Asp Glu Lys Val Met Ala Gln Ser Leu Ala Thr Thr Val Val
 290 295 300
 Ala Arg Arg Leu Gln Leu Val Val Ala Asp Leu His Asp Lys Ser Arg
 305 310 315 320
 Pro Leu Ser Asn Phe Leu Phe Thr Gly Pro Thr Gly Val Gly Lys Thr
 325 330 335
 Glu Leu Val Lys Gln Leu Ala Arg Val Leu Phe Gly Asp Asp Thr Gly
 340 345 350
 Arg Leu Ile Arg Phe Asp Met Ser Glu Phe Ala Leu Glu Ser Ser Leu
 355 360 365
 Asp Leu Phe Arg Ser Glu Leu Thr Arg Arg Val Ala Asp Gln Gly Asn
 370 375 380
 Ala Ile Val Leu Leu Asp Glu Val Glu Lys Ala Asp Arg Ala Ile Ala
 385 390 395 400
 Arg Leu Leu Leu Gln Val Leu Asp Asp Gly Arg Leu Ser Asp Asp Tyr
 405 410 415
 Asn Arg Glu Val Ser Phe Leu Asn Thr Tyr Ile Val Met Thr Thr Asn
 420 425 430
 Ala Gly Ser Glu Ile Phe Glu Thr Ile Ser Asn Tyr Ala Thr Asp Asp
 435 440 445
 Thr Gly Asp Gly Arg Ala Ile Lys Asp Phe Val Lys Asn Ile His Thr
 450 455 460
 Ser Ile Lys Asn Lys Gly Phe Pro Pro Glu Leu Leu Gly Arg Val Asp
 465 470 475 480
 Glu Ile Val Pro

<210> 2521
 <211> 1644
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1621)

<223> RXA01976

<400> 2521

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agtatattaa ttacttgatt taattgaagg gggtttatagt atg acg caa aca ctt 115
Met Thr Gln Thr Leu 5
1

gct ggc gag cgc aga atc gtc acc acg gca gag ctt aaa gcg atg ctg 163
Ala Gly Glu Arg Arg Ile Val Thr Thr Ala Glu Leu Lys Ala Met Leu 20
10 15

gca cga ggg gat aag gtg ttt ctg cct ggt gtc gca gcg cgg gcg cca 211
Ala Arg Gly Asp Lys Val Phe Leu Pro Gly Val Ala Ala Arg Ala Pro 35
25 30

gag atc ctc gac aac ttc gat cca gca gat cgg gca cgt ctc gac gtg 259
Glu Ile Leu Asp Asn Phe Asp Pro Ala Asp Arg Ala Arg Leu Asp Val 50
40 45

ccc gca gca gac aat gaa atc gtc tct gta gaa ttc tcc cgc cgc gat 307
Pro Ala Ala Asp Asn Glu Ile Val Ser Val Glu Phe Ser Arg Arg Asp 65
55 60

acc gtg caa tgc atc agc att gcc gac cgt gac cat ctc tac atc act 355
Thr Val Gln Cys Ile Ser Ile Ala Asp Arg Asp His Leu Tyr Ile Thr 85
70 75 80

gac gat atg atc ccg acc cac aac acg tcc aac att atc ttc ttg aaa 403
Asp Asp Met Ile Pro Thr His Asn Thr Ser Asn Ile Ile Phe Leu Lys 100
90 95

tcc aca gac gaa aca atg att aag acg ttg gtg gat tgg tca ggt gag 451
Ser Thr Asp Glu Thr Met Ile Lys Thr Leu Val Asp Trp Ser Gly Glu 115
105 110

cga cat gtt gta cgc aga aat tca aag acc gta acc cgt gac ttg gca 499
Arg His Val Val Arg Arg Asn Ser Lys Thr Val Thr Arg Asp Leu Ala 130
120 125

cag tta gtt atg cgc acc gag ggt aaa gtg tcg tac acg tct gca act 547
Gln Leu Val Met Arg Thr Glu Gly Lys Val Ser Tyr Thr Ser Ala Thr 145
135 140

gaa aaa gag ccg gtg gtg tct tat aat gac cta aat act ctg cca tcg 595
Glu Lys Glu Pro Val Val Ser Tyr Asn Asp Leu Asn Thr Leu Pro Ser 165
150 155 160 165

cag aac gcc atc gtc ttc cgt gcg ggt cag tat ccg gtg tgg tca cgc 643
Gln Asn Ala Ile Val Phe Arg Ala Gly Gln Tyr Pro Val Trp Ser Arg 180
170 175

aat gaa acg att tgg ccg atg tcg ttc atg ttg ttt gct aac cag att 691
Asn Glu Thr Ile Trp Pro Met Ser Phe Met Leu Phe Ala Asn Gln Ile 195
185 190

atc caa ccg ggt cgc gaa tac tcg ttg cag act att cca aca ctg tcg 739
Ile Gln Pro Gly Arg Glu Tyr Ser Leu Gln Thr Ile Pro Thr Leu Ser 210
200 205 210

agc gct aat gaa ttc gat gtg aat caa aat gca ccg gac ttt atg gcg	787
Ser Ala Asn Glu Phe Asp Val Asn Gln Asn Ala Pro Asp Phe Met Ala	
215 220 225	
atg ctg gaa aag cgc atg gcg cag tcg att cgt act cag cgt gcc gtc	835
Met Leu Glu Lys Arg Met Ala Gln Ser Ile Arg Thr Gln Arg Ala Val	
230 235 240 245	
gat att tat aaa aag gcg act ggg ctc gat gac tct gat att gca cgc	883
Asp Ile Tyr Lys Lys Ala Thr Gly Leu Asp Asp Ser Asp Ile Ala Arg	
250 255 260	
ctg gat atg gat gtg tat tca gca gaa atc atg gac atc gtg gac acg	931
Leu Asp Met Asp Val Tyr Ser Ala Glu Ile Met Asp Ile Val Asp Thr	
265 270 275	
atg atc gcg aaa gat gag tac gat gac acg ccg gat tat gac gag ggg	979
Met Ile Ala Lys Asp Glu Tyr Asp Asp Thr Pro Asp Tyr Asp Glu Gly	
280 285 290	
gat gag tct gtc atg aat gct cgt gat ttc atg gag tct gaa tat gac	1027
Asp Glu Ser Val Met Asn Ala Arg Asp Phe Met Glu Ser Glu Tyr Asp	
295 300 305	
gtt ttt gat gat gag ttc gaa gac agt gct cag ggc ttc ccc gtg gct	1075
Val Phe Asp Asp Glu Phe Glu Asp Ser Ala Gln Gly Phe Pro Val Ala	
310 315 320 325	
act ggt acg aag gtg aaa aag aaa tct ctg tct gaa gaa gca gag gtc	1123
Thr Gly Thr Lys Val Lys Lys Ser Leu Ser Glu Glu Ala Glu Val	
330 335 340	
aat gat gaa ttc att cac gat cag gag aat gca gaa cat aag ctc gct	1171
Asn Asp Glu Phe Ile His Asp Gln Glu Asn Ala Glu His Lys Leu Ala	
345 350 355	
gac atg ccg ttg aag cgt tat gcc gaa ggc aag gtg tca cga gat atg	1219
Asp Met Arg Leu Lys Arg Tyr Ala Glu Gly Lys Val Ser Arg Asp Met	
360 365 370	
ctg gct gat caa ttc ggc cac atc ctg cag gac tca ctc gaa gat gag	1267
Leu Ala Asp Gln Phe Gly His Ile Leu Gln Asp Ser Leu Glu Asp Glu	
375 380 385	
ctc act gca gcc tat gat gag agc ctg cac gct ttt gct caa gat ccg	1315
Leu Thr Ala Ala Tyr Asp Glu Ser Leu His Ala Phe Ala Gln Asp Pro	
390 395 400 405	
aat ttc ccg gtg act gct aac aac ggc ttg gtt aat gct gtc gat ggc	1363
Asn Phe Arg Val Thr Ala Asn Asn Gly Leu Val Asn Ala Val Asp Gly	
410 415 420	
act gtg ttg att gag gcg ttg tcg cag gaa gat att gca ctt atg cgc	1411
Thr Val Leu Ile Glu Ala Leu Ser Gln Glu Asp Ile Ala Leu Met Arg	
425 430 435	
gcg caa gca gga gtg gag cag tcg cgt gtc tac tct gag ggt gaa gaa	1459
Ala Gln Ala Gly Val Glu Gln Ser Arg Val Tyr Ser Glu Gly Glu Glu	
440 445 450	
gct cta tct ggc aca gag gat gat ccg ctg tct gct atg ggt aaa tat	1507

Ala Leu Ser Gly Thr Glu Asp Asp Pro Leu Ser Ala Met Gly Lys Tyr
 455 460 465

aag acc acc cga gca ttc cgc atc atg ctg gtg gag ctt ccg cat tgg 1555
 Lys Thr Thr Arg Ala Phe Arg Ile Met Leu Val Glu Leu Pro His Trp
 470 475 480 485

cgt gat ctc gcc cag ggt cac ttt gat aaa gaa gtc gcg cga gcc ttt 1603
 Arg Asp Leu Ala Gln Gly His Phe Asp Lys Glu Val Ala Arg Ala Phe
 490 495 500

agg cgt att gaa gat gct taagtgtcgt gagcgataaa aaa 1644
 Arg Arg Ile Glu Asp Ala
 505

<210> 2522

<211> 507

<212> PRF

<213> *Corynebacterium glutamicum*

<400> 2522

Met Thr Gln Thr Leu Ala Gly Glu Arg Arg Ile Val Thr Thr Ala Glu
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Leu Lys Ala Met Leu Ala Arg Gly Asp Lys Val Phe Leu Pro Gly Val
 20 25 30

Ala Ala Arg Ala Pro Glu Ile Leu Asp Asn Phe Asp Pro Ala Asp Arg
 35 40 45

Ala Arg Leu Asp Val Pro Ala Ala Asp Asn Glu Ile Val Ser Val Glu
 50 55 60

Phe Ser Arg Arg Asp Thr Val Gln Cys Ile Ser Ile Ala Asp Arg Asp
 65 70 75 80

His Leu Tyr Ile Thr Asp Asp Met Ile Pro Thr His Asn Thr Ser Asn
 85 90 95

Ile Ile Phe Leu Lys Ser Thr Asp Glu Thr Met Ile Lys Thr Leu Val
 100 105 110

Asp Trp Ser Gly Glu Arg His Val Val Arg Arg Asn Ser Lys Thr Val
 115 120 125

Thr Arg Asp Leu Ala Gln Leu Val Met Arg Thr Glu Gly Lys Val Ser
 130 135 140

Tyr Thr Ser Ala Thr Glu Lys Glu Pro Val Val Ser Tyr Asn Asp Leu
 145 150 155 160

Asn Thr Leu Pro Ser Gln Asn Ala Ile Val Phe Arg Ala Gly Gln Tyr
 165 170 175

Pro Val Trp Ser Arg Asn Glu Thr Ile Trp Pro Met Ser Phe Met Leu
 180 185 190

Phe Ala Asn Gln Ile Ile Gln Pro Gly Arg Glu Tyr Ser Leu Gln Thr
 195 200 205

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Ile Pro Thr Leu Ser Ser Ala Asn Glu Phe Asp Val Asn Gln Asn Ala
 210                215                220

Pro Asp Phe Met Ala Met Leu Glu Lys Arg Met Ala Gln Ser Ile Arg
 225                230                235                240

Thr Gln Arg Ala Val Asp Ile Tyr Lys Lys Ala Thr Gly Leu Asp Asp
                245                250                255

Ser Asp Ile Ala Arg Leu Asp Met Asp Val Tyr Ser Ala Glu Ile Met
                260                265                270

Asp Ile Val Asp Thr Met Ile Ala Lys Asp Glu Tyr Asp Asp Thr Pro
 275                280                285

Asp Tyr Asp Glu Gly Asp Glu Ser Val Met Asn Ala Arg Asp Phe Met
 290                295                300

Glu Ser Glu Tyr Asp Val Phe Asp Asp Glu Phe Glu Asp Ser Ala Gln
 305                310                315                320

Gly Phe Pro Val Ala Thr Gly Thr Lys Val Lys Lys Lys Ser Leu Ser
                325                330                335

Glu Glu Ala Glu Val Asn Asp Glu Phe Ile His Asp Gln Glu Asn Ala
 340                345                350

Glu His Lys Leu Ala Asp Met Arg Leu Lys Arg Tyr Ala Glu Gly Lys
 355                360                365

Val Ser Arg Asp Met Leu Ala Asp Gln Phe Gly His Ile Leu Gln Asp
 370                375                380

Ser Leu Glu Asp Glu Leu Thr Ala Ala Tyr Asp Glu Ser Leu His Ala
 385                390                395                400

Phe Ala Gln Asp Pro Asn Phe Arg Val Thr Ala Asn Asn Gly Leu Val
                405                410                415

Asn Ala Val Asp Gly Thr Val Leu Ile Glu Ala Leu Ser Gln Glu Asp
                420                425                430

Ile Ala Leu Met Arg Ala Gln Ala Gly Val Glu Gln Ser Arg Val Tyr
 435                440                445

Ser Glu Gly Glu Glu Ala Leu Ser Gly Thr Glu Asp Asp Pro Leu Ser
 450                455                460

Ala Met Gly Lys Tyr Lys Thr Thr Arg Ala Phe Arg Ile Met Leu Val
 465                470                475                480

Glu Leu Pro His Trp Arg Asp Leu Ala Gln Gly His Phe Asp Lys Glu
                485                490                495

Val Ala Arg Ala Phe Arg Arg Ile Glu Asp Ala
 500                505

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<210> 2523

<211> 699

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(676)

<223> RXA01977

<400> 2523

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gggcacagac gatcctagca atagtcaaat tgcaggaagt atg ttg cgc aca tta 115
 Met Leu Arg Thr Leu 5
 1

ttc gtc cgc aag att aga gcg ctg ctg ctg gtt ttg atg att gcg cca 163
 Phe Val Arg Lys Ile Arg Ala Leu Leu Leu Val Leu Met Ile Ala Pro 20
 10 15

act cca ttg gtc gaa ggg cta act tcg act gca atg att gta tcc gta 211
 Thr Pro Leu Val Glu Gly Leu Thr Ser Thr Ala Met Ile Val Ser Val 35
 25 30

gta atc ctg gcg atc tac atg gcg ata aca atg tat aga gta gtg cac 259
 Val Ile Leu Ala Ile Tyr Met Ala Ile Thr Met Tyr Arg Val Val His 50
 40 45

ggt cgc cat gag ttc gcg cat atc gca cgt cgc atg gcg ctt tac gtc 307
 Gly Arg His Glu Phe Ala His Ile Ala Arg Arg Met Ala Leu Tyr Val 65
 55 60

aac aag act tct tct agg ttc agt gtt gtt att gct tat gta gta tta 355
 Asn Lys Thr Ser Ser Arg Phe Ser Val Val Ile Ala Tyr Val Val Leu 85
 70 75 80

att gct att tat gcg cta cta att ccc gga ctt gtc tac tct gtt aca 403
 Ile Ala Ile Tyr Ala Leu Leu Ile Pro Gly Leu Val Tyr Ser Val Thr 100
 90 95

ttt gga ttc atc gtc cca agc aca cct aat acg ttt agt gat gca cct 451
 Phe Gly Phe Ile Val Pro Ser Thr Pro Asn Thr Phe Ser Asp Ala Pro 115
 105 110

gca tgg att atg tgc gta tcg ctg ctg ctc att gca gtc gcc agt ttc 499
 Ala Trp Ile Met Cys Val Ser Leu Leu Leu Ile Ala Val Ala Ser Phe 130
 120 125

atc aca tca atc atg gat gac ttt att gat ggc ata ctc act gat ttt 547
 Ile Thr Ser Ile Met Asp Asp Phe Ile Asp Gly Ile Leu Thr Asp Phe 145
 135 140

tat gac gaa gat aat gct gat agc ccc gat agt cct gcc gag gat ata 595
 Tyr Asp Glu Asp Asn Ala Asp Ser Pro Asp Ser Pro Ala Glu Asp Ile 165
 150 155 160

gcc acc cgt cct gtc gag agc gca aca aca agt gct ctt gct gga ttt 643
 Ala Thr Arg Pro Val Glu Ser Ala Thr Thr Ser Ala Leu Ala Gly Phe 180
 170 175

gct gtt ggt tat att tgt ggg cgc ttt aat cgc taacacttaa aacacttctc 696
 Ala Val Gly Tyr Ile Cys Gly Arg Phe Asn Arg 190
 185

aac

699

<210> 2524

<211> 192

<212> PRT

<213> Corynebacterium glutamicum

<400> 2524

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20 25 30Met Ile Val Ser Val Val Ile Leu Ala Ile Tyr Met Ala Ile Thr Met
35 40 45Tyr Arg Val Val His Gly Arg His Glu Phe Ala His Ile Ala Arg Arg
50 55 60Met Ala Leu Tyr Val Asn Lys Thr Ser Ser Arg Phe Ser Val Val Ile
65 70 75 80Ala Tyr Val Val Leu Ile Ala Ile Tyr Ala Leu Leu Ile Pro Gly Leu
85 90 95Val Tyr Ser Val Thr Phe Gly Phe Ile Val Pro Ser Thr Pro Asn Thr
100 105 110Phe Ser Asp Ala Pro Ala Trp Ile Met Cys Val Ser Leu Leu Ile
115 120 125Ala Val Ala Ser Phe Ile Thr Ser Ile Met Asp Asp Phe Ile Asp Gly
130 135 140Ile Leu Thr Asp Phe Tyr Asp Glu Asp Asn Ala Asp Ser Pro Asp Ser
145 150 155 160Pro Ala Glu Asp Ile Ala Thr Arg Pro Val Glu Ser Ala Thr Thr Ser
165 170 175Ala Leu Ala Gly Phe Ala Val Gly Tyr Ile Cys Gly Arg Phe Asn Arg
180 185 190

<210> 2525

<211> 1281

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1258)

<223> RXA01982

<400> 2525

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cttcacccca	ctcatcatct	actgaagaa	ggcttctgct	atg	gct acc acc agc	115
				Met Ala Thr Thr Ser	5	
ctc ccc acg acg att aca ccg gat tcc gag gag acc gta gaa aag cgt	163					
Leu Pro Thr Thr Ile Thr Pro Asp Ser Glu Glu Thr Val Glu Lys Arg						
	10		15		20	
cac tcc ctg acc ccg atc ctg gat tca ctt ccc tgc gag tca gtt ccc	211					
His Ser Leu Thr Pro Ile Leu Asp Ser Leu Pro Cys Glu Ser Val Pro						
	25		30		35	
tat gct ctg gct gca ggt gag gga caa caa cac cag ctt ggc ccc tac	259					
Tyr Ala Leu Ala Ala Gly Glu Gly Gln Gln His Gln Leu Gly Pro Tyr						
	40		45		50	
cat ctc aca gtt atg tcc cgt ccc gaa gac aac ggt gga ata ttt tcg	307					
His Leu Thr Val Met Ser Arg Pro Glu Asp Asn Gly Gly Ile Phe Ser						
	55		60		65	
ctg gct cgt gtg agc gca ggc aag act ccc gcc acc cgg ttc ttc tct	355					
Leu Ala Arg Val Ser Ala Gly Lys Thr Pro Ala Thr Arg Phe Phe Ser						
	70		75		80	85
gtc gca gga ccg acg ttc ctc tac atg atg gag ggg cgg ttg act ctc	403					
Val Ala Gly Pro Thr Phe Leu Tyr Met Met Glu Gly Arg Leu Thr Leu						
	90		95		100	
tgg ttc gct gat gga cgt caa gag atc atc gct ggc ggc agt gcc acc	451					
Trp Phe Ala Asp Gly Arg Gln Glu Ile Ile Ala Gly Gly Ser Ala Thr						
	105		110		115	
att cct acg aat acg ccc tgg tcc ttc gcc tgt gag ggc cta gta aat	499					
Ile Pro Thr Asn Thr Pro Trp Ser Phe Ala Cys Glu Gly Leu Val Asn						
	120		125		130	
tca gct cta gtg tac tac tca tcc tgg aat gca ttc cta cac gcg gca	547					
Ser Ala Leu Val Tyr Tyr Ser Ser Ser Asn Ala Phe Leu His Ala Ala						
	135		140		145	
gag aaa ctt ggc acg tcc tgg ttc tcc cac acc ttc cgc gtc agt ggc	595					
Glu Lys Leu Gly Thr Ser Ser Phe Ser His Thr Phe Arg Val Ser Gly						
	150		155		160	165
gag gtc aca ggg att ccc tac gag gaa ctg gag gat tgc gga ttc aca	643					
Glu Val Thr Gly Ile Pro Tyr Glu Glu Leu Glu Asp Cys Gly Phe Thr						
	170		175		180	
ttc tat gag cgg gac cac ctt gcc gag ctc ggg ccg cat ttc gat cgc	691					
Phe Tyr Glu Arg Asp His Leu Ala Glu Leu Gly Pro His Phe Asp Arg						
	185		190		195	
ctc cca gaa gat atg aag gcg ttt gcc ctg aac gat ggt gag ggg gac	739					
Leu Pro Glu Asp Met Lys Ala Phe Ala Leu Asn Asp Gly Glu Gly Asp						
	200		205		210	
cgg ctt gag cag ttc gag cag atc aac agc ttc gtc tgc cgt ccg aga	787					
Arg Leu Glu Gln Phe Glu Gln Ile Asn Ser Phe Val Cys Arg Pro Arg						
	215		220		225	

cac acc gga aat cag ttc ctc gct atg cag acc aag ggt gcc aag acg 835
 His Thr Gly Asn Gln Phe Leu Ala Met Gln Thr Lys Gly Ala Lys Thr
 230 235 240 245

cct tat ata cct cgt cat ttc cac cgc ctt cac acc gaa aac ttc atc 883
 Pro Tyr Ile Pro Arg His Phe His Arg Leu His Thr Glu Asn Phe Ile
 250 255 260

tgt ctg gac ggg cgc gtc aaa ctg cac gtc aac ggt caa gag atc atc 931
 Cys Leu Asp Gly Arg Val Lys Leu His Val Asn Gly Gln Glu Ile Ile
 265 270 275

ctc tcc cgt ggg gat tac gtt cat gcc cca gcc gga acc atc cac tct 979
 Leu Ser Arg Gly Asp Tyr Val His Ala Pro Ala Gly Thr Ile His Ser
 280 285 290

ttc gcc ttc gca ggg cac aat acc cag atg ctg gga gtg ctc acc aca 1027
 Phe Ala Phe Ala Gly His Asn Thr Gln Met Leu Gly Val Leu Thr Thr
 295 300 305

gag gta ttc gag aag ttc ttt gac tac ata aac act ccg act aat gct 1075
 Glu Val Phe Glu Lys Phe Phe Asp Tyr Ile Asn Thr Pro Thr Asn Ala
 310 315 320 325

cga gtt cag ctg gag gac ggg ggg aag cca ttt ttt cct gct gaa gca 1123
 Arg Val Gln Leu Glu Asp Gly Gly Lys Pro Phe Phe Pro Ala Glu Ala
 330 335 340

ttc gcg aaa gtc caa gct gaa ctc gat gtc gtg gtg gtc ggc ccc cca 1171
 Phe Ala Lys Val Gln Ala Glu Leu Asp Val Val Val Val Gly Pro Pro
 345 350 355

cga att agt acc ctg gat gtt gtt aca aac tcg cgt ttc gaa cca att 1219
 Arg Ile Ser Thr Leu Asp Val Val Thr Asn Ser Arg Phe Glu Pro Ile
 360 365 370

aac aga act atc acc tat cgt gcg ctg gac gct aac caa tagtgagtga 1268
 Asn Arg Thr Ile Thr Tyr Arg Ala Leu Asp Ala Asn Gln
 375 380 385

gccgaaatcc ctg 1281

<210> 2526

<211> 386

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2526

Met Ala Thr Thr Ser Leu Pro Thr Thr Ile Thr Pro Asp Ser Glu Glu
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Thr Val Glu Lys Arg His Ser Leu Thr Pro Ile Leu Asp Ser Leu Pro
 20 25 30

Cys Glu Ser Val Pro Tyr Ala Leu Ala Ala Gly Glu Gly Gln Gln His
 35 40 45

Gln Leu Gly Pro Tyr His Leu Thr Val Met Ser Arg Pro Glu Asp Asn
 50 55 60

Gly Gly Ile Phe Ser Leu Ala Arg Val Ser Ala Gly Lys Thr Pro Ala
 65 70 75 80
 Thr Arg Phe Phe Ser Val Ala Gly Pro Thr Phe Leu Tyr Met Met Glu
 85 90 95
 Gly Arg Leu Thr Leu Trp Phe Ala Asp Gly Arg Gln Glu Ile Ile Ala
 100 105 110
 Gly Gly Ser Ala Thr Ile Pro Thr Asn Thr Pro Trp Ser Phe Ala Cys
 115 120 125
 Glu Gly Leu Val Asn Ser Ala Leu Val Tyr Tyr Ser Ser Ser Asn Ala
 130 135 140
 Phe Leu His Ala Ala Glu Lys Leu Gly Thr Ser Ser Phe Ser His Thr
 145 150 155 160
 Phe Arg Val Ser Gly Glu Val Thr Gly Ile Pro Tyr Glu Glu Leu Glu
 165 170 175
 Asp Cys Gly Phe Thr Phe Tyr Glu Arg Asp His Leu Ala Glu Leu Gly
 180 185 190
 Pro His Phe Asp Arg Leu Pro Glu Asp Met Lys Ala Phe Ala Leu Asn
 195 200 205
 Asp Gly Glu Gly Asp Arg Leu Glu Gln Phe Glu Gln Ile Asn Ser Phe
 210 215 220
 Val Cys Arg Pro Arg His Thr Gly Asn Gln Phe Leu Ala Met Gln Thr
 225 230 235 240
 Lys Gly Ala Lys Thr Pro Tyr Ile Pro Arg His Phe His Arg Leu His
 245 250 255
 Thr Glu Asn Phe Ile Cys Leu Asp Gly Arg Val Lys Leu His Val Asn
 260 265 270
 Gly Gln Glu Ile Ile Leu Ser Arg Gly Asp Tyr Val His Ala Pro Ala
 275 280 285
 Gly Thr Ile His Ser Phe Ala Phe Ala Gly His Asn Thr Gln Met Leu
 290 295 300
 Gly Val Leu Thr Thr Glu Val Phe Glu Lys Phe Phe Asp Tyr Ile Asn
 305 310 315 320
 Thr Pro Thr Asn Ala Arg Val Gln Leu Glu Asp Gly Gly Lys Pro Phe
 325 330 335
 Phe Pro Ala Glu Ala Phe Ala Lys Val Gln Ala Glu Leu Asp Val Val
 340 345 350
 Val Val Gly Pro Pro Arg Ile Ser Thr Leu Asp Val Val Thr Asn Ser
 355 360 365
 Arg Phe Glu Pro Ile Asn Arg Thr Ile Thr Tyr Arg Ala Leu Asp Ala
 370 375 380

Asn Gln
385

<210> 2527

<211> 1022

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(999)

<223> RXA01990

<400> 2527

aca tct gat cat gtg gca cag ttt ggt atg gca act gcg tct gct gcg 48
Thr Ser Asp His Val Ala Gln Phe Gly Met Ala Thr Ala Ser Ala Ala
1 5 10 15

acg ttg ccg gac agt att gtg acc agt gtt tct tat acg ttg aac ggg 96
Thr Leu Pro Asp Ser Ile Val Thr Ser Val Ser Tyr Thr Leu Asn Gly
20 25 30

ctg tca ttt tct gac ccg gtt gag ctg ggt atc agt gac aac gac aag 144
Leu Ser Phe Ser Asp Pro Val Glu Leu Gly Ile Ser Asp Asn Asp Lys
35 40 45

cgt gaa gag ctt cta gga gac atc acc aag ggt gaa ctg cga ttg cag 192
Arg Glu Glu Leu Leu Gly Asp Ile Thr Lys Gly Glu Leu Arg Leu Gln
50 55 60

atg gag ttt tcg atc ccg gat tca gca act gcc gag gat gag tac gtc 240
Met Glu Phe Ser Ile Pro Asp Ser Ala Thr Ala Glu Asp Glu Tyr Val
65 70 75 80

ttt aat ctc acc gcc gat gga ctt cgg ttt ttc aat tca aac gat cgc 288
Phe Asn Leu Thr Thr Gly Asp Gly Leu Arg Phe Phe Asn Ser Asn Asp Arg
85 90 95

acc gtc cct gta cgc aat gat gca ggt att cgt gtc gca gat ctt ttg 336
Thr Val Pro Val Arg Asn Asp Ala Gly Ile Arg Val Ala Asp Leu Leu
100 105 110

gtg agc aac ggt ggt acg cgc ggt acg ttg aca aac ttt agt tcg gat 384
Val Ser Asn Gly Gly Thr Arg Gly Thr Leu Thr Asn Phe Ser Ser Asp
115 120 125

gct gcc act act tct cgc acc gca gct ctt gat atg gaa ctg tac ggg 432
Ala Gly Thr Thr Ser Arg Thr Thr Ala Ala Leu Asp Met Glu Leu Tyr Gly
130 135 140

tgg gtg agt agc gcc cag cag acg ggt gag cga cca att caa gac tgg 480
Trp Val Ser Ser Ala Gln Gln Thr Gly Glu Arg Pro Ile Gln Asp Trp
145 150 155 160

act gtg ggt aag act gag ggt cag gtt gag aac aag gta gtc cgc tac 528
Thr Val Gly Lys Thr Glu Gly Gln Val Glu Asn Lys Val Val Arg Tyr
165 170 175

ggc gtt gct gga cac ccg tgg att atc agt act gtc cag cac acg tgg 576
Gly Val Ala Gly His Pro Trp Ile Ile Ser Thr Val Gln His Thr Trp

	180	185	190	
	gtt aag tct acg cag acc gtg tgc cat ttc cga agt gaa caa gac tgg			624
	Val Lys Ser Thr Gln Thr Val Ser His Phe Arg Ser Glu Gln Asp Trp			
	195	200	205	
	aag att aat caa cca cca gct gtt gat atg ggc gca tta gca tac gca			672
	Lys Ile Asn Gln Pro Pro Ala Val Asp Met Gly Ala Leu Ala Tyr Ala			
	210	215	220	
	gct cca ctt ggc gtc gtg gtc ggg cac gcc aat gtt gtc att agc aat			720
	Ala Pro Leu Gly Val Val Val Gly His Ala Asn Val Val Ile Ser Asn			
	225	230	235	240
	aac aac ggt gct gga ttc cgg ggt gcg ctt gtc aat acc aca ccc acc			768
	Asn Asn Gly Ala Gly Phe Arg Gly Ala Leu Val Asn Thr Thr Pro Thr			
	245	250	255	
	aca cgc gac gtg ata ctt aat ttc aca gcc gca gac gga gcc act tta			816
	Thr Arg Asp Val Ile Leu Asn Phe Thr Ala Ala Asp Gly Ala Thr Leu			
	260	265	270	
	cgc gaa cgt tcc gga ggt gga ttt gag gat ttc gac gtt ttc tgc gaa			864
	Arg Glu Arg Ser Gly Gly Gly Phe Glu Asp Phe Asp Val Phe Ser Glu			
	275	280	285	
	gtt cct cgg gta gag gaa aca tgc acg agg atc agc tat tct tac aaa			912
	Val Pro Arg Val Glu Glu Thr Ser Thr Arg Ile Ser Tyr Ser Tyr Lys			
	290	295	300	
	aat tca ttt gaa tat gac gaa ttt gtt gcc gca ttt ccc gag tac cga			960
	Asn Ser Phe Glu Tyr Asp Glu Glu Phe Val Ala Ala Phe Pro Glu Tyr Arg			
	305	310	315	320
	cgt agc tgc gtg gga acc aac cgt tgt gta ttc agc gga taagaccaca			1009
	Arg Ser Cys Val Gly Thr Asn Arg Cys Val Phe Ser Gly			
	325	330		
	gcaacagcga cgt			1022
	<210> 2528			
	<211> 333			
	<212> PRT			
	<213> Corynebacterium glutamicum			
	<400> 2528			
	Thr Ser Asp His Val Ala Gln Phe Gly Met Ala Thr Ala Ser Ala Ala			
	1	5	10	15
	Thr Leu Pro Asp Ser Ile Val Thr Ser Val Ser Tyr Thr Leu Asn Gly			
	20	25	30	
	Leu Ser Phe Ser Asp Pro Val Glu Leu Gly Ile Ser Asp Asn Asp Lys			
	35	40	45	
	Arg Glu Glu Leu Leu Gly Asp Ile Thr Lys Gly Glu Leu Arg Leu Gln			
	50	55	60	
	Met Glu Phe Ser Ile Pro Asp Ser Ala Thr Ala Glu Asp Glu Tyr Val			
	65	70	75	80

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Phe Asn Leu Thr Gly Asp Gly Leu Arg Phe Phe Asn Ser Asn Asp Arg
      85                      90                      95

Thr Val Pro Val Arg Asn Asp Ala Gly Ile Arg Val Ala Asp Leu Leu
      100                    105                    110

Val Ser Asn Gly Gly Thr Arg Gly Thr Leu Thr Asn Phe Ser Ser Asp
      115                    120                    125

Ala Gly Thr Thr Ser Arg Thr Ala Ala Leu Asp Met Glu Leu Tyr Gly
      130                    135                    140

Trp Val Ser Ser Ala Gln Gln Thr Gly Glu Arg Pro Ile Gln Asp Trp
      145                    150                    155

Thr Val Gly Lys Thr Glu Gly Gln Val Glu Asn Lys Val Val Arg Tyr
      165                    170                    175

Gly Val Ala Gly His Pro Trp Ile Ile Ser Thr Val Gln His Thr Trp
      180                    185                    190

Val Lys Ser Thr Gln Thr Val Ser His Phe Arg Ser Glu Gln Asp Trp
      195                    200                    205

Lys Ile Asn Gln Pro Pro Ala Val Asp Met Gly Ala Leu Ala Tyr Ala
      210                    215                    220

Ala Pro Leu Gly Val Val Val Gly His Ala Asn Val Val Ile Ser Asn
      225                    230                    235

Asn Asn Gly Ala Gly Phe Arg Gly Ala Leu Val Asn Thr Thr Pro Thr
      245                    250                    255

Thr Arg Asp Val Ile Leu Asn Phe Thr Ala Ala Asp Gly Ala Thr Leu
      260                    265                    270

Arg Glu Arg Ser Gly Gly Gly Phe Glu Asp Phe Asp Val Phe Ser Glu
      275                    280                    285

Val Pro Arg Val Glu Glu Thr Ser Thr Arg Ile Ser Tyr Ser Tyr Lys
      290                    295                    300

Asn Ser Phe Glu Tyr Asp Glu Phe Val Ala Ala Phe Pro Glu Tyr Arg
      305                    310                    315

Arg Ser Cys Val Gly Thr Asn Arg Cys Val Phe Ser Gly
      325                    330

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<210> 2529

<211> 573

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(550)

<223> RXA01992

<400> 2529

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tgcttgaagt cgaagtaagt gagggggaga ggatccgtta gtg tac tgc cca ttt 115
Val Tyr Cys Pro Phe
1 5

tgc caa cat gat cat tca aaa gtc att gac tcc cgc gtc att gac gcc 163
Cys Gln His Asp His Ser Lys Val Ile Asp Ser Arg Val Ile Asp Ala
10 15 20

gga agc gcc att cgc agg cgc cgc gag tgc agc aaa tgc gaa ggc cgt 211
Gly Ser Ala Ile Arg Arg Arg Arg Glu Cys Ser Lys Cys Glu Gly Arg
25 30 35

ttc acc acc atc gaa aaa gct gtt ctc ctc gtt gtt aaa aga aac ggc 259
Phe Thr Thr Ile Glu Lys Ala Val Leu Leu Val Val Lys Arg Asn Gly
40 45 50

gtc act gaa ccg ttc agt cga gaa aaa gta gtc acc ggt gtc cgt cgt 307
Val Thr Glu Pro Phe Ser Arg Glu Lys Val Val Thr Gly Val Arg Arg
55 60 65

gca tgc caa ggc cgc gac gta tca gat gac gcg ttg aaa cgc cta gct 355
Ala Cys Gln Gly Arg Asp Val Ser Asp Asp Ala Leu Lys Arg Leu Ala
70 75 80 85

cag caa gtg gaa gaa aca gtc cgc agc aac gga agc tct caa gta cgc 403
Gln Gln Val Glu Glu Thr Val Arg Ser Asn Gly Ser Ser Gln Val Arg
90 95 100

gct aac gat att ggt tta gcc att ctc gat cca ctg aga gaa ctc gac 451
Ala Asn Asp Ile Gly Leu Ala Ile Leu Asp Pro Leu Arg Glu Leu Asp
105 110 115

gag gta gcg tac cta cgc ttt gcc tct gtg tat aag tct ttt gac agt 499
Glu Val Ala Tyr Leu Arg Phe Ala Ser Val Tyr Lys Ser Phe Asp Ser
120 125 130

gct gac gac ttt gaa aaa gaa atc cgc ctc atg cgc aga cgc gga agg 547
Ala Asp Asp Phe Glu Lys Glu Ile Arg Leu Met Arg Arg Arg Gly Arg
135 140 145

gac tagcagacac aaagtcttaa cta 573
Asp
150

<210> 2530
<211> 150
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 2530
Val Tyr Cys Pro Phe Cys Gln His Asp His Ser Lys Val Ile Asp Ser
1 5 10 15
Arg Val Ile Asp Ala Gly Ser Ala Ile Arg Arg Arg Arg Glu Cys Ser
20 25 30
Lys Cys Glu Gly Arg Phe Thr Thr Ile Glu Lys Ala Val Leu Leu Val
35 40 45

Val Lys Arg Asn Gly Val Thr Glu Pro Phe Ser Arg Glu Lys Val Val
 50 55 60

Thr Gly Val Arg Arg Ala Cys Gln Gly Arg Asp Val Ser Asp Asp Ala
 65 70 75 80

Leu Lys Arg Leu Ala Gln Gln Val Glu Glu Thr Val Arg Ser Asn Gly
 85 90 95

Ser Ser Gln Val Arg Ala Asn Asp Ile Gly Leu Ala Ile Leu Asp Pro
 100 105 110

Leu Arg Glu Leu Asp Glu Val Ala Tyr Leu Arg Phe Ala Ser Val Tyr
 115 120 125

Lys Ser Phe Asp Ser Ala Asp Asp Phe Glu Lys Glu Ile Arg Leu Met
 130 135 140

Arg Arg Arg Gly Arg Asp
 145 150

<210> 2531
 <211> 594
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(571)
 <223> RXA01999

<400> 2531
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 atacttgacc atatcgaaat ctctaccagc tcgaggcatc atg act ctc ccc acc 115
 Met Thr Leu Pro Thr
 1 5

cct aca cat tcc acc aaa ggc agt tca ggc cgc atg aaa cga atg gcc 163
 Pro Thr His Ser Thr Lys Gly Ser Ser Gly Arg Met Lys Arg Met Ala
 10 15 20

ctt atc gcc tcc tcg ctc att att tcc atg gga ctt att act gcg tgc 211
 Leu Ile Gly Ser Ser Leu Ile Ile Ser Met Gly Leu Ile Thr Ala Cys
 25 30 35

ggt tcg gcc gct gca gaa ccc gaa gcc cct gca cca aca gtt acc gaa 259
 Gly Ser Ala Ala Glu Pro Glu Ala Pro Ala Pro Thr Val Thr Glu
 40 45 50

act gta aca gcc acg gtg aca acc aca gct aaa gcc agc acg atc acc 307
 Thr Val Thr Ala Thr Val Thr Thr Thr Ala Lys Ala Ser Thr Ile Thr
 55 60 65

tcg aca gtg acg gaa act acc tcc gcg gaa gat ctt gcc caa gaa att 355
 Ser Thr Val Thr Glu Thr Thr Ser Ala Glu Asp Leu Ala Gln Glu Ile
 70 75 80 85

gtg aag cca gcg gcc gtg gag gaa tat tca gag cct cag gta aat acg 403

Val Lys Pro Ala Ala Val Glu Glu Tyr Ser Glu Pro Gln Val Asn Thr
 90 95 100

cca cag cag ttt gcg gcc atc ccg gaa cct gca ccg gcg gtt gca cca 451
 Pro Gln Gln Phe Ala Ala Ile Pro Glu Pro Ala Pro Ala Val Ala Pro
 105 110 115

gct caa acg tat tac gcc aac tgc gcg gca gtt cgt gcg gcg ggt gca 499
 Ala Gln Thr Tyr Tyr Ala Asn Cys Ala Ala Val Arg Ala Ala Gly Ala
 120 125 130

gct ccc ctt tat gcg gga tca cct gga tat agt tcc aag ctt gat cgc 547
 Ala Pro Leu Tyr Ala Gly Ser Pro Gly Tyr Ser Ser Lys Leu Asp Arg
 135 140 145

gat ggc gac gga att gcc tgc gaa taaataggaa tagttaaaaa cac 594
 Asp Gly Asp Gly Ile Ala Cys Glu
 150 155

<210> 2532

<211> 157

<212> PRT

<213> Corynebacterium glutamicum

<400> 2532

Met Thr Leu Pro Thr Pro Thr His Ser Thr Lys Gly Ser Ser Gly Arg
 1 5 10 15

Met Lys Arg Met Ala Leu Ile Gly Ser Ser Leu Ile Ile Ser Met Gly
 20 25 30

Leu Ile Thr Ala Cys Gly Ser Ala Ala Ala Glu Pro Glu Ala Pro Ala
 35 40 45

Pro Thr Val Thr Glu Thr Val Thr Ala Thr Val Thr Thr Thr Ala Lys
 50 55 60

Ala Ser Thr Ile Thr Ser Thr Val Thr Glu Thr Thr Ser Ala Glu Asp
 65 70 75 80

Leu Ala Gln Glu Ile Val Lys Pro Ala Ala Val Glu Glu Tyr Ser Glu
 85 90 95

Pro Gln Val Asn Thr Pro Gln Gln Phe Ala Ala Ile Pro Glu Pro Ala
 100 105 110

Pro Ala Val Ala Pro Ala Gln Thr Tyr Tyr Ala Asn Cys Ala Ala Val
 115 120 125

Arg Ala Ala Gly Ala Ala Pro Leu Tyr Ala Gly Ser Pro Gly Tyr Ser
 130 135 140

Ser Lys Leu Asp Arg Asp Gly Asp Gly Ile Ala Cys Glu
 145 150 155

<210> 2533

<211> 572

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(549)

<223> RXA02001

<400> 2533

acc cgc gac ccc atc gtc gca gcc gtc gga att gtc caa gcg ttt caa 48
 Thr Arg Asp Pro Ile Val Ala Ala Val Gly Ile Val Gln Ala Phe Gln
 1 5 10 15

acg ata gtc agc cgg aat cac aat ccg gtc gag gac ctt gtc gtg tcg 96
 Thr Ile Val Ser Arg Asn His Asn Pro Val Glu Asp Leu Val Val Ser
 20 25 30

gtc acg caa atc cac acc gcc agc gcc gat aat atc atc ccc gaa acc 144
 Val Thr Gln Ile His Thr Gly Ser Ala Asp Asn Ile Ile Pro Glu Thr
 35 40 45

gcc tat atc aac gcc act gtc cgc acc ttc aac aaa gac gtg cag gcc 192
 Ala Tyr Ile Asn Gly Thr Val Arg Thr Phe Asn Lys Asp Val Gln Ala
 50 55 60

atg gtc atc acg cgg atg gaa gaa atc gtc cgc gcc caa gct gca gcc 240
 Met Val Ile Thr Arg Met Glu Glu Ile Val Ala Gly Gln Ala Ala Ala
 65 70 75 80

tat ggg gtc gag gcg acg ctg acc tac aac cgc aac tat ccc gcc acc 288
 Tyr Gly Val Glu Ala Thr Leu Thr Tyr Asn Arg Asn Tyr Pro Ala Thr
 85 90 95

att aac gac gcc gcc aaa gcc gcc atc gct gcc gaa gtc gcg gcc gag 336
 Ile Asn Asp Ala Ala Lys Ala Ala Ile Ala Ala Glu Val Ala Gly Glu
 100 105 110

gtc gcc ctc ggg gtc aac ccg aac gcc tcg cgc ggg atg ggg gcc gag 384
 Val Gly Leu Gly Val Asn Pro Asn Gly Ser Arg Gly Met Gly Ala Glu
 115 120 125

gat ttc tcg tat ttc ctc gaa aag cgc ccg ggt gcc tac ctg ttc gtc 432
 Asp Phe Ser Tyr Phe Leu Glu Lys Arg Pro Gly Ala Tyr Leu Phe Val
 130 135 140

ggt aat ggc gac agc gcg gcc ctt cac aac ccc gcc tat aat ttc aac 480
 Gly Asn Gly Asp Ser Ala Gly Leu His Asn Pro Ala Tyr Asn Phe Asn
 145 150 155 160

gac gag gcc gcg ccc tac gcc gca tcg ttc ttg gcc cgc atg gca gaa 528
 Asp Glu Ala Ala Pro Tyr Gly Ala Ser Phe Leu Ala Arg Met Ala Glu
 165 170 175

cgc ccc ttg ccg tta aag gcc tgatccatgg cgctcgaaga tgc 572
 Arg Pro Leu Pro Leu Lys Gly
 180

<210> 2534

<211> 183

<212> PRT

<213> Corynebacterium glutamicum

<400> 2534

Thr Arg Asp Pro Ile Val Ala Ala Val Gly Ile Val Gln Ala Phe Gln
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Thr Ile Val Ser Arg Asn His Asn Pro Val Glu Asp Leu Val Val Ser
 20 25 30

Val Thr Gln Ile His Thr Gly Ser Ala Asp Asn Ile Ile Pro Glu Thr
 35 40 45

Ala Tyr Ile Asn Gly Thr Val Arg Thr Phe Asn Lys Asp Val Gln Ala
 50 55 60

Met Val Ile Thr Arg Met Glu Glu Ile Val Ala Gly Gln Ala Ala Ala
 65 70 75 80

Tyr Gly Val Glu Ala Thr Leu Thr Tyr Asn Arg Asn Tyr Pro Ala Thr
 85 90 95

Ile Asn Asp Ala Ala Lys Ala Ala Ile Ala Ala Glu Val Ala Gly Glu
 100 105 110

Val Gly Leu Gly Val Asn Pro Asn Gly Ser Arg Gly Met Gly Ala Glu
 115 120 125

Asp Phe Ser Tyr Phe Leu Glu Lys Arg Pro Gly Ala Tyr Leu Phe Val
 130 135 140

Gly Asn Gly Asp Ser Ala Gly Leu His Asn Pro Ala Tyr Asn Phe Asn
 145 150 155 160

Asp Glu Ala Ala Pro Tyr Gly Ala Ser Phe Leu Ala Arg Met Ala Glu
 165 170 175

Arg Pro Leu Pro Leu Lys Gly
 180

<210> 2535

<211> 230

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(207)

<223> RXA02004

<400> 2535

cgc gtc ggc cgt ctg atg cgt cag aac ggc att ctc atc atc cgc agc 48
 Arg Val Gly Arg Leu Met Arg Gln Asn Gly Ile Leu Ile Ile Arg Ser
 1 5 10 15

cgg aag ttc aag cgc acg acc ggc agc gat cat acc ttc aac atc gca 96
 Arg Lys Phe Lys Arg Thr Thr Gly Ser Asp His Thr Phe Asn Ile Ala
 20 25 30

cgg aac ttt ctg cag cag gac ttt atg gcg agc agg cgg aac cag aag 144
 Pro Asn Phe Leu Gln Gln Asp Phe Met Ala Ser Arg Pro Asn Gln Lys
 35 40 45

tct ggc cga cat tct tgacctttat cccgcgcggg tga 230
Ser Gly Arg His Ser
65

<213> Corynebacterium glutamicum

Ser Gly Arg His Ser
65

<213> Corynebacterium glutamicum

<223> RXA02006

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tat ctc att gac gag tca ctc ttt caa gag act gta gaa acc tct ccg 301

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Tyr Leu Ile Asp Glu Ser Leu Phe Gln Glu Thr Val Glu Thr Ser Pro
      65              70              75

atc gta gtc agc gac aat gaa gat gca gcc caa gat ccc ggt ttc ggc 349
Ile Val Val Ser Asp Asn Glu Asp Ala Ala Gln Asp Pro Gly Phe Gly
      80              85              90

ctt ttc acc aca aat cct gtg aaa cac aca gat gag cac att ggc gct 397
Leu Phe Thr Thr Asn Pro Val Lys His Thr Asp Glu His Ile Gly Ala
      95              100             105

cta tac ttc tcc gac cta cca ggt att tcc aat ctt acg tgc act gcc 445
Leu Tyr Phe Ser Asp Leu Pro Gly Ile Ser Asn Leu Thr Cys Thr Ala
      110             115             120             125

aac tac atc ggt gga aaa ttc tgg acc aca gca cat cat tgt gtt gaa 493
Asn Tyr Ile Gly Gly Lys Phe Trp Thr Thr Ala His His Cys Val Glu
      130             135             140

ggc cgc agt cgc ttc gtc ggc ttc atc gag cag tcg gac gga caa tat 541
Gly Arg Ser Arg Phe Val Gly Phe Ile Glu Gln Ser Asp Gly Gln Tyr
      145             150             155

gca ggc att gag cat gtt tac aca 565
Ala Gly Ile Glu His Val Tyr Thr
      160             165

<210> 2538
<211> 165
<212> PRT
<213> Corynebacterium glutamicum

<400> 2538
Met Thr Val Ala His Lys Arg Ser Leu Thr Trp Ile Lys Arg Leu Ser
  1              5              10             15

Ala Thr Thr Phe Ala Ala Phe Leu Gly Ile Gln Leu Val Thr Pro Ala
      20              25              30

His Ser Ile Glu Asn Thr Thr Gln Ile Pro Glu Ser Glu Leu His Asn
      35              40              45

Leu Gly Leu Thr Asp Glu Glu Ile Gln Glu Phe Asn Gln Tyr Leu Ile
      50              55              60

Asp Glu Ser Leu Phe Gln Glu Thr Val Glu Thr Ser Pro Ile Val Val
      65              70              75             80

Ser Asp Asn Glu Asp Ala Ala Gln Asp Pro Gly Phe Gly Leu Phe Thr
      85              90              95

Thr Asn Pro Val Lys His Thr Asp Glu His Ile Gly Ala Leu Tyr Phe
      100             105             110

Ser Asp Leu Pro Gly Ile Ser Asn Leu Thr Cys Thr Ala Asn Tyr Ile
      115             120             125

Gly Gly Lys Phe Trp Thr Thr Ala His His Cys Val Glu Gly Arg Ser
      130             135             140

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Arg Phe Val Gly Phe Ile Glu Gln Ser Asp Gly Gln Tyr Ala Gly Ile
 145 150 155 160

Glu His Val Tyr Thr
 165

<210> 2539
 <211> 223
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(223)
 <223> RXA02009

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gcttaaaaaa actcaatcgt ccattcaag aaaagagcac atg acc atg tac aac 115
 Met Thr Met Tyr Asn
 1 5

gcc gca aag acc ctt gtt ccc cag att gtt gct ttc gat gac aca gca 163
 Ala Ala Lys Thr Leu Val Pro Gln Ile Val Ala Phe Asp Asp Thr Ala
 10 15 20

atc atc gca ctc gac caa gcc gcg gaa gat gaa ttc cgc aag gct aac 211
 Ile Ile Ala Leu Asp Gln Ala Ala Glu Asp Glu Phe Arg Lys Ala Asn
 25 30 35

tac ccc gag gtt 223
 Tyr Pro Glu Val
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<210> 2540
 <211> 41
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 2540
 Met Thr Met Tyr Asn Ala Ala Lys Thr Leu Val Pro Gln Ile Val Ala
 1 5 10 15

Phe Asp Asp Thr Ala Ile Ile Ala Leu Asp Gln Ala Ala Glu Asp Glu
 20 25 30

Phe Arg Lys Ala Asn Tyr Pro Glu Val
 35 40

<210> 2541
 <211> 649
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(649)

<223> RXA02013

<400> 2541

atcaccgcgc tggcgacaat ttcagaaaaac tcccacaaag cactgcttgg cctttatttg 60

tccggtcttta	aacacggcat	gatggctaac	atcggagaac	atg	acg	gaa	agt	cct	115
				Met	Thr	Glu	Ser	Pro	
				1				5	

gat	cta	gca	gtt	tcc	ttt	tta	gcc	gcc	ttc	aat	gac	atc	gaa	gcg	cac	163
Asp	Leu	Ala	Val	Ser	Phe	Leu	Ala	Ala	Phe	Asn	Asp	Ile	Glu	Ala	His	
			10						15					20		

ctt	cga	acc	cag	ctc	cgc	gct	aaa	cgc	tcc	gac	agt	ttc	aga	tggt	atg	211
Leu	Arg	Thr	Gln	Leu	Arg	Ala	Lys	Arg	Ser	Asp	Ser	Phe	Arg	Trp	Met	
			25						30					35		

gta	cgt	atc	gcc	gag	aaa	cag	cat	ctg	att	tcc	aaa	gaa	caa	gca	gaa	259
Val	Arg	Ile	Ala	Glu	Lys	Gln	His	Leu	Ile	Ser	Lys	Glu	Gln	Ala	Glu	
			40					45				50				

acc	ctt	gat	gct	ttt	gcg	gag	ctg	cgc	aac	gca	att	agc	cac	ggc	caa	307
Thr	Leu	Asp	Ala	Phe	Ala	Glu	Leu	Arg	Asn	Ala	Ile	Ser	His	Gly	Gln	
			55			60					65					

tac	aac	gat	cta	cgc	ccg	att	gcc	gat	ccc	cgc	ccc	gac	acc	gtg	gac	355
Tyr	Asn	Asp	Leu	Arg	Pro	Ile	Ala	Asp	Pro	Arg	Pro	Asp	Thr	Val	Asp	
			70			75				80				85		

acc	att	gag	aag	att	cgc	tcc	ctc	ctt	ctc	aat	cct	cca	att	gcg	tta	403
Thr	Ile	Glu	Lys	Ile	Arg	Ser	Leu	Leu	Leu	Asn	Pro	Pro	Ile	Ala	Leu	
										95				100		

aac	gtc	ctc	ccg	gag	caa	aag	gtc	cgc	tcc	tac	tca	ott	gaa	gat	cca	451
Asn	Val	Leu	Pro	Glu	Gln	Lys	Val	Arg	Ser	Tyr	Ser	Leu	Glu	Asp	Pro	
			105				110						115			

gtg	agt	agg	gcc	tta	gaa	gtt	gtg	cac	acc	acg	gag	atc	tcc	caa	ttc	499
Val	Ser	Arg	Ala	Leu	Glu	Val	Val	His	Thr	Thr	Glu	Ile	Ser	Gln	Phe	
			120				125						130			

ccc	ata	tat	aag	gga	acg	gaa	tac	gtg	gca	ctg	cta	act	acc	aac	aca	547
Pro	Ile	Tyr	Lys	Gly	Thr	Glu	Tyr	Val	Ala	Leu	Leu	Thr	Thr	Asn	Thr	
			135			140					145					

atc	gct	cgc	tggt	gcc	tcc	gat	tta	cat	gac	aat	gcc	cag	ctg	gat	595	
Ile	Ala	Arg	Trp	Val	Ala	Ser	Asp	Leu	His	Asp	Asn	Ala	Gln	Leu	Asp	
			150			155				160				165		

gca	cgt	tct	atc	aaa	gag	gtt	ctg	gat	tat	gca	gaa	tcc	tct	gac	act	643
Ala	Arg	Ser	Ile	Lys	Glu	Val	Leu	Asp	Tyr	Ala	Glu	Ser	Ser	Asp	Thr	
			170						175					180		

gca	gtt															649
Ala	Val															

<210> 2542

<211> 183

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2542

Met Thr Glu Ser Pro Asp Leu Ala Val Ser Phe Leu Ala Ala Phe Asn
 1 5 10 15

Asp Ile Glu Ala His Leu Arg Thr Gln Leu Arg Ala Lys Arg Ser Asp
 20 25 30

Ser Phe Arg Trp Met Val Arg Ile Ala Glu Lys Gln His Leu Ile Ser
 35 40 45

Lys Glu Gln Ala Glu Thr Leu Asp Ala Phe Ala Glu Leu Arg Asn Ala
 50 55 60

Ile Ser His Gly Gln Tyr Asn Asp Leu Arg Pro Ile Ala Asp Pro Arg
 65 70 75 80

Pro Asp Thr Val Asp Thr Ile Glu Lys Ile Arg Ser Leu Leu Leu Asn
 85 90 95

Pro Pro Ile Ala Leu Asn Val Leu Pro Glu Gln Lys Val Arg Ser Tyr
 100 105 110

Ser Leu Glu Asp Pro Val Ser Arg Ala Leu Glu Val Val His Thr Thr
 115 120 125

Glu Ile Ser Gln Phe Pro Ile Tyr Lys Gly Thr Glu Tyr Val Ala Leu
 130 135 140

Leu Thr Thr Asn Thr Ile Ala Arg Trp Val Ala Ser Asp Leu His Asp
 145 150 155 160

Asn Ala Gln Leu Asp Ala Arg Ser Ile Lys Glu Val Leu Asp Tyr Ala
 165 170 175

Glu Ser Ser Asp Thr Ala Val
 180

<210> 2543

<211> 1071

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1048)

<223> RXA02021

<400> 2543

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aaaccttagt taaaacatga tggaagcggg cgattaaaaa atg agt gaa aac att 115
 Met Ser Glu Asn Ile
 1 5

cgc gga gcc caa gca gtt gga atc gca aat atc gcc atg gac ggg acc 163
 Arg Gly Ala Gln Ala Val Gly Ile Ala Asn Ile Ala Met Asp Gly Thr
 10 15 20

atc ctg gac acg tgg tac cca gaa ccc caa att ttc aac ccg gat cag	211
Ile Leu Asp Thr Trp Tyr Pro Glu Pro Gln Ile Phe Asn Pro Asp Gln	
25 30 35	
tgg gct gaa cgc tac cca ttg gaa gtg ggc acc aca cgc ctc gga gca	259
Trp Ala Glu Arg Tyr Pro Leu Glu Val Gly Thr Thr Arg Leu Gly Ala	
40 45 50	
aac gaa ctc acc cca cgg atg ctg cag ttg gta aaa ctg gac caa gat	307
Asn Glu Leu Thr Pro Arg Met Leu Gln Leu Val Lys Leu Asp Gln Asp	
55 60 65	
cgc ctc gtc gaa cag gta gca gtc cgc acc gtt atc ccc gat ctg tct	355
Arg Leu Val Glu Gln Val Ala Val Arg Thr Val Ile Pro Asp Leu Ser	
70 75 80 85	
caa cct cca gta gac gcg cac gat gtt tac ctg cgc ctc cac ctg ctt	403
Gln Pro Pro Val Asp Ala His Asp Val Tyr Leu Arg Leu His Leu Leu	
90 95 100	
tcc cac cgg ctg gtc cgc ccc cac gaa atg cac atg caa aac acc ttg	451
Ser His Arg Leu Val Arg Pro His Glu Met His Met Gln Asn Thr Leu	
105 110 115	
gag ctg ctg tcc gac gtg gtg tgg aca aac aag ggc cct tgc ctt cct	499
Glu Leu Leu Ser Asp Val Val Trp Thr Asn Lys Gly Pro Cys Leu Pro	
120 125 130	
gaa aac ttt gag tgg gtg cgt ggt gct ctg cgg tcc cgc gga ctc atc	547
Glu Asn Phe Glu Trp Val Arg Gly Ala Leu Arg Ser Arg Gly Leu Ile	
135 140 145	
cac gtc tac tgt gtg gac cgt ctt ccc cgc atg gtc gac tat gtg gtt	595
His Val Tyr Cys Val Asp Arg Leu Pro Arg Met Val Asp Tyr Val Val	
150 155 160 165	
ccc cct gga gtc cgc atc tcc gaa gca gaa cgc gtg cgc cta ggt gca	643
Pro Pro Gly Val Arg Ile Ser Glu Ala Glu Arg Val Arg Leu Gly Ala	
170 175 180	
tac ctt gct ccg ggt acc tct gtg ctg cgt gaa ggt ttc gtg tct ttc	691
Tyr Leu Ala Pro Gly Thr Ser Val Leu Arg Glu Gly Phe Val Ser Phe	
185 190 195	
aac tcc gcc acc ttg ggt gcc gca aag gtg gaa ggc cgc ctg agt tcc	739
Asn Ser Gly Thr Leu Gly Ala Ala Lys Val Glu Gly Arg Leu Ser Ser	
200 205 210	
ggt gtg gtc atc ggt gaa ggt tcc gag att gga ctg tct tct act att	787
Gly Val Val Ile Gly Glu Gly Ser Glu Ile Gly Leu Ser Ser Thr Ile	
215 220 225	
cag tcc ccg aga gat gaa cag cgc cgc cgt ttg ccg ttg agc atc ggc	835
Gln Ser Pro Arg Asp Glu Gln Arg Arg Arg Leu Pro Leu Ser Ile Gly	
230 235 240 245	
caa aac tgc aac ttt ggt gtc agc tcc gga atc atc gga gtc agt ctg	883
Gln Asn Cys Asn Phe Gly Val Ser Ser Gly Ile Ile Gly Val Ser Leu	
250 255 260	
gga gac aat tgc gac atc gga aat aac att gtc ttg gat gga gat acc	931

Gly Asp Asn Cys Asp Ile Gly Asn Asn Ile Val Leu Asp Gly Asp Thr
 265 270 275
 ccc att tgg ttc gca gcc gat gag gag tta cgc act atc gac tcc atc 979
 Pro Ile Trp Phe Ala Ala Asp Glu Glu Leu Arg Thr Ile Asp Ser Ile
 280 285 290
 gaa ggc caa gca aat tgg tca atc aag cgt gaa tcc ggc ttc cat gag 1027
 Glu Gly Gln Ala Asn Trp Ser Ile Lys Arg Glu Ser Gly Phe His Glu
 295 300 305
 cca gtt gcc cgc ctc aaa gct tgacccattt tcataaccag tgc 1071
 Pro Val Ala Arg Leu Lys Ala
 310 315

<210> 2544

<211> 316

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2544

Met Ser Glu Asn Ile Arg Gly Ala Gln Ala Val Gly Ile Ala Asn Ile
 1 5 10 15
 Ala Met Asp Gly Thr Ile Leu Asp Thr Trp Tyr Pro Glu Pro Gln Ile
 20 25 30
 Phe Asn Pro Asp Gln Trp Ala Glu Arg Tyr Pro Leu Glu Val Gly Thr
 35 40 45
 Thr Arg Leu Gly Ala Asn Glu Leu Thr Pro Arg Met Leu Gln Leu Val
 50 55 60
 Lys Leu Asp Gln Asp Arg Leu Val Glu Gln Val Ala Val Arg Thr Val
 65 70 75 80
 Ile Pro Asp Leu Ser Gln Pro Pro Val Asp Ala His Asp Val Tyr Leu
 85 90 95
 Arg Leu His Leu Leu Ser His Arg Leu Val Arg Pro His Glu Met His
 100 105 110
 Met Gln Asn Thr Leu Glu Leu Leu Ser Asp Val Val Trp Thr Asn Lys
 115 120 125
 Gly Pro Cys Leu Pro Glu Asn Phe Glu Trp Val Arg Gly Ala Leu Arg
 130 135 140
 Ser Arg Gly Leu Ile His Val Tyr Cys Val Asp Arg Leu Pro Arg Met
 145 150 155 160
 Val Asp Tyr Val Val Pro Pro Gly Val Arg Ile Ser Glu Ala Glu Arg
 165 170 175
 Val Arg Leu Gly Ala Tyr Leu Ala Pro Gly Thr Ser Val Leu Arg Glu
 180 185 190
 Gly Phe Val Ser Phe Asn Ser Gly Thr Leu Gly Ala Ala Lys Val Glu
 195 200 205

Gly Arg Leu Ser Ser Gly Val Val Ile Gly Glu Gly Ser Glu Ile Gly
210 215

Leu Ser Ser Thr Ile Gln Ser Pro Arg Asp Glu Gln Arg Arg Arg Leu
225 230 235 240

Pro Leu Ser Ile Gly Gln Asn Cys Asn Phe Gly Val Ser Ser Gly Ile
245 250 255

Ile Gly Val Ser Leu Gly Asp Asn Cys Asp Ile Gly Asn Asn Ile Val
260 265 270

Leu Asp Gly Asp Thr Pro Ile Trp Phe Ala Ala Asp Glu Glu Leu Arg
275 280 285

Thr Ile Asp Ser Ile Glu Gly Gln Ala Asn Trp Ser Ile Lys Arg Glu
290 295 300

Ser Gly Phe His Glu Pro Val Ala Arg Leu Lys Ala
305 310 315

<210> 2545

<211> 504

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(481)

<223> RXA02036

<400> 2545

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gccctcatct ctgctgcagt ggcggetctc ggagggtggt gtg cat att cct ttt 115
Val His Ile Pro Phe
1 5

ggg cac ctc gcc gac acc gtc tcc tgg gac tgc ggg gga ggc agc tgc 163
Gly His Leu Ala Asp Thr Val Ser Trp Asp Cys Gly Gly Gly Ser Cys
10 15 20

gcc acc aac gat ttg gta tcc ctg ttc atg ccg gcc gcc ttc atg agt 211
Ala Thr Asn Asp Leu Val Ser Leu Phe Met Pro Ala Ala Phe Met Ser
25 30 35

acc ctc gcc gcc tgc gta ttt ggc gcg tgg gcc ata ggt ttg atc gct 259
Thr Leu Ala Ala Cys Val Phe Gly Ala Trp Ala Ile Gly Leu Ile Ala
40 45 50

ccc gca cta ttc atc gcg gtg act gcc tgg gca ttt cgc tcc gcc gtg 307
Pro Ala Leu Phe Ile Ala Val Thr Ala Trp Ala Phe Arg Ser Gly Val
55 60 65

cag gct gcg att gcc gac gcc tac acg tcc gcg act tcc gtc gcc ttc 355
Gln Ala Ala Ile Ala Asp Gly Tyr Thr Ser Ala Thr Ser Val Gly Phe
70 75 80 85

gaa atg act gtc tcg ctc att ctt ttc atc atc gca ggt ctg tgc ttt 403
Glu Met Thr Val Ser Leu Ile Leu Phe Ile Ile Ala Gly Leu Cys Phe

	90	95	100	
ctg ggc tgg atc ccc atg ttc atc aac aac cgc caa gtc gcg cgc aag				451
Leu Gly Trp Ile Pro Met Phe Ile Asn Asn Arg Gln Val Ala Arg Lys				
	105	110	115	
gtc cgc gag agg gct gcg ggc ttg agc aat taggctctcg ctttcgacg				501
Val Arg Glu Arg Ala Ala Gly Leu Ser Asn				
	120	125		
ttt				504

<210> 2546

<211> 127

<212> PRT

<213> Corynebacterium glutamicum

<400> 2546

Val His Ile Pro Phe Gly His Leu Ala Asp Thr Val Ser Trp Asp Cys				
1	5	10	15	
Gly Gly Gly Ser Cys Ala Thr Asn Asp Leu Val Ser Leu Phe Met Pro				
20	25	30		
Ala Ala Phe Met Ser Thr Leu Ala Ala Cys Val Phe Gly Ala Trp Ala				
35	40	45		
Ile Gly Leu Ile Ala Pro Ala Leu Phe Ile Ala Val Thr Ala Trp Ala				
50	55	60		
Phe Arg Ser Gly Val Gln Ala Ala Ile Ala Asp Gly Tyr Thr Ser Ala				
65	70	75	80	
Thr Ser Val Gly Phe Glu Met Thr Val Ser Leu Ile Leu Phe Ile Ile				
85	90	95		
Ala Gly Leu Cys Phe Leu Gly Trp Ile Pro Met Phe Ile Asn Asn Arg				
100	105	110		
Gln Val Ala Arg Lys Val Arg Glu Arg Ala Ala Gly Leu Ser Asn				
115	120	125		

<210> 2547

<211> 551

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(528)

<223> RXA02040

<400> 2547

tac ata cct ttt gtc att tgg tcc gat ctc ggt gag gct gcc gaa ggt				48
Tyr Ile Pro Phe Val Ile Trp Ser Asp Leu Gly Glu Ala Ala Glu Gly				
1	5	10	15	
gag aac ttt gct cgc ttc tgg tcc tgg ctg aaa tgc cgc cgg gac aaa				96
Glu Asn Phe Ala Arg Phe Trp Ser Trp Leu Lys Ser Arg Arg Asp Lys				

	20	25	30	
	gct cgc cag cag gga caa acc ttc ggt gtg ttc tgc tat gcc agc aac			144
	Ala Arg Gln Gln Gly Gln Thr Phe Gly Val Phe Cys Tyr Ala Ser Asn			
	35	40	45	
	ggc gaa aac cac tgg atg ctc tcc act gct cgc aga ttc ttc ggc aaa			192
	Gly Glu Asn His Trp Met Leu Ser Thr Ala Arg Arg Phe Phe Gly Lys			
	50	55	60	
	gtc aaa ggt gtg ccc gac gag caa gaa atc cgc agc ttc att agc tct			240
	Val Lys Gly Val Pro Asp Glu Gln Glu Ile Arg Ser Phe Ile Ser Ser			
	65	70	75	80
	gac caa tgg aat gac atg ttt gct gtc gcg cgc tcc caa ctt gtt ggc			288
	Asp Gln Trp Asn Asp Met Phe Ala Val Ala Arg Ser Gln Leu Val Gly			
	85	90	95	
	ccc ggt ggt tta ggt ctg aaa caa ctc gcg ccg gca gct gga ttc cat			336
	Pro Gly Gly Leu Gly Leu Lys Gln Leu Ala Pro Ala Ala Gly Phe His			
	100	105	110	
	tgg gag gaa gaa gac ttc gca ggt gaa gat agc ctc cac gca tat ctc			384
	Trp Glu Glu Glu Asp Phe Ala Gly Glu Asp Ser Leu His Ala Tyr Leu			
	115	120	125	
	att gct tcc acg gct gcc gaa cca gaa gct gag gcc gct cgt gct caa			432
	Ile Ala Ser Thr Ala Ala Glu Pro Glu Ala Glu Ala Ala Arg Ala Gln			
	130	135	140	
	ttg ctc agc tac aac ggc gat gat tgc agg gcc acc gca gcg gtt cgc			480
	Leu Leu Ser Tyr Asn Gly Asp Asp Cys Arg Ala Thr Ala Ala Val Arg			
	145	150	155	160
	cat tgg ctt cga caa ggt gcg cgc acg gca cct gtg ctg ggg aat att			528
	His Trp Leu Arg Gln Gly Ala Arg Thr Ala Pro Val Leu Gly Asn Ile			
	165	170	175	
	taaaccaagg aaggattctc cag			551

<210> 2548

<211> 176

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2548

Tyr Ile Pro Phe Val Ile Trp Ser Asp Leu Gly Glu Ala Ala Glu Gly

1

5

10

15

Glu Asn Phe Ala Arg Phe Trp Ser Trp Leu Lys Ser Arg Arg Asp Lys

20

25

30

Ala Arg Gln Gln Gly Gln Thr Phe Gly Val Phe Cys Tyr Ala Ser Asn

35

40

45

Gly Glu Asn His Trp Met Leu Ser Thr Ala Arg Arg Phe Phe Gly Lys

50

55

60

Val Lys Gly Val Pro Asp Glu Gln Glu Ile Arg Ser Phe Ile Ser Ser

65

70

75

80

Asp	Gln	Trp	Asn	Asp	Met	Phe	Ala	Val	Ala	Arg	Ser	Gln	Leu	Val	Gly
			85						90					95	
Pro	Gly	Gly	Leu	Gly	Leu	Lys	Gln	Leu	Ala	Pro	Ala	Ala	Gly	Phe	His
			100					105					110		
Trp	Glu	Glu	Glu	Asp	Phe	Ala	Gly	Glu	Asp	Ser	Leu	His	Ala	Tyr	Leu
			115				120					125			
Ile	Ala	Ser	Thr	Ala	Ala	Glu	Pro	Glu	Ala	Glu	Ala	Ala	Arg	Ala	Gln
						135					140				
Leu	Leu	Ser	Tyr	Asn	Gly	Asp	Asp	Cys	Arg	Ala	Thr	Ala	Ala	Val	Arg
					150					155					160
His	Trp	Leu	Arg	Gln	Gly	Ala	Arg	Thr	Ala	Pro	Val	Leu	Gly	Asn	Ile
				165					170					175	

<210> 2549
<211> 364
<212> DNA
<213> *Corynebacterium glutamicum*

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<220>
<221> CDS
<222> (101)..(364)
<223> RXA02046
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400> 2549	
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aaattattaa catccgcgcg aacgccttag gagagtcttc atg aaa gag aca ctg	115
	Met Lys Glu Thr Leu 1 5
acc acc ggt tta acc cac caa atg acc tac ata gtg cca gca aac cgc	163
Thr Thr Gly Leu Thr His Gln Met Thr Tyr Ile Val Pro Ala Asn Arg	
	10 15 20
aca gtt ccg cat ctg ctt ccc gaa gca gca gaa ttt gaa acc atg cca	211
Thr Val Pro His Leu Leu Pro Glu Ala Ala Glu Phe Glu Thr Met Pro	
	25 30 35
gat gtc ctg gcc act gga tat atg gtc ggc atc atc gag tgg gcc tgc	259
Asp Val Leu Ala Thr Gly Tyr Met Val Gly Ile Ile Glu Trp Ala Cys	
	40 45 50
atg gaa ctt ctg cgt ccc cat ttg gac gac ggt gaa atc tcg ctg gcc	307
Met Glu Leu Leu Arg Pro His Leu Asp Asp Gly Glu Ile Ser Leu Gly	
	55 60 65
act cat gtg aac ttc tcc cac gca gct cca acg gtt cct gga tcc acg	355
Thr His Val Asn Phe Ser His Ala Ala Pro Thr Val Pro Gly Ser Thr	
	70 75 80 85
gtc acc atc	364

Val Thr Ile

<210> 2550

<211> 88

<212> PRT

<213> Corynebacterium glutamicum

<400> 2550

Met Lys Glu Thr Leu Thr Thr Gly Leu Thr His Gln Met Thr Tyr Ile
 1 5 10 15

Val Pro Ala Asn Arg Thr Val Pro His Leu Leu Pro Glu Ala Ala Glu
 20 25 30

Phe Glu Thr Met Pro Asp Val Leu Ala Thr Gly Tyr Met Val Gly Ile
 35 40 45

Ile Glu Trp Ala Cys Met Glu Leu Leu Arg Pro His Leu Asp Asp Gly
 50 55 60

Glu Ile Ser Leu Gly Thr His Val Asn Phe Ser His Ala Ala Pro Thr
 65 70 75 80

Val Pro Gly Ser Thr Val Thr Ile
 85

<210> 2551

<211> 621

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(598)

<223> RXA02051

<400> 2551

cgcaactgac ggtgtagtaa ctggcggtat ttgctgcta attaaactgc aaaacgggtga 60

gcagacatca tcttcaactc gcacaacagt caatgactcc atg gtc atc aga gct 115
 Met Val Ile Arg Ala
 1 5

ctc cag cgc gaa gaa gaa atc gtc ctt ctc agc gcc gga gca ctt gga 163
 Leu Gln Arg Glu Glu Glu Ile Val Leu Leu Ser Ala Gly Ala Leu Gly
 10 15 20

atc cat gag aaa acc gtt gaa cgt aca att cgt gga aaa cgt att cct 211
 Ile His Glu Lys Thr Val Glu Arg Thr Ile Arg Gly Lys Arg Ile Pro
 25 30 35

ggc acg caa aag acc gtg cac gtc caa tac agc tac acc gga aaa ctc 259
 Gly Thr Gln Lys Thr Val His Val Gln Tyr Ser Tyr Thr Gly Lys Leu
 40 45 50

gga atc gat gcc tca gat gtt gaa atc aaa tcc gca ggt gac aat aag 307
 Gly Ile Asp Ala Ser Asp Val Glu Ile Lys Ser Ala Gly Asp Asn Lys
 55 60 65

ctt tcc atc act atc cct gag ttc atc ttc atc gga tac gac gat cta 355
 Leu Ser Ile Thr Ile Pro Glu Phe Ile Phe Ile Gly Tyr Asp Asp Leu 85
 70 75 80

aag ttt aag acc ata gcc gaa gat gac ggt tgg atc agt ttc agc act 403
 Lys Phe Lys Thr Ile Ala Glu Asp Asp Gly Trp Ile Ser Phe Ser Thr 100
 90 95

gac gat atc gat act gca gaa gta gtt tct gag atc atg agc caa gag 451
 Asp Asp Ile Asp Thr Ala Glu Val Val Ser Glu Ile Met Ser Gln Glu 115
 105 110

aac ttc gtc gag caa gta acc act aac cgg gaa atg ttg gaa gat caa 499
 Asn Phe Val Glu Gln Val Thr Thr Asn Arg Glu Met Leu Glu Asp Gln 130
 120 125

gcg gtt gat ttc tac aac gac ctg ctc cac gaa ttc acc gag aaa ctc 547
 Ala Val Asp Phe Tyr Asn Asp Leu Leu His Glu Phe Thr Glu Lys Leu 145
 135 140

gat aca gat cga tac gaa gac acc aag att gag ctc gaa ttc gag ttt 595
 Asp Thr Asp Arg Tyr Glu Asp Thr Lys Ile Glu Leu Glu Phe Glu Phe 165
 150 155 160

gag tagatagtgc ttggaagaca gtt 621
 Glu

<210> 2552
 <211> 166
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2552
 Met Val Ile Arg Ala Leu Gln Arg Glu Glu Glu Ile Val Leu Leu Ser 15
 1 5 10

Ala Gly Ala Leu Gly Ile His Glu Lys Thr Val Glu Arg Thr Ile Arg 30
 20 25

Gly Lys Arg Ile Pro Gly Thr Gln Lys Thr Val His Val Gln Tyr Ser 45
 35 40

Tyr Thr Gly Lys Leu Gly Ile Asp Ala Ser Asp Val Glu Ile Lys Ser 60
 50 55

Ala Gly Asp Asn Lys Leu Ser Ile Thr Ile Pro Glu Phe Ile Phe Ile 80
 65 70 75

Gly Tyr Asp Asp Leu Lys Phe Lys Thr Ile Ala Glu Asp Asp Gly Trp 95
 85 90

Ile Ser Phe Ser Thr Asp Asp Ile Asp Thr Ala Glu Val Val Ser Glu 110
 100 105

Ile Met Ser Gln Glu Asn Phe Val Glu Gln Val Thr Thr Asn Arg Glu 125
 115 120

Met Leu Glu Asp Gln Ala Val Asp Phe Tyr Asn Asp Leu Leu His Glu

130 135 140
 Phe Thr Glu Lys Leu Asp Thr Asp Arg Tyr Glu Asp Thr Lys Ile Glu
 145 150 155 160
 Leu Glu Phe Glu Phe Glu
 165

<210> 2553

<211> 702

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(679)

<223> RXA02053

<400> 2553

aaccagccag aaactatctc caaaagctaa taaaaccctt gcactgacaa ataaggcgac 60

ctaccatgac tctgtttcca acacataaaa aggataaaaa atg tca ctt tca gtc 115
 Met Ser Leu Ser Val
 1 5

gtc gag gcg att acc aac cgc cgc gcc acc cgc aaa tac acc gat gaa 163
 Val Glu Ala Ile Thr Asn Arg Arg Ala Thr Arg Lys Tyr Thr Asp Glu
 10 15 20

gct cct acc cct gag ctg atc gac aaa atc gtt gac ctt gcc ctg gag 211
 Ala Pro Thr Pro Glu Leu Ile Asp Lys Ile Val Asp Leu Ala Leu Glu
 25 30 35

gca ccc agt gcg ttc aat gcg cag caa cgt gaa att gtt gtg att act 259
 Ala Pro Ser Ala Phe Asn Ala Gln Gln Arg Glu Ile Val Val Ile Thr
 40 45 50

gat ccc gca cag aag cag aag ctt tac gag gcc tcc cat cag aaa caa 307
 Asp Pro Ala Gln Lys Gln Lys Leu Tyr Glu Ala Ser His Gln Lys Gln
 55 60 65

ttc etc acc gca cct gta act ttc att gcg gtt gcc cgc gtg gaa aac 355
 Phe Leu Thr Ala Pro Val Thr Phe Ile Ala Val Ala Arg Val Glu Asn
 70 75 80 85

gag cct gag gat ttg gaa gag att ctt ggt acg gaa agg gct gaa cgt 403
 Glu Pro Glu Asp Leu Glu Glu Ile Leu Gly Thr Glu Arg Ala Glu Arg
 90 95 100

gtc gcg gga ttc atc aac ggt cgc agc att cag cag gca cgc gaa gca 451
 Val Ala Gly Phe Ile Asn Gly Arg Ser Ile Gln Gln Ala Arg Glu Ala
 105 110 115

acg ttg agg gat gcc agc ctc gcg gcg gct ttt cta att ctg gct gcc 499
 Thr Leu Arg Asp Ala Ser Leu Ala Ala Phe Leu Ile Leu Ala Ala
 120 125 130

cag gcg gag ggt ttg agt acc agc ccg act act ggt tgg gat gag gaa 547
 Gln Ala Glu Gly Leu Ser Thr Ser Pro Thr Thr Gly Trp Asp Glu Glu
 135 140 145


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aaa gtg aag gaa gca atc ggt ctc ggc ggg cgt gag gat cgt gca atc 595
Lys Val Lys Glu Ala Ile Gly Leu Gly Gly Arg Glu Asp Arg Ala Ile
150 155 160 165

gcc ctt gtt att gct acc gga ttc cct aat gaa cag ccg gag cac cct 643
Ala Leu Val Ile Ala Thr Gly Phe Pro Asn Glu Gln Pro Glu His Pro
170 175 180

ggt cgt ttg cag aat agg cgc atc gac aac agc tac taactctgcc 689
Gly Arg Leu Gln Asn Arg Arg Ile Asp Asn Ser Tyr
185 190

agctgcgccg gac 702

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<210> 2554

<211> 193

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2554

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Met Ser Leu Ser Val Val Glu Ala Ile Thr Asn Arg Arg Ala Thr Arg
1 5 10 15

Lys Tyr Thr Asp Glu Ala Pro Thr Pro Glu Leu Ile Asp Lys Ile Val
20 25 30

Asp Leu Ala Leu Glu Ala Pro Ser Ala Phe Asn Ala Gln Gln Arg Glu
35 40 45

Ile Val Val Ile Thr Asp Pro Ala Gln Lys Gln Lys Leu Tyr Glu Ala
50 55 60

Ser His Gln Lys Gln Phe Leu Thr Ala Pro Val Thr Phe Ile Ala Val
65 70 75 80

Ala Arg Val Glu Asn Glu Pro Glu Asp Leu Glu Glu Ile Leu Gly Thr
85 90 95

Glu Arg Ala Glu Arg Val Ala Gly Phe Ile Asn Gly Arg Ser Ile Gln
100 105 110

Gln Ala Arg Glu Ala Thr Leu Arg Asp Ala Ser Leu Ala Ala Ala Phe
115 120 125

Leu Ile Leu Ala Ala Gln Ala Glu Gly Leu Ser Thr Ser Pro Thr Thr
130 135 140

Gly Trp Asp Glu Glu Lys Val Lys Glu Ala Ile Gly Leu Gly Gly Arg
145 150 155 160

Glu Asp Arg Ala Ile Ala Leu Val Ile Ala Thr Gly Phe Pro Asn Glu
165 170 175

Gln Pro Glu His Pro Gly Arg Leu Gln Asn Arg Arg Ile Asp Asn Ser
180 185 190

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Tyr

<210> 2555
 <211> 654
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(631)
 <223> RXA02057

<400> 2555
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 acggcccttt ttgctgcggt ggttgccctaa ggtggaaggt atg aaa cga atc tgt 115
 Ala Val Arg Ile Cys
 1 5
 gcg gtc gcg atc tct tca gta ctt ttg tta agt ggc tgc tcc tcc act 163
 Ala Val Ala Ile Ser Ser Val Leu Leu Ser Gly Cys Ser Ser Thr
 10 15 20
 tcc aca acg cag ctc gag gga ttc gat gga cgc tca gcg cag gag atc 211
 Ser Thr Thr Gln Leu Glu Gly Phe Asp Gly Arg Ser Ala Gln Glu Ile
 25 30 35
 atc aca gaa ctt gat caa acc cca gtc gca gac aga gca act aac ctc 259
 Ile Thr Glu Leu Asp Gln Thr Pro Val Ala Asp Arg Ala Thr Asn Leu
 40 45 50
 atg gcc tcc att cgg gca gat gag tta att ctg tgc gat caa agc gga 307
 Met Ala Ser Ile Arg Ala Asp Glu Leu Ile Leu Ser Asp Gln Ser Gly
 55 60 65
 cag ctc agc att gac atg cct gca gat gag ttc tat atc tcc gca gcc 355
 Gln Leu Ser Ile Asp Met Pro Ala Asp Glu Phe Tyr Ile Ser Ala Ala
 70 75 80 85
 ccg tac acc acc aca acc cac gag tgc ttc tat cac agc ctc acc aca 403
 Pro Tyr Thr Thr Thr His Glu Cys Phe Tyr His Ser Leu Thr Thr
 90 95 100
 tgt act ggt gaa ctc gcc aac acc cca gtg aaa gta acg gtg gtg gca 451
 Cys Thr Gly Glu Leu Ala Asn Thr Pro Val Lys Val Thr Val Val Ala
 105 110 115
 gat aat gga gaa acc atc ctc gaa gag gac acc atc acc tac gat aat 499
 Asp Asn Gly Glu Thr Ile Leu Glu Glu Asp Thr Ile Thr Tyr Asp Asn
 120 125 130
 gga ttt gtt ggg atg tgg ctc ccc cgc aac att gat gcc aca ctc acc 547
 Gly Phe Val Gly Met Trp Leu Pro Arg Asn Ile Asp Ala Thr Leu Thr
 135 140 145
 atc gaa cat gac gcc ctg aaa tcc acc cag ccg atc tct acg ggt gat 595
 Ile Glu His Asp Gly Leu Lys Ser Thr Gln Pro Ile Ser Thr Gly Asp
 150 155 160 165
 gac gcc ccc acg tgc atc acc acg gct gaa cta gcg tgaaaaatcct 641
 Asp Ala Pro Thr Cys Ile Thr Thr Ala Glu Leu Ala
 170 175

ttagacaata aga

654

<210> 2556

<211> 177

<212> PRT

<213> Corynebacterium glutamicum

<400> 2556

Met Lys Arg Ile Cys Ala Val Ala Ile Ser Ser Val Leu Leu Leu Ser
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Gly Cys Ser Ser Thr Ser Thr Thr Gln Leu Glu Gly Phe Asp Gly Arg
 20 25 30

Ser Ala Gln Glu Ile Ile Thr Glu Leu Asp Gln Thr Pro Val Ala Asp
 35 40 45

Arg Ala Thr Asn Leu Met Ala Ser Ile Arg Ala Asp Glu Leu Ile Leu
 50 55 60

Ser Asp Gln Ser Gly Gln Leu Ser Ile Asp Met Pro Ala Asp Glu Phe
 65 70 75 80

Tyr Ile Ser Ala Ala Pro Tyr Thr Thr Thr His Glu Cys Phe Tyr
 85 90 95

His Ser Leu Thr Thr Cys Thr Gly Glu Leu Ala Asn Thr Pro Val Lys
 100 105 110

Val Thr Val Val Ala Asp Asn Gly Glu Thr Ile Leu Glu Glu Asp Thr
 115 120

Ile Thr Tyr Asp Asn Gly Phe Val Gly Met Trp Leu Pro Arg Asn Ile
 130 135 140

Asp Ala Thr Leu Thr Ile Glu His Asp Gly Leu Lys Ser Thr Gln Pro
 145 150 155 160

Ile Ser Thr Gly Asp Asp Ala Pro Thr Cys Ile Thr Thr Ala Glu Leu
 165 170 175

Ala

<210> 2557

<211> 675

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(652)

<223> RXA02058

<400> 2557

gaagcggatt ttagtccttg cgttggtg ctcggtagcg ggatgctcaa cgctttccca 60

agaaccttca ccacctgttc cgttgggaaa cgttgatact gtg cag att gtc tct 115

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Val Gln Ile Val Ser
1 5
ccc aat ggg gag att gag tct ttt gtg ctg ggg aag ctg tat gag acc 163
Pro Asn Gly Glu Ile Glu Ser Phe Val Leu Gly Lys Leu Tyr Glu Thr
10 15 20

gca tta gtg gaa cgt ggc aga tct gca tca gtt cag ctg att gag ggc 211
Ala Leu Val Glu Arg Gly Arg Ser Ala Ser Val Gln Leu Ile Asp Gly
25 30 35

gac ttg gat gag caa cta tct atg ctg cga gat gac agc act gat ttg 259
Asp Leu Asp Glu Gln Leu Ser Met Leu Arg Asp Asp Ser Thr Asp Leu
40 45 50

gtg att gct tgc tca gga caa tta ctg gaa tat tac aac cca gat tta 307
Val Ile Ala Cys Ser Gly Gln Leu Leu Glu Tyr Tyr Asn Pro Asp Leu
55 60 65

gcc tcc gag ttt gcc gtc gaa tac gct aat cag aca gcc ttt gat aaa 355
Ala Ser Glu Phe Ala Val Glu Tyr Ala Asn Gln Thr Ala Phe Asp Lys
70 75 80 85

aac tct ggt gaa tgg cgc gaa aaa gtc tac gat gct ctc caa gga tcg 403
Asn Ser Gly Glu Trp Arg Glu Lys Val Tyr Asp Ala Leu Gln Gly Ser
90 95 100

ctg ccg gac tcc atc gtg gcc acc gat cct tcc aat gct att ggt tgt 451
Leu Pro Asp Ser Ile Val Ala Thr Asp Pro Ser Asn Ala Ile Gly Cys
105 110 115

aag gac gat acg tcg ctg cct caa aac atc gtg cca att tat aga aag 499
Lys Asp Asp Thr Ser Leu Pro Gln Asn Ile Val Pro Ile Tyr Arg Lys
120 125 130

ccc aat ctg gat agg gac aat cgg gac acc ctg aac ttt gtg agc ggt 547
Pro Asn Leu Asp Arg Asp Asn Arg Asp Thr Leu Asn Phe Val Ser Gly
135 140 145

tct ttg ggt aca agc gat ttg gaa gca ttg gtc aag gac gcc caa aca 595
Ser Leu Gly Thr Ser Asp Leu Glu Ala Leu Val Lys Asp Ala Gln Thr
150 155 160 165

aca ggc aca acc tct gaa act gcg ctg gat ttc tta ttg tct aaa gga 643
Thr Gly Thr Thr Ser Glu Thr Ala Leu Asp Phe Leu Leu Ser Lys Gly
170 175 180

ttt tca cgc tagttcagcc gtggtgatgc acg 675
Phe Ser Arg

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<210> 2558

<211> 184

<212> PRT

<213> Corynebacterium glutamicum

<400> 2558

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Val Gln Ile Val Ser Pro Asn Gly Glu Ile Glu Ser Phe Val Leu Gly
1 5 10 15

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Lys	Leu	Tyr	Glu	Thr	Ala	Leu	Val	Glu	Arg	Gly	Arg	Ser	Ala	Ser	Val				
						20								25				30	
Gln	Leu	Ile	Asp	Gly	Asp	Leu	Asp	Glu	Gln	Leu	Ser	Met	Leu	Arg	Asp				
			35				40									45			
Asp	Ser	Thr	Asp	Leu	Val	Ile	Ala	Cys	Ser	Gly	Gln	Leu	Leu	Glu	Tyr				
		50				55										60			
Tyr	Asn	Pro	Asp	Leu	Ala	Ser	Glu	Phe	Ala	Val	Glu	Tyr	Ala	Asn	Gln				
						70									75				80
Thr	Ala	Phe	Asp	Lys	Asn	Ser	Gly	Glu	Trp	Arg	Glu	Lys	Val	Tyr	Asp				
			85								90						95		
Ala	Leu	Gln	Gly	Ser	Leu	Pro	Asp	Ser	Ile	Val	Ala	Thr	Asp	Pro	Ser				
			100					105								110			
Asn	Ala	Ile	Gly	Cys	Lys	Asp	Asp	Thr	Ser	Leu	Pro	Gln	Asn	Ile	Val				
			115								120						125		
Pro	Ile	Tyr	Arg	Lys	Pro	Asn	Leu	Asp	Arg	Asp	Asn	Arg	Asp	Thr	Leu				
			130					135									140		
Asn	Phe	Val	Ser	Gly	Ser	Leu	Gly	Thr	Ser	Asp	Leu	Glu	Ala	Leu	Val				
			145					150								155			160
Lys	Asp	Ala	Gln	Thr	Thr	Gly	Thr	Thr	Ser	Glu	Thr	Ala	Leu	Asp	Phe				
						165									170				175
Leu	Leu	Ser	Lys	Gly	Phe	Ser	Arg												
			180																

<210> 2559
<211> 702
<212> DNA
<213> *Corynebacterium glutamicum*

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<220>  
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<222> (101)..(679)  
<223> RXA02069
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tggcgcgcagc	ccggaatccg accaggaaa gagcacaccc atg gct gat ttc aac	115
	Met Ala Asp Phe Asn	
	1 5	
cgc tct gaa tta gac agc cca ctt ttt gga tcc cgc aaa cga ttt aaa		163
Arg Ser Glu Leu Asp Ser Pro Leu Phe Gly Ser Arg Lys Arg Phe Phe		
	10 15 20	
ttc gac gat gac acc att ggt gcc tac gcc gaa aaa gta gcc cgq ttc		211
Phe Asp Asp Asp Thr Ile Gly Ala Tyr Ala Glu Lys Val Ala Arg Phe		
	25 30 35	
ttt ggc acg gga cag tac ctg ttt tgg caa acc att ttc gtg gtg gtg		259
Phe Gly Thr Gly Gln Tyr Leu Phe Trp Gln Thr Ile Phe Val Val Val		

40	45	50	
tgg att ttc ctc aac atc ggt ggt tgg gcc tgg agt tgg gac ccc tac			307
Trp Ile Phe Leu Asn Ile Gly Gly Trp Ala Trp Ser Trp Asp Pro Tyr			
55	60	65	
cct ttc atc ctg ctc aac ctg gca ttc tcc acg cag gct gct tat gct			355
Pro Phe Ile Leu Leu Asn Leu Ala Phe Ser Thr Gln Ala Ala Tyr Ala			
70	75	80	85
gct ccg ctg atc ctg ttg gcg caa aac cgt caa gaa gac cgc gat aag			403
Ala Pro Leu Ile Leu Leu Ala Gln Asn Arg Gln Glu Asp Arg Asp Lys			
90	95	100	
cac acc att ttg gcg gat cgt cgg cgt gct gaa gag aca aaa gcc gat			451
His Thr Ile Leu Ala Asp Arg Arg Arg Ala Glu Glu Thr Lys Ala Asp			
105	110	115	
act gaa ttc ctc gca cgg gaa ctc gca ggc gtt cgc tta gcc ttg gga			499
Thr Glu Phe Leu Ala Arg Glu Leu Ala Gly Val Arg Leu Ala Leu Gly			
120	125	130	
gat act gtc aca cgt gac tat ttg cgc cat gag tta gaa gat ctc cgc			547
Asp Thr Val Thr Arg Asp Tyr Leu Arg His Glu Glu Asp Leu Arg			
135	140	145	
gga ctt ctt gac cgc att gaa gcc aag ctc gac gac gag gca gcg tcc			595
Gly Leu Leu Asp Arg Ile Glu Ala Lys Leu Asp Asp Glu Ala Ala Ser			
150	155	160	165
cgt att gca gac cgc cac gaa cag cac gga tca gga cct caa gat ttg			643
Arg Ile Ala Asp Arg His Glu Gln His Gly Ser Gly Pro Gln Asp Leu			
170	175	180	
tct gac ccc act cag ggt gat gtt gca gac gaa ttt tagggagtat			689
Ser Asp Pro Thr Gln Gly Asp Val Ala Asp Glu Phe			
185	190		
caaaacttgg gac			702
<210> 2560			
<211> 193			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 2560			
Met Ala Asp Phe Asn Arg Ser Glu Leu Asp Ser Pro Leu Phe Gly Ser			
1	5	10	15
Arg Lys Arg Phe Lys Phe Asp Asp Asp Thr Ile Gly Ala Tyr Ala Glu			
20	25	30	
Lys Val Ala Arg Phe Phe Gly Thr Gly Gln Tyr Leu Phe Trp Gln Thr			
35	40	45	
Ile Phe Val Val Val Trp Ile Phe Leu Asn Ile Gly Gly Trp Ala Trp			
50	55	60	
Ser Trp Asp Pro Tyr Pro Phe Ile Leu Leu Asn Leu Ala Phe Ser Thr			
65	70	75	80

Phe

400> 2561	agcaccggatc aggcacctcaa gatttgtctg accccactca gggtgatgtt gcagacgaat	60
	tttagggagt atcaaaaactt gggactacta togatacgtg	115
	Met Thr Gln Val Thr	5
	gaa tcc gct gtc cgc agc gcg cta tcc cgc gta gag gat cca gag atc	163
Glu Ser Ala Val Arg Ser Ala Leu Ser Arg Val Glu Asp Pro Glu Ile	10 15 20	
	ggt aag ccc atc aca gag ctc ggc atg gtc aaa tca gtg tcc atc gac	211
Gly Lys Pro Ile Thr Glu Leu Gly Met Val Lys Ser Val Ser Ile Asp	25 30 35	
	ggc tct gat gtc cag gtg gag gtc tac ctg acg atc gcg gct tgc ccg	259
Gly Ser Asp Val Gln Val Glu Val Tyr Leu Thr Ile Ala Ala Cys Pro	40 45 50	
	atg aaa acc acc att gtc acc aac act gaa gca gct ctc aaa gac atc	307
Met Lys Thr Thr Ile Val Thr Asn Thr Glu Ala Ala Leu Lys Asp Ile	55 60 65	
	gac ggg gtt ggc caa gtt cat gtc acc acc gac gat gtc atg agt gat gaa	355
Asp Gly Val Gly Gln Val His Val Thr Thr Asp Val Met Ser Asp Glu		

70	75	80	85
cag cgc cgt gcg ctc cgc gtc tcc ctg cgc ggt gaa act tct gag cca Gln Arg Arg Ala Leu Arg Val Ser Leu Arg Gly Glu Thr Ser Glu Pro	90	95	100
403			
gtg att cca ttc gct cag cct ggt tcc act acc cgc gtt tac gct gtt Val Ile Pro Phe Ala Gln Pro Gly Ser Thr Thr Arg Val Tyr Ala Val	105	110	115
451			
gct tcc ggc aaa ggt ggc gta gga aaa tcc tcc atg acg gtg aac ttg Ala Ser Gly Lys Gly Gly Val Gly Lys Ser Ser Met Thr Val Asn Leu	120	125	130
499			
gct gca gcc cta gcc aag cgc ggg ctg tct gtg gga att ttg gat gcc Ala Ala Ala Leu Ala Lys Arg Gly Leu Ser Val Gly Ile Leu Asp Ala	135	140	145
547			
gat att tac gga cac tca gtg ccc gga atg ctc ggc tcg gac caa cgc Asp Ile Tyr Gly His Ser Val Pro Gly Met Leu Gly Ser Asp Gln Arg	150	155	160
595			
cca cac cag gtc gat gac atg atc atg cct ccc cag gcg cac ggc gtg Pro His Gln Val Asp Met Ile Met Pro Pro Gln Ala His Gly Val	170	175	180
643			
aag atg ata tcc att gct cac ttc acc gaa gga aat gct cct gtg gtg Lys Met Ile Ser Ile Ala His Phe Thr Glu Gly Asn Ala Pro Val Val	185	190	195
691			
tgg cgt gga cca atg ctg cac cgt gcc atc cag caa ttc ctc act gac Trp Arg Gly Pro Met Leu His Arg Ala Ile Gln Gln Phe Leu Thr Asp	200	205	210
739			
gtg ttc tgg ggc gac ctg gat att ttg ctg ctg gat ctt cct cca gga Val Phe Trp Gly Asp Leu Asp Ile Leu Leu Leu Asp Leu Pro Pro Gly	215	220	225
787			
act ggt gac atc gcc atc acc gtt gcc caa ttg atc ccg aat gct gag Thr Gly Asp Ile Ala Ile Thr Val Ala Gln Leu Ile Pro Asn Ala Glu	230	235	240
835			
ttg ctc att gtg acc act cct cag gct gcc gca gct gag gtt gcc gag Leu Leu Ile Val Thr Thr Pro Gln Ala Ala Ala Glu Val Ala Glu	250	255	260
883			
cga gca gga acg atc tct gtg cag acc aac cag aag gtt gct ggc gtg Arg Ala Gly Thr Ile Ser Val Gln Thr Asn Gln Lys Val Ala Gly Val	265	270	275
931			
att gaa aac atg tct gcc atg gtg ctt cct gat ggc acc acc atg gat Ile Glu Asn Met Ser Ala Met Val Leu Pro Asp Gly Thr Thr Met Asp	280	285	290
979			
gtt ttc ggc acc ggc ggc ggt caa aag att gct gat cgt ctt acc gct Val Phe Gly Thr Gly Gly Gly Gln Lys Ile Ala Asp Arg Leu Thr Ala	295	300	305
1027			
gtg aca ggt gaa gag gtc aag gtt atc gga tct gtt cca ttg gat ccg Val Thr Gly Glu Val Lys Val Ile Gly Ser Val Pro Leu Asp Pro	310	315	320
1075			

aac ctg cgt atc ggt ggc gat gtg gga aat cct att gcg att tct gaa 1123
 Asn Leu Arg Ile Gly Gly Asp Val Gly Asn Pro Ile Ala Ile Ser Glu
 330 335 340

cca cac tcc cca acc gct gca gcg atc aat gag atc gct gaa cac cta 1171
 Pro His Ser Pro Thr Ala Ala Ala Ile Asn Glu Ile Ala Glu His Leu
 345 350 355

gct cac cgc aag gta tcg ccc acc aaa tgaccagaa ccacaccgca 1218
 Ala His Arg Lys Val Ser Pro Thr Lys
 360 365

aac 1221

<210> 2562

<211> 366

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2562

Met Thr Gln Val Thr Glu Ser Ala Val Arg Ser Ala Leu Ser Arg Val
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Glu Asp Pro Glu Ile Gly Lys Pro Ile Thr Glu Leu Gly Met Val Lys
 20 25 30

Ser Val Ser Ile Asp Gly Ser Asp Val Gln Val Glu Val Tyr Leu Thr
 35 40 45

Ile Ala Ala Cys Pro Met Lys Thr Thr Ile Val Thr Asn Thr Glu Ala
 50 55 60

Ala Leu Lys Asp Ile Asp Gly Val Gly Gln Val His Val Thr Thr Asp
 65 70 75 80

Val Met Ser Asp Glu Gln Arg Arg Ala Leu Arg Val Ser Leu Arg Gly
 85 90 95

Glu Thr Ser Glu Pro Val Ile Pro Phe Ala Gln Pro Gly Ser Thr Thr
 100 105 110

Arg Val Tyr Ala Val Ala Ser Gly Lys Gly Gly Val Gly Lys Ser Ser
 115 120 125

Met Thr Val Asn Leu Ala Ala Ala Leu Ala Lys Arg Gly Leu Ser Val
 130 135 140

Gly Ile Leu Asp Ala Asp Ile Tyr Gly His Ser Val Pro Gly Met Leu
 145 150 155 160

Gly Ser Asp Gln Arg Pro His Gln Val Asp Asp Met Ile Met Pro Pro
 165 170 175

Gln Ala His Gly Val Lys Met Ile Ser Ile Ala His Phe Thr Glu Gly
 180 185 190

Asn Ala Pro Val Val Trp Arg Gly Pro Met Leu His Arg Ala Ile Gln
 195 200 205

Gln Phe Leu Thr Asp Val Phe Trp Gly Asp Leu Asp Ile Leu Leu Leu
210 215 220

Asp Leu Pro Pro Gly Thr Gly Asp Ile Ala Ile Thr Val Ala Gln Leu
225 230 235 240

Ile Pro Asn Ala Glu Leu Leu Ile Val Thr Thr Pro Gln Ala Ala Ala
245 250 255

Ala Glu Val Ala Glu Arg Ala Gly Thr Ile Ser Val Gln Thr Asn Gln
260 265 270

Lys Val Ala Gly Val Ile Glu Asn Met Ser Ala Met Val Leu Pro Asp
275 280 285

Gly Thr Thr Met Asp Val Phe Gly Thr Gly Gly Gly Gln Lys Ile Ala
290 295 300

Asp Arg Leu Thr Ala Val Thr Gly Glu Glu Val Lys Val Ile Gly Ser
305 310 315 320

Val Pro Leu Asp Pro Asn Leu Arg Ile Gly Gly Asp Val Gly Asn Pro
325 330 335

Ile Ala Ile Ser Glu Pro His Ser Pro Thr Ala Ala Ala Ile Asn Glu
340 345 350

Ile Ala Glu His Leu Ala His Arg Lys Val Ser Pro Thr Lys
355 360 365

<210> 2563

<211> 930

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(907)

<223> RXA02080

<400> 2563

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tttgtcctgt tgcttattgt gcaggaattc ggaggcggac atg tca atc gag tgg 115
Met Ser Ile Glu Trp
1 5

tta caa att gtt gaa tta gga gcg atc ttt ggt gca ggt ttc ctc gca 163
Leu Gln Ile Val Glu Leu Gly Ala Ile Phe Gly Ala Gly Phe Leu Ala
10 15 20

gga agc atc aat gta att gtc gga gca gga aca tta gtg tgg ttt cct 211
Gly Ser Ile Asn Val Ile Val Gly Ala Gly Thr Leu Val Ser Phe Pro
25 30 35

att ctc gtg ttc ctg ggc ctt cca cgg ttg act gcc acc atc gcc aac 259
Ile Leu Val Phe Leu Gly Leu Pro Pro Leu Thr Ala Thr Ile Ala Asn
40 45 50

acc atc ggc atc gtt cct gga agt att tcg ggt gtg gtt gct tat aga 307

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Thr Ile Gly Ile Val Pro Gly Ser Ile Ser Gly Val Val Ala Tyr Arg
  55                      60                      65

cgt gaa cta cac gcc cat gta aaa acc atc aga ttt ctg ctg cca gca 355
Arg Glu Leu His Ala His Val Lys Thr Ile Arg Phe Leu Leu Pro Ala
  70                      75                      80                      85

tca atc ctc gga ggg atc acc ggc gcc tcg ctc ttg ctg cat ttc tcc 403
Ser Ile Leu Gly Gly Ile Thr Gly Ala Ser Leu Leu Leu His Phe Ser
                      90                      95                      100

gca gat gtt ttt aca gca gta att ccc tgg ctg att gga ttc ggc acg 451
Ala Asp Val Phe Thr Ala Val Ile Pro Trp Leu Ile Gly Phe Gly Thr
                      105                      110                      115

ctg ttg gtt atc gca ggt cca tca att aag aag cat gtt ggc gct cat 499
Leu Leu Val Ile Ala Gly Pro Ser Ile Lys Lys His Val Gly Ala His
                      120                      125                      130

act tca ggt ggc atc tct gct ggg ttt agg caa ttg cct ttc ccg agc 547
Thr Ser Gly Gly Ile Ser Ala Gly Phe Arg Gln Leu Pro Phe Pro Ser
                      135                      140                      145

cga acc acc ttc atc gtc tca gta tgt ggt gcc ctg ttg ctg ggc atg 595
Arg Thr Thr Phe Ile Val Ser Val Cys Gly Ala Leu Leu Leu Gly Met
                      150                      155                      160                      165

tat gga ggg tac ttc agc gca gct caa ggc att ctt ctc atc gca ttg 643
Tyr Gly Gly Tyr Phe Ser Ala Ala Gln Gly Ile Leu Leu Ile Ala Leu
                      170                      175                      180

ctt ggc atc aca tca acg ctg cag atg cag gaa ctc aac gcc atc aaa 691
Leu Gly Ile Thr Ser Thr Leu Leu Gln Met Gln Glu Leu Asn Ala Ile Lys
                      185                      190                      195

aac ctc aca gtg gcg gca gtt aat ctc atc gca gcc agt gtt ttt ata 739
Asn Leu Thr Val Ala Ala Val Asn Leu Ile Ala Ala Ser Val Phe Ile
                      200                      205                      210

atc atc tcc cct gag ttg atc tcc tgg ccg acc gtt gcc tta atc gcg 787
Ile Ile Ser Pro Glu Leu Ile Ser Trp Pro Thr Val Ala Leu Ile Ala
                      215                      220                      225

ctt ggc tca gct tta ggt gga tac atc ggc gga cgg tac gcc cgc cga 835
Leu Gly Ser Ala Leu Gly Gly Tyr Ile Gly Gly Arg Tyr Ala Arg Arg
                      230                      235                      240                      245

ctt cgc ccc agt gtt ttt aga gca gta gtc atc gtc gga atc acc 883
Leu Arg Pro Ser Val Phe Arg Ala Phe Val Val Ile Val Gly Ile Thr
                      250                      255                      260

acg gtc atc gtt atg acg atc ggt taatgcagca gactagtaac ccc 930
Thr Val Ile Val Met Thr Ile Gly
                      265

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<210> 2564

<211> 269

<212> PRT

<213> Corynebacterium glutamicum

<400> 2564

Met Ser Ile Glu Trp Leu Gln Ile Val Glu Leu Gly Ala Ile Phe Gly
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Ala Gly Phe Leu Ala Gly Ser Ile Asn Val Ile Val Gly Ala Gly Thr
 20 25 30

Leu Val Ser Phe Pro Ile Leu Val Phe Leu Gly Leu Pro Pro Leu Thr
 35 40 45

Ala Thr Ile Ala Asn Thr Ile Gly Ile Val Pro Gly Ser Ile Ser Gly
 50 55 60

Val Val Ala Tyr Arg Arg Glu Leu His Ala His Val Lys Thr Ile Arg
 65 70 75 80

Phe Leu Leu Pro Ala Ser Ile Leu Gly Gly Ile Thr Gly Ala Ser Leu
 85 90 95

Leu Leu His Phe Ser Ala Asp Val Phe Thr Ala Val Ile Pro Trp Leu
 100 105 110

Ile Gly Phe Gly Thr Leu Leu Val Ile Ala Gly Pro Ser Ile Lys Lys
 115 120 125

His Val Gly Ala His Thr Ser Gly Gly Ile Ser Ala Gly Phe Arg Gln
 130 135 140

Leu Pro Phe Pro Ser Arg Thr Thr Phe Ile Val Ser Val Cys Gly Ala
 145 150 155 160

Leu Leu Leu Gly Met Tyr Gly Gly Tyr Phe Ser Ala Ala Gln Gly Ile
 165 170 175

Leu Leu Ile Ala Leu Leu Gly Ile Thr Ser Thr Leu Gln Met Gln Glu
 180 185 190

Leu Asn Ala Ile Lys Asn Leu Thr Val Ala Ala Val Asn Leu Ile Ala
 195 200 205

Ala Ser Val Phe Ile Ile Ile Ser Pro Glu Leu Ile Ser Trp Pro Thr
 210 215 220

Val Ala Leu Ile Ala Leu Gly Ser Ala Leu Gly Gly Tyr Ile Gly Gly
 225 230 235 240

Arg Tyr Ala Arg Arg Leu Arg Pro Ser Val Phe Arg Ala Phe Val Val
 245 250 255

Ile Val Gly Ile Thr Thr Val Ile Val Met Thr Ile Gly
 260 265

<210> 2565

<211> 1752

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1729)

<223> RXA02081

<400> 2565

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agctcaacat aattttgcgg tgccaccggg acaaaaacat atg acg tta agt ggc 115
 Met Thr Leu Ser Gly
 1 5

ttg gag ctt tta gag ttc gag cgt cga aca gct gcg atg gaa acc agg 163
 Leu Glu Leu Leu Glu Phe Glu Arg Arg Thr Ala Ala Met Glu Thr Arg
 10 15 20

ctt ggt cgg cat aat cgg gga gcg ggt ggc gca ttt cct gag gcg gtg 211
 Leu Gly Arg His Asn Arg Gly Ala Gly Gly Ala Phe Pro Glu Ala Val
 25 30 35

gtg tct cga agc gtg gag ttg cca ctt ttt gta cag gcc cgg aat ttc 259
 Val Ser Arg Ser Val Glu Leu Pro Leu Phe Val Gln Ala Arg Asn Phe
 40 45 50

ctc aac aat cag cag atc aga gct caa gtg cat cgc cgt att ttg gag 307
 Leu Asn Asn Gln Gln Ile Arg Ala Gln Val His Arg Arg Ile Leu Glu
 55 60 65

cag ctt cca acc gag gga gag att gtg ctg ttg ggg cac agt ttg ggg 355
 Gln Leu Pro Thr Glu Gly Glu Ile Val Leu Leu Gly His Ser Leu Gly
 70 75 80 85

tcg gta att gct gca gac ctt ttg agg cga ttg ccg cca gag ctt acg 403
 Ser Val Ile Ala Ala Asp Leu Leu Arg Arg Leu Pro Pro Glu Leu Thr
 90 95 100

gtg aag gga ttt gtc acc atc ggt agt ccg ttg gca aat ggt caa ttc 451
 Val Lys Gly Phe Val Thr Ile Gly Ser Pro Leu Ala Asn Gly Gln Phe
 105 110 115

aat gtg gat gat ttg ttt aag ttg ctg cgc acg ccg ttg agc aat gtg 499
 Asn Val Asp Asp Leu Phe Lys Leu Leu Arg Thr Pro Leu Ser Asn Val
 120 125 130

tcg tgg tgg gtg aat ttt tgg agt gga tct gat cct gtt gca gca aaa 547
 Ser Trp Trp Val Asn Phe Trp Ser Gly Ser Asp Pro Val Ala Ala Lys
 135 140 145

cgc gga gtg tcg gtg gct gtt ccg tgg gta ttg gat ttt cgt gtg aaa 595
 Arg Gly Val Ser Val Ala Val Pro Trp Val Leu Asp Phe Arg Val Lys
 150 155 160 165

acc tca ctg gtc cca ggc cct ggg cat tct tcg ccg gaa tac tgt gcc 643
 Thr Ser Leu Val Pro Gly Pro Gly His Ser Ser Arg Glu Tyr Cys Ala
 170 175 180

aat gat gca gtg gcg gaa gca att ggg ttt ggg ctg ttc gga tcg cgc 691
 Asn Asp Ala Val Ala Glu Ala Ile Gly Phe Gly Leu Phe Gly Ser Arg
 185 190 195

agc aaa gaa atc gtc ctt gcg gag aaa aat ctg cag att ccg ctc aat 739
 Ser Lys Glu Ile Val Leu Ala Glu Lys Asn Leu Gln Ile Pro Leu Asn
 200 205 210

gac gcg gag att ttt gtg ctg cag gcg ctg cgt tat tgt tac ctc att 787
 Asp Ala Glu Ile Phe Val Leu Gln Ala Leu Arg Tyr Cys Tyr Leu Ile
 215 220 225

ttg caa cgg ctc aaa ggc gat gaa gcc tta agg tat gag tac gca ctt 835
 Leu Gln Arg Leu Lys Gly Asp Glu Ala Leu Arg Tyr Glu Tyr Ala Leu
 230 235 240 245

cgg gag act cag gat cgc ctg att gag gag att aaa tcc aga aac gcc 883
 Arg Glu Thr Gln Asp Arg Leu Ile Glu Glu Ile Lys Ser Arg Asn Ala
 250 255 260

gaa gag ggc cgg ccg att ccg aag gaa atc gca cgc ctg gat ttt gat 931
 Glu Glu Gly Arg Pro Ile Pro Lys Glu Ile Ala Arg Leu Asp Phe Asp
 265 270 275

aac ggt gat cca aac gca gca gct cct gtt cca ggt ttg agc cca ttt 979
 Asn Gly Asp Pro Asn Ala Ala Pro Val Pro Gly Leu Ser Pro Phe
 280 285 290

atg ccc aaa gag cag gca att gag cgg ctt tta gag atc att gga cag 1027
 Met Pro Lys Glu Gln Ala Ile Glu Arg Leu Leu Glu Ile Ile Gly Gln
 295 300 305

aac ctg ctg ctg cct ttt gag atc gag gtg ccg gag aaa att cag cgg 1075
 Asn Leu Leu Leu Pro Phe Glu Ile Glu Val Pro Glu Lys Ile Gln Arg
 310 315 320 325

gaa gca ctg agg gat ttc acg gcg gaa act caa ttg ggt tcc acc gtg 1123
 Glu Ala Leu Arg Asp Phe Thr Ala Glu Thr Gln Leu Gly Ser Thr Val
 330 335 340

ggc gct gat att ttt gat gca ttg caa atg gct gtt ggg gtg gtg tcg 1171
 Gly Ala Asp Ile Phe Asp Ala Leu Gln Met Ala Val Gly Val Val Ser
 345 350 355

gga agc gcg aag agc aat tgg cgc aaa tgg gga gcg ttt ggt gtg ggg 1219
 Gly Ser Ala Lys Ser Asn Trp Arg Lys Trp Gly Ala Phe Gly Val Gly
 360 365 370

gct gca gct ttg acc gct gca acg ggt ggt ttg gct ttg gcg gct gtg 1267
 Ala Ala Ala Leu Thr Ala Ala Thr Gly Gly Leu Ala Leu Ala Ala Val
 375 380 385

ccg act gtt gct gga gta gcc act gtt gcc tcg aca ctc gca gca ttt 1315
 Pro Thr Val Ala Gly Val Ala Thr Val Ala Ser Thr Leu Ala Ala Phe
 390 395 400 405

ggt cca ggt ggg atg atg ggc ggt ttg gtc act gca gga aca ctg ctc 1363
 Gly Pro Gly Gly Met Met Gly Gly Leu Val Thr Ala Gly Thr Leu Leu
 410 415 420

aca gtt ggt ggc ggc agt tta acc gct ggg gtg ttg agc tcg gtg aac 1411
 Thr Val Gly Gly Gly Ser Leu Thr Ala Gly Val Leu Ser Ser Val Asn
 425 430 435

acc acg gaa gag atc gaa gcg ctc gtt gta cag aag cta agt ttg gct 1459
 Thr Thr Glu Glu Ile Glu Ala Leu Val Val Gln Lys Leu Ser Leu Ala
 440 445 450

att ttg tgg cag cgc cat gag ata gat aga act cat gag gtg tgg gaa 1507

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Ile Leu Trp Gln Arg His Glu Ile Asp Arg Thr His Glu Val Trp Glu
455                               460                               465

gaa ttc gcg gag gca gaa cgt ctg att gtg cgg gag cac acg cgt gtg 1555
Glu Phe Ala Glu Ala Glu Arg Leu Ile Val Arg Glu His Thr Arg Val
470                               475                               480

aaa aac gtg tcg gat agt tct tcg ccc att ttg aaa gct ttc gag cag 1603
Lys Asn Val Ser Asp Ser Ser Ser Pro Ile Leu Lys Ala Phe Glu Gln
490                               495                               500

cag cgt tcg act att gag cgg cgg ttg aag tat ttg agc gat cat ggg 1651
Gln Arg Ser Thr Ile Glu Arg Ala Leu Lys Tyr Leu Ser Asp His Gly
505                               510                               515

atg gaa cct ggc tgg ttt gaa gaa ctg gaa cca cca gcc cca aca ccg 1699
Met Glu Pro Gly Trp Phe Glu Glu Leu Glu Pro Pro Ala Pro Thr Pro
520                               525                               530

ttt cta aaa ctg cgg gct aag aaa act gat taggagaaac acaatggaga 1749
Phe Leu Lys Leu Arg Ala Lys Lys Thr Asp
535                               540

aag 1752

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<211> 543
<212> PRT
<213> Corynebacterium glutamicum

<400> 2566
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20 25 30

Phe Pro Glu Ala Val Val Ser Arg Ser Val Glu Leu Pro Leu Phe Val
35 40 45

Gln Ala Arg Asn Phe Leu Asn Asn Gln Gln Ile Arg Ala Gln Val His
50 55 60

Arg Arg Ile Leu Glu Gln Leu Pro Thr Glu Gly Glu Ile Val Leu Leu
65 70 75 80

Gly His Ser Leu Gly Ser Val Ile Ala Ala Asp Leu Leu Arg Arg Leu
85 90 95

Pro Pro Glu Leu Thr Val Lys Gly Phe Val Thr Ile Gly Ser Pro Leu
100 105 110

Ala Asn Gly Gln Phe Asn Val Asp Asp Leu Phe Lys Leu Leu Arg Thr
115 120 125

Pro Leu Ser Asn Val Ser Trp Trp Val Asn Phe Trp Ser Gly Ser Asp
130 135 140

Pro Val Ala Ala Lys Arg Gly Val Ser Val Ala Val Pro Trp Val Leu
145 150 155 160

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Asp Phe Arg Val Lys Thr Ser Leu Val Pro Gly Pro Gly His Ser Ser
 165 170 175
 Arg Glu Tyr Cys Ala Asn Asp Ala Val Ala Glu Ala Ile Gly Phe Gly
 180 185 190
 Leu Phe Gly Ser Arg Ser Lys Glu Ile Val Leu Ala Glu Lys Asn Leu
 195 200 205
 Gln Ile Pro Leu Asn Asp Ala Glu Ile Phe Val Leu Gln Ala Leu Arg
 210 215 220
 Tyr Cys Tyr Leu Ile Leu Gln Arg Leu Lys Gly Asp Glu Ala Leu Arg
 225 230 235 240
 Tyr Glu Tyr Ala Leu Arg Glu Thr Gln Asp Arg Leu Ile Glu Glu Ile
 245 250 255
 Lys Ser Arg Asn Ala Glu Glu Gly Arg Pro Ile Pro Lys Glu Ile Ala
 260 265 270
 Arg Leu Asp Phe Asp Asn Gly Asp Pro Asn Ala Ala Ala Pro Val Pro
 275 280 285
 Gly Leu Ser Pro Phe Met Pro Lys Glu Gln Ala Ile Glu Arg Leu Leu
 290 295 300
 Glu Ile Ile Gly Gln Asn Leu Leu Leu Pro Phe Glu Ile Glu Val Pro
 305 310 315 320
 Glu Lys Ile Gln Arg Glu Ala Leu Arg Asp Phe Thr Ala Glu Thr Gln
 325 330 335
 Leu Gly Ser Thr Val Gly Ala Asp Ile Phe Asp Ala Leu Gln Met Ala
 340 345 350
 Val Gly Val Val Ser Gly Ser Ala Lys Ser Asn Trp Arg Lys Trp Gly
 355 360 365
 Ala Phe Gly Val Gly Ala Ala Leu Thr Ala Ala Thr Gly Gly Leu
 370 375 380
 Ala Leu Ala Ala Val Pro Thr Val Ala Gly Val Ala Thr Val Ala Ser
 385 390 395 400
 Thr Leu Ala Ala Phe Gly Pro Gly Gly Met Met Gly Gly Leu Val Thr
 405 410 415
 Ala Gly Thr Leu Leu Thr Val Gly Gly Ser Leu Thr Ala Gly Val
 420 425 430
 Leu Ser Ser Val Asn Thr Thr Glu Glu Ile Glu Ala Leu Val Val Gln
 435 440 445
 Lys Leu Ser Leu Ala Ile Leu Trp Gln Arg His Glu Ile Asp Arg Thr
 450 455 460
 His Glu Val Trp Glu Glu Phe Ala Glu Ala Glu Arg Leu Ile Val Arg
 465 470 475 480

Glu His Thr Arg Val Lys Asn Val Ser Asp Ser Ser Ser Pro Ile Leu
 485 490
 Lys Ala Phe Glu Gln Gln Arg Ser Thr Ile Glu Arg Ala Leu Lys Tyr
 500 505 510
 Leu Ser Asp His Gly Met Glu Pro Gly Trp Phe Glu Glu Leu Glu Pro
 515 520 525
 Pro Ala Pro Thr Pro Phe Leu Lys Leu Arg Ala Lys Lys Thr Asp
 530 535 540

<210> 2567

<211> 468

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(445)

<223> RXA02084

<400> 2567

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 gaaattgaaa gtacttaaga aacatgtcac gctaggagac gtg ata atc att gca 115
 Val Ile Ile Ile Ala
 1 5
 agc gtt gtt ttc ctc ctc gtt ggc gca atg ttg gcg aat gct gcc gct 163
 Ser Val Val Phe Leu Leu Val Gly Ala Met Leu Ala Asn Ala Ala Ala
 10 15 20
 gcg ctc ttt agt gcc agc gag cca ttc gga cga att tcc tac ctc att 211
 Ala Leu Phe Ser Ala Ser Glu Pro Phe Gly Arg Ile Ser Tyr Leu Ile
 25 30 35
 ggc cta cct aac gaa gac gac ttc gtg cgg tac tca cta cgg ttc gtg 259
 Gly Leu Pro Asn Glu Asp Asp Phe Val Pro Tyr Ser Leu Arg Phe Val
 40 45 50
 gcc ttt ttc cca ctg atg ctc tcc gca tcg atg gca gca tcc ttc ttc 307
 Ala Phe Phe Pro Leu Met Leu Ser Ala Ser Met Ala Ala Ser Phe Phe
 55 60 65
 ggg gtg tgg gca gta cta atc att cct ttc ggt tac ttc cca tca ctg 355
 Gly Val Trp Ala Val Leu Ile Ile Pro Phe Gly Tyr Phe Pro Ser Leu
 70 75 80 85
 atg atg gtt cat aag cac aac aag cag gta cag cga acc tgg gat tcc 403
 Met Met Val His Lys His Asn Lys Gln Val Gln Arg Thr Trp Asp Ser
 90 95 100
 gtc acc gtt gct gac ttc tac gag gat tcc acc cct ctg gtc 445
 Val Thr Val Ala Asp Phe Tyr Glu Asp Ser Thr Pro Leu Val
 105 110 115
 taatttcgat ttctaaatgt cat 468

ggc gaa gat ccc ctc acc ctc acc ttg tca cgt cac cgc qca qgc ccc 307

Gly Glu Asp Pro Leu Thr Leu Thr Leu Ser Arg His Arg Ala Gly Pro
 55 60 65
 gcc gcc cgc caa atc atc cgc gag ttc ggt gag caa cgt gaa ccc gcc 355
 Ala Ala Arg Gln Ile Ile Arg Glu Phe Gly Glu Gln Arg Glu Pro Ala 85
 70 75 80
 tat ctc atc acc atc cgc atc acc agc cca gag ggc ttc aaa gta tcc 403
 Tyr Leu Ile Thr Ile Arg Ile Thr Ser Pro Glu Gly Phe Lys Val Ser 100
 90 95
 acc cgc ctc gcc gaa ggc tgg atc cgc gca att ctc agc acc gcg cac 451
 Thr Arg Leu Ala Glu Gly Trp Ile Arg Ala Ile Leu Ser Thr Ala His 115
 105 110
 agc ggc act gtc cac cag ctc acc gat gag cgc gca cgc acg ttt tgc 499
 Ser Gly Thr Val His Gln Leu Thr Asp Glu Pro Ala Pro Thr Phe Cys 130
 120 125
 tgg ctt gtc gac gcc cac ttt gat cgc gtg cgt tcc cct tcc ttc ctt 547
 Trp Leu Val Asp Ala His Phe Asp Pro Val Arg Ser Pro Ser Phe Leu 145
 135 140
 ttc gaa tat tcc aaa agt gca gcc tagaaaaatga cgaacccctg gat 594
 Phe Glu Tyr Ser Lys Ser Ala Ala 155
 150 155
 <210> 2570
 <211> 157
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 2570
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 20 25 30
 Arg Ser Leu Ala Arg Ala Ile Pro Thr Trp Arg Pro Pro Ser Ile Pro
 35 40 45
 Leu Pro Ser Leu Pro Gly Glu Asp Pro Leu Thr Leu Thr Leu Ser Arg
 50 55 60
 His Arg Ala Gly Pro Ala Ala Arg Gln Ile Ile Arg Glu Phe Gly Glu
 65 70 75 80
 Gln Arg Glu Pro Ala Tyr Leu Ile Thr Ile Arg Ile Thr Ser Pro Glu
 85 90 95
 Gly Phe Lys Val Ser Thr Arg Leu Ala Glu Gly Trp Ile Arg Ala Ile
 100 105 110
 Leu Ser Thr Ala His Ser Gly Thr Val His Gln Leu Thr Asp Glu Pro
 115 120 125
 Ala Pro Thr Phe Cys Trp Leu Val Asp Ala His Phe Asp Pro Val Arg
 130 135 140

Ser Pro Ser Phe Leu Phe Glu Tyr Ser Lys Ser Ala Ala
145 150 155

<210> 2571

<211> 924

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(901)

<223> RXA02090

<400> 2571

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ggacgtcccc agcacaacc agatggaagg tcatacagaac atg agc ttt ttt gag 115
Met Ser Phe Phe Glu
1 5

gac atc gcg gct gga ctt gat agt gac ggt atc gag tcc cgc gta aac 163
Asp Ile Ala Ala Gly Leu Asp Ser Asp Gly Ile Glu Ser Arg Val Asn
10 15 20

ggc gac aca atg ttc gtt ccg atc acc tct gac ttg gaa atc cag ttc 211
Gly Asp Thr Met Phe Val Pro Ile Thr Ser Asp Leu Glu Ile Gln Phe
25 30 35

gtg gag atc gat tcc ctc cta cct gca gca aac gtt tat atc gct gca 259
Val Glu Ile Asp Ser Leu Leu Pro Ala Ala Asn Val Tyr Ile Ala Ala
40 45 50

gcc aat gtt gat gaa gac gat gat gag ttc gag gca gtt ctc gtt tcg 307
Ala Asn Val Asp Glu Asp Asp Asp Glu Phe Glu Ala Val Leu Val Ser
55 60 65

gtg gtg ttc tct gtt gag gat gct gtc gct gct gtc gca aag cat gtt 355
Val Val Phe Ser Val Glu Asp Ala Val Ala Val Ala Lys His Val
70 75 80 85

gct act gat cag gtg gtg act gtg ctg cgt gat cta ctt gaa gga act 403
Ala Thr Asp Gln Val Val Thr Val Leu Arg Asp Leu Leu Glu Gly Thr
90 95 100

gat gaa cgc atc cag gat ttg gag ttt ttc cag gat gca gtg aat gca 451
Asp Glu Arg Ile Gln Asp Leu Glu Phe Phe Gln Asp Ala Val Asn Ala
105 110 115

aat ttg gtt cgt gcg gaa gtc ggc cag aat tct gag ctt cag gtt ttg 499
Asn Leu Val Arg Ala Glu Val Gly Gln Asn Ser Glu Gln Val Leu
120 125 130

gtc gag gtt gaa gac ggc gtc cca acc gca acg gtc aat ttc atc gcg 547
Val Glu Val Glu Asp Gly Val Pro Thr Ala Thr Val Asn Phe Ile Ala
135 140 145

atc ggt gag tcc ttt gaa gat ctg att gat cag gcc att gaa gaa ttg 595
Ile Gly Glu Ser Phe Glu Asp Leu Ile Asp Gln Ala Ile Glu Glu Leu
150 155 160 165

tgg gaa tcc gac ggc gac gca gtt cta tcg gat gaa gat cgc caa cgc 643
 Trp Glu Ser Asp Gly Asp Ala Val Leu Ser Asp Glu Asp Arg Gln Arg 180
 170 175

atg ttc gct gat ttg acc tcc gag ttg gaa ttt gtc act gat gaa gtc 691
 Met Phe Ala Asp Leu Thr Ser Glu Leu Glu Phe Val Thr Asp Glu Val 195
 185 190

ctc gac ttg ggt acc ttc act gat ttt gat cga ctt ttc gat atc ctt 739
 Leu Asp Leu Gly Thr Phe Thr Asp Phe Asp Arg Leu Phe Asp Ile Leu 210
 200 205

tcc ctc gcc gat gac cag gct gag gat tgg gaa gca cag ctc gtt cct 787
 Ser Leu Ala Asp Asp Gln Ala Glu Asp Trp Glu Ala Gln Leu Val Pro 225
 215 220

ttt gag gac gag gaa ttt gat gag cgc gat gtt tat gac ctt ttc gtc 835
 Phe Glu Asp Glu Phe Asp Glu Pro Asp Val Tyr Asp Leu Phe Val 245
 230 235 240

gat gac tct gaa gaa gat gac gac gac ctc gat gat gac gag gac gat 883
 Asp Asp Ser Glu Glu Asp Asp Asp Asp Leu Asp Asp Glu Asp Asp 260
 250 255

gag gat gat gac gaa gac tagatttttag ctttgtcgc ggt 924
 Glu Asp Asp Asp Glu Asp 265

<210> 2572
 <211> 267
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 2572
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Glu Ser Arg Val Asn Gly Asp Thr Met Phe Val Pro Ile Thr Ser Asp 30
 20 25

Leu Glu Ile Gln Phe Val Glu Ile Asp Ser Leu Leu Pro Ala Ala Asn 45
 35 40

Val Tyr Ile Ala Ala Ala Asn Val Asp Glu Asp Asp Asp Glu Phe Glu 60
 50 55

Ala Val Leu Val Ser Val Val Phe Ser Val Glu Asp Ala Val Ala Ala 80
 65 70 75

Val Ala Lys His Val Ala Thr Asp Gln Val Val Thr Val Leu Arg Asp 95
 85 90

Leu Leu Glu Gly Thr Asp Glu Arg Ile Gln Asp Leu Glu Phe Phe Gln 110
 100 105

Asp Ala Val Asn Ala Asn Leu Val Arg Ala Glu Val Gly Gln Asn Ser 125
 115 120

Glu Leu Gln Val Leu Val Glu Val Glu Asp Gly Val Pro Thr Ala Thr 140
 130 135

Val Asn Phe Ile Ala Ile Gly Glu Ser Phe Glu Asp Leu Ile Asp Gln
145 150 155 160

Ala Ile Glu Glu Leu Trp Glu Ser Asp Gly Asp Ala Val Leu Ser Asp
165 170 175

Glu Asp Arg Gln Arg Met Phe Ala Asp Leu Thr Ser Glu Leu Glu Phe
180 185 190

Val Thr Asp Glu Val Leu Asp Leu Gly Thr Phe Thr Asp Phe Asp Arg
195 200 205

Leu Phe Asp Ile Leu Ser Leu Ala Asp Asp Gln Ala Glu Asp Trp Glu
210 215 220

Ala Gln Leu Val Pro Phe Glu Asp Glu Glu Phe Asp Glu Pro Asp Val
225 230 235 240

Tyr Asp Leu Phe Val Asp Asp Ser Glu Glu Asp Asp Asp Asp Leu Asp
245 250 255

Asp Asp Glu Asp Asp Glu Asp Asp Asp Glu Asp
260 265

<210> 2573

<211> 774

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> {101}..(751)

<223> RXA02091

<400> 2573

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gaagtggctt agccttatgc agtttttttg aagtagataa atg agc atc tgg aaa 115
Met Ser Ile Trp Lys
1 5

cgt ctg tta gtg cag tac ccg cgc ttc gcc gac acc ctc aca gcc ggc 163
Arg Leu Leu Val Gln Tyr Pro Arg Phe Ala Asp Thr Leu Thr Ala Gly
10 15 20

caa ccc atc acg ctc gag gaa tta gca acc ccg gaa gtg atc ttg gaa 211
Gln Pro Ile Thr Leu Glu Glu Ala Thr Pro Glu Val Ile Leu Glu
25 30 35

gct gtt gcc aaa ggc caa gaa att ttc ggc att gag cag cca aaa cat 259
Ala Val Ala Lys Gly Gln Glu Ile Phe Gly Ile Glu Gln Pro Lys His
40 45 50

gca gca caa ctc tgg ttt cac tcc ctg tgc acc gca att gtc ggc ccc 307
Ala Ala Gln Leu Trp Phe His Ser Leu Cys Thr Ala Ile Val Gly Pro
55 60 65

gcc gtc acc gcc atg gtg gaa ttc gat gtc atc ccc agc ctc gac ata 355
Ala Val Thr Ala Met Val Glu Phe Asp Val Ile Pro Ser Leu Asp Ile

70	75	80	85	
cgt cga ggt cag	ctg cat aac atc gac	ggt tac tgg ttc ggc	ttc agg	403
Arg Arg Gly Gln	Leu His Asn Ile Asp	Gly Tyr Trp Phe	Gly Phe Arg	
	90	95	100	
ccg gag gag atg	ctt gtc gac gcc	tcg ctc cac	ctg tgc ggc	acc caa
Pro Glu Glu Met	Leu Val Asp Ala	Ser Leu His	Leu Ser Gly Thr	Gln
	105	110	115	451
ttc ggc gag agt	atc cgc gtg gtg	att gat gca	tta tgc gct	gcc acg
Phe Gly Glu Ser	Ile Arg Val Val	Ile Asp Ala	Leu Cys Ala	Ala Thr
	120	125	130	499
gat ctg cga	ccg gca ccc	ctg tgg gcg	gtt gcc	tca gat
Asp Leu Arg	Pro Ala Pro	Leu Trp Ala	Val Ala	Ser Asp
	135	140	145	547
atc gca gct agc	ggc gca ggt	gtc gag gcc	ttt gaa	gaa gaa
Ile Ala Ala Ser	Gly Ala Gly	Val Glu Ala	Phe Glu	Glu Glu
	150	155	160	165
cgc gag gtg gcg	gaa gcc ctc	att gaa gga	atg aat	agt gtg
Arg Glu Val Ala	Glu Ala Leu	Ile Glu Gly	Met Asn	Ser Val
	170	175	180	643
gtt cca tgc	ccg cgg ttt	aac gac gac	gat tat	ttc att
Val Pro Ser Pro	Arg Phe Asn	Asp Asp	Asp Tyr	Phe Ile
	185	190	195	691
tgc tgc atg att	ttc cac tca	cca cga gct	gat ttt	tgc acg
Cys Cys Met Ile	Phe His Ser	Pro Arg Ala	Asp Phe	Cys Thr
	200	205	210	739
cca cag aag agg	tgaaggcta	ggcgcggtatt	cgt	774
Pro Gln Lys Arg				
	215			
<210> 2574				
<211> 217				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 2574				
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	20	25	30	35
Glu Val Ile	Leu Glu Ala	Val Ala Lys	Gly Gln	Glu Ile
	35	40	45	50
Glu Gln Pro	Lys His Ala	Ala Gln	Leu Trp	Phe His
	50	55	60	65
Ala Ile Val	Gly Pro Ala	Val Thr	Ala Met	Val Glu
	65	70	75	80
Pro Ser Leu	Asp Ile Arg	Arg Gly Gln	Leu His	Asn Ile
				Asp Gly
				Tyr

85										90										95																																			
Trp	Phe	Gly	Phe	Arg	Pro	Glu	Glu	Met	Leu	Val	Asp	Ala	Ser	Leu	His																																								
100										105										110																																			
Leu	Ser	Gly	Thr	Gln	Phe	Gly	Glu	Ser	Ile	Arg	Val	Val	Ile	Asp	Ala																																								
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Leu	Cys	Ala	Ala	Thr	Asp	Leu	Arg	Pro	Ala	Pro	Leu	Trp	Ala	Val	Ala																																								
130										135										140																																			
Ser	Asp	Ala	Leu	Gly	Ile	Ala	Ala	Ser	Gly	Ala	Gly	Val	Glu	Ala	Phe																																								
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Glu	Glu	Glu	His	Ala	Arg	Glu	Val	Ala	Glu	Ala	Leu	Ile	Glu	Gly	Met																																								
165										170										175																																			
Asn	Ser	Val	Asn	Ser	Val	Pro	Ser	Pro	Arg	Phe	Asn	Asp	Asp	Asp	Tyr																																								
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Phe	Ile	Arg	Ala	Gly	Cys	Cys	Met	Ile	Phe	His	Ser	Pro	Arg	Ala	Asp																																								
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 Met Pro Ala Gly Ile
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 gca gac atg aca gat tca ttg ctc gga tgg gca tca caa act gag ctg 163
 Ala Asp Met Thr Asp Ser Leu Leu Gly Trp Ala Ser Gln Thr Glu Leu
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 gat ctg aac cag cgt ctt gca ggg gta gag tac ttt cca caa att cag 211
 Asp Leu Asn Gln Arg Leu Ala Gly Val Glu Tyr Phe Pro Gln Ile Gln
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 ctg cga cac gat gag ctc gag cgc att cat cgg ttt tac ggc acc ttt 259
 Leu Arg His Asp Glu Leu Glu Arg Ile His Arg Phe Tyr Gly Thr Phe
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 ttg tcc cgc cag gta ggc gcg ggc gca agc ctt ggg gat ctt ttt gaa 307
 Leu Ser Arg Gln Val Gly Ala Gly Ala Ser Leu Gly Asp Leu Phe Glu
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 atg acc cca tgc ctg aca gtc acc acc ttg gtg tct cgg gcg tca cgg 355

Met Thr Pro Cys Leu Thr Val Thr Thr Leu Val Ser Arg Ala Ser Arg	
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atc agc gat cca gca gat ttc ttc ggt gaa tac atc gga gga ctg gga	403
Ile Ser Asp Pro Ala Asp Phe Phe Gly Glu Tyr Ile Gly Gly Leu Gly	
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ctt agc gca gaa cac gca gca gtt gtt gaa ggg ttg acc gaa aag ctc	451
Leu Ser Ala Glu His Ala Ala Val Val Glu Gly Leu Thr Glu Lys Leu	
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ttc gca cag gct ggc ctg ctc gtt cct gag gga att gca tct cca ttg	499
Phe Ala Gln Ala Gly Leu Leu Val Pro Glu Gly Ile Ala Ser Pro Leu	
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gag ttg tta tcc atc cac gca ggc att agt aac cac gaa gtg gcc gca	547
Glu Leu Leu Ser Ile His Ala Gly Ile Ser Asn His Glu Val Ala Ala	
135 140 145	
gtg ctg acc gaa gtg gaa aac ggc acc acc gaa tat cca ttc atg ttc	595
Val Leu Thr Glu Val Glu Asn Gly Thr Thr Glu Tyr Pro Phe Met Phe	
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gac gct gtc ctg cgc cta acc cct gag tgg gca cag acc ctt atc ggc	643
Asp Ala Val Leu Arg Leu Thr Pro Glu Trp Ala Gln Thr Leu Ile Gly	
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gga gtt caa gaa ctc att gaa ttt gcc acc acc cca cga act tct tgg	691
Gly Val Gln Glu Leu Ile Glu Phe Ala Thr Thr His Arg Thr Ser Trp	
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tca gac cgc cag cgc gaa tcc tca ctg cca gcc atg atc gat gag atc	739
Ser Asp Arg Gln Arg Glu Ser Ser Leu Pro Ala Met Ile Asp Glu Ile	
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gtt gtg gcg gaa ctt cgg gaa cgc cca gtt ggt act gcc gac cgt gaa	787
Val Val Ala Glu Leu Arg Glu Arg Pro Val Gly Thr Ala Asp Arg Glu	
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Asn Ser Val Gly Val Ala Leu Arg Glu Leu Arg Pro Arg Leu Ile Leu	
230 235 240 245	
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Asp Ala Glu Arg Arg Lys Val Cys Leu Arg Leu Pro Glu Gln Arg Val	
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agc gac gat gaa atc aac tgg cga gtc agc cta gaa ggc acc acc cgg	931
Ser Asp Asp Glu Ile Asn Trp Arg Val Ser Leu Glu Gly Thr Arg	
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att ttc tcc acc cgc cga gca tgg ggc gat act tct gga tac tcc gaa	979
Ile Phe Ser Thr Arg Arg Ala Trp Gly Asp Thr Ser Gly Tyr Ser Glu	
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Ala Leu Asp Ile Thr Val Glu Arg Gln Ile Arg Glu Thr Thr Val Thr	
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Asp Thr Ser Asn Gln Ile Thr Trp Val Val Pro Val Val Asp Phe Asn	

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gtc tcc ctg cac cat caa gag att tac gtt ctc gcg cca gcg gaa gca 1171 Val Ser Leu His His Gln Glu Ile Tyr Val Leu Ala Pro Ala Glu Ala 345	345	350	355
aaa ctc gaa gac atg gtc act ggc cag cca gta cca gtt att gag caa 1219 Lys Leu Glu Asp Met Val Thr Gly Gln Pro Val Pro Val Ile Glu Gln 360	365	370	375
ttc ctc gta gag ggc tgg aac tca tgg gtg tgc tcc cgc gtg gac gcc 1267 Phe Leu Val Glu Gly Trp Asn Ser Trp Val Cys Ser Arg Val Asp Ala 375	380	385	390
cgt ggc ctg tcc tct ctg aag gtc aac aaa gaa gtc cga tgc att gac 1315 Arg Gly Leu Ser Ser Leu Lys Val Asn Lys Glu Val Arg Cys Ile Asp 390	395	400	405
cca cgt cga cgc gtt gcc ttc cac cac cca gcc gaa ttg gtc cct cac 1363 Pro Arg Arg Arg Val Ala Phe His His Pro Ala Glu Leu Val Pro His 410	415	420	425
gta cga tcc att tcc gga ctc ccc gta cac gcg cag tcc ctg atc gcc 1411 Val Arg Ser Ile Ser Gly Leu Pro Val His Ala Gln Ser Leu Ile Ala 425	430	435	440
gag ttc cca cca acc ctg agc gga caa gac gaa acc tgg atg ctc tcc 1459 Glu Phe Pro Pro Thr Leu Ser Gly Gln Asp Glu Thr Trp Met Leu Ser 440	445	450	455
atc tcg gct ttc gca ggt gta ggc gct gct ggt gaa gaa atc gcc gag 1507 Ile Ser Ala Phe Ala Gly Val Gly Ala Ala Gly Glu Glu Ile Ala Glu 455	460	465	470
cca gag cct ttg gaa gtc cct gcc gac ggt ggc ctt ttc gcc atc ttc 1555 Pro Glu Pro Leu Glu Val Pro Ala Asp Gly Gly Leu Phe Ala Ile Phe 470	475	480	485
gac cca gaa ata tac gac gcc cca tgg gtg ggt gaa tac ctg gtc cga 1603 Asp Pro Glu Ile Tyr Asp Ala Pro Trp Val Gly Glu Tyr Leu Val Arg 490	495	500	505
ctc cgc ggc cca cgc aat gaa tcc ttc cga ccc gaa ttc gcc atc gtc 1651 Leu Arg Gly Pro Arg Asn Glu Ser Phe Arg Pro Glu Phe Ala Ile Val 505	510	515	520
gaa gac atg acc acc gaa ttc gaa gtc gcc tca ggt gca tca ttt cga 1699 Glu Asp Met Thr Thr Glu Phe Glu Val Ala Ser Gly Ala Ser Phe Arg 520	525	530	535
atc cca acc acc act ggt ctc agc gaa gcc agc cta cgc gtg cgt tcc 1747 Ile Pro Thr Thr Thr Gly Leu Ser Glu Ala Ser Leu Arg Val Arg Ser 535	540	545	550
ggt gaa aag cac ttc acc gca gag cca cgc ctg gtc acc gtt gaa gca 1795 Gly Glu Lys His Phe Thr Ala Glu Pro Arg Leu Val Thr Val Glu Ala 550	555	560	565

acc gac ccc aac gca tca ttc gtg gtc acc acc gat gaa ggc gat caa	1843
Thr Asp Pro Asn Ala Ser Phe Val Val Thr Thr Asp Glu Gly Asp Gln	
570 575 580	
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Met Pro Leu Arg Phe Val Pro Pro Gln Ile Ala Ile Glu Leu Pro Leu	
585 590 595	
acc acc gag cca cca acc tgg cgc gtc acc cgt act gtc tgt gga cca	1939
Thr Thr Glu Pro Pro Thr Trp Arg Val Thr Arg Thr Val Cys Gly Pro	
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Arg Asp Leu Asp Gly Ala Gly Glu Leu Arg Ile Arg Thr Gly Val Asp	
615 620 625	
gtc ggc gat cca aag gtc agt gtg cgc aac cac cac ggt tca cca ctg	2035
Val Gly Asp Pro Lys Val Ser Val Arg Asn His Gly Ser Pro Leu	
630 635 640 645	
cga acc gtg aaa atg gtc acc cct gac aac ggc cgt acc tgg att gcc	2083
Arg Thr Val Lys Met Val Thr Pro Asp Asn Gly Arg Thr Trp Ile Ala	
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Ser Met Lys Glu Ile Ala Ala Ser Thr Phe Val Met Pro Arg Gly Ser	
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Ile Glu Phe Glu Trp Thr Asp Arg Lys Val Asp Arg Val Ser Val	
680 685 690	
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Thr Ile Ala Val Ile Asp Lys Thr Glu Asn Phe Thr Gly Ile Thr Ile	
695 700 705	
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Glu Asp Gly Lys Leu Val Phe Glu Glu Leu Ala Ala Gly Arg Gln Leu	
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Leu Ala Val Thr Gly Pro Glu Leu Glu Leu Pro Glu Val Leu Val Gly	
745 750 755	
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Ala Gly Asn Leu Ile Val Gln Leu His Thr Ala Asp Pro Phe Thr Thr	
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Phe Phe Gly Gly Glu Val Glu Glu Pro Pro Ile Ser Asp Ala Val Val	
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ccc gca ctt tgg gat gtt tcc cat atc tgg acc gaa cag gga aac acc	2611
Pro Ala Leu Trp Asp Val Ser His Ile Trp Thr Glu Gln Gly Asn Thr	
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Glu His Leu Pro Val Val His Ala Ala Leu Arg Ser Ser Pro Ala Ala	
840 845 850	
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Ala Leu Lys Gly Leu Ser Ala Ser Leu Val Pro Ala Gln Ala Leu Pro	
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Asn Arg Thr Pro Leu Leu Pro Ile Leu Gly Gln Leu Glu Glu Val Ala	
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Gly Lys Asn Ile Leu Ser Thr Leu Ala Thr Gly Arg Asp Ser Thr Leu	
935 940 945	
gac acc gca tgc atc gac caa tcc acc gtt gcg att gcc ggc atg aac	2995
Asp Thr Ala Cys Ile Asp Gln Ser Thr Val Ala Ile Ala Gly Met Asn	
950 955 960 965	
gaa acc cag caa aaa gcc ctg ctg gac atg ttc ttc agc aac gcc gac	3043
Glu Thr Gln Gln Lys Ala Leu Leu Asp Met Phe Phe Ser Asn Ala Asp	
970 975 980	
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Ile Val Pro Gly Pro Leu Met Glu Asp Asn Thr Arg Leu Met Ala Val	
985 990 995	
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Phe Glu Thr Phe Lys Lys Arg Asp Ala Leu Arg Glu Val Leu Gln Thr	
1000 1005 1010	
gaa ggc ttg att aag acc gct gta gaa ctt ctt cgt gcc atg cgt gga	3187
Glu Gly Leu Ile Lys Thr Ala Val Glu Leu Leu Arg Ala Met Arg Gly	
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acc cag cgt cag ctg tat tcc tcc gca cgt att cga ttc gac aag ctc	3235
Thr Gln Arg Gln Leu Tyr Ser Ser Ala Arg Ile Arg Phe Asp Lys Leu	
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gat ggt gtc aac act gac aac cca gaa aac atg tgg gca ctc acc cca	3283

Asp Gly Val Asn Thr Asp Asn Pro Glu Asn Met Trp Ala Leu Thr Pro
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 Val Val Ser Leu Val Phe Ala Leu Ser Ser Arg Leu His Ala His Glu
 1065 1070 1075

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 Arg Ile Ala Asp Leu Val Pro Asp Leu Val Thr Gly Asp Leu Ile Ser
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<400> 2576

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Phe Tyr Gly Thr Phe Leu Ser Arg Gln Val Gly Ala Gly Ala Ser Leu
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Gly Asp Leu Phe Glu Met Thr Pro Cys Leu Thr Val Thr Thr Leu Val
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Ser Arg Ala Ser Arg Ile Ser Asp Pro Ala Asp Phe Phe Gly Glu Tyr
 85 90 95

Ile Gly Gly Leu Gly Leu Ser Ala Glu His Ala Ala Val Val Glu Gly
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Leu Thr Glu Lys Leu Phe Ala Gln Ala Gly Leu Leu Val Pro Glu Gly
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Ile Ala Ser Pro Leu Glu Leu Leu Ser Ile His Ala Gly Ile Ser Asn
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His Glu Val Ala Ala Val Leu Thr Glu Val Glu Asn Gly Thr Thr Glu
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Tyr Pro Phe Met Phe Asp Ala Val Leu Arg Leu Thr Pro Glu Trp Ala
 165 170 175

Gln Thr Leu Ile Gly Gly Val Gln Glu Leu Ile Glu Phe Ala Thr Thr
 180 185 190
 His Arg Thr Ser Trp Ser Asp Arg Gln Arg Glu Ser Ser Leu Pro Ala
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 Met Ile Asp Glu Ile Val Val Ala Glu Leu Arg Glu Arg Pro Val Gly
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 Thr Ala Asp Arg Glu Asn Ser Val Gly Val Ala Leu Arg Glu Leu Arg
 225 230 235 240
 Pro Arg Leu Ile Leu Asp Ala Glu Arg Arg Lys Val Cys Leu Arg Leu
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 Pro Glu Gln Arg Val Ser Asp Asp Glu Ile Asn Trp Arg Val Ser Leu
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 Glu Gly Thr Thr Arg Ile Phe Ser Thr Arg Arg Ala Trp Gly Asp Thr
 275 280 285
 Ser Gly Tyr Ser Glu Ala Leu Asp Ile Thr Val Glu Arg Gln Ile Arg
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 305 310 315 320
 Val Val Asp Phe Asn Asp Pro Val Leu Val Phe Ser Ala Arg Gly Glu
 325 330 335
 Asn Leu Thr Asp Lys Val Ser Leu His His Gln Glu Ile Tyr Val Leu
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 Ala Pro Ala Glu Ala Lys Leu Glu Asp Met Val Thr Gly Gln Pro Val
 355 360 365
 Pro Val Ile Glu Gln Phe Leu Val Glu Gly Trp Asn Ser Trp Val Cys
 370 375 380
 Ser Arg Val Asp Ala Arg Gly Leu Ser Ser Leu Lys Val Asn Lys Glu
 385 390 395 400
 Val Arg Cys Ile Asp Pro Arg Arg Arg Val Ala Phe His His Pro Ala
 405 410 415
 Glu Leu Val Pro His Val Arg Ser Ile Ser Gly Leu Pro Val His Ala
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 Gln Ser Leu Ile Ala Glu Phe Pro Pro Thr Leu Ser Gly Gln Asp Glu
 435 440 445
 Thr Trp Met Leu Ser Ile Ser Ala Phe Ala Gly Val Gly Ala Ala Gly
 450 455 460
 Glu Glu Ile Ala Glu Pro Glu Pro Leu Glu Val Pro Ala Asp Gly Gly
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 Leu Phe Ala Ile Phe Asp Pro Glu Ile Tyr Asp Ala Pro Trp Val Gly
 485 490 495
 Glu Tyr Leu Val Arg Leu Arg Gly Pro Arg Asn Glu Ser Phe Arg Pro

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Ala	Gly	Arg	Gln	Leu	Ala	Ala	Trp	Val	Trp	Pro	Gln	Thr	Ala	Pro	Trp															
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Glu	Val	Leu	Val	Gly	Ala	Gly	Asn	Leu	Ile	Val	Gln	Leu	His	Thr	Ala															
755					760					765																				
Asp	Pro	Phe	Thr	Thr	Ser	Val	Thr	Pro	Leu	Ser	Pro	Gly	Lys	Ala	Ala															
770					775					780																				
Val	Thr	Val	Glu	Gln	Glu	Gly	Tyr	Tyr	Ser	Ala	Gln	Thr	Glu	Glu	Tyr															
785					790					795					800															
Ala	Gln	Leu	Ser	Ala	Phe	Phe	Gly	Gly	Glu	Val	Glu	Glu	Pro	Pro	Ile															
805					810					815																				
Ser	Asp	Ala	Val	Val	Pro	Ala	Leu	Trp	Asp	Val	Ser	His	Ile	Trp	Thr															
820					825					830																				

Glu Gln Gly Asn Thr Glu His Leu Pro Val Val His Ala Ala Leu Arg
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 Ser Ser Pro Ala Ala Ala Leu Lys Gly Leu Ser Ala Ser Leu Val Pro
 850 855 860
 Ala Gln Ala Leu Pro Gly Lys Val Ile Ser Ser Gly Leu Ala Ala Ser
 865 870 875 880
 Pro Phe Thr Thr Glu Ser Pro Ala Thr Glu Val His Arg Thr Ala Trp
 885 890 895
 Ile Gly Thr Leu Gln Leu Leu Gly Ala Leu Pro Ser Ala Phe Lys Glu
 900 905 910
 Ala Glu Glu Leu Gly Asn Arg Thr Pro Leu Leu Pro Ile Leu Gly Gln
 915 920 925
 Leu Glu Glu Val Ala Gly Lys Asn Ile Leu Ser Thr Leu Ala Thr Gly
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 Arg Asp Ser Thr Leu Asp Thr Ala Cys Ile Asp Gln Ser Thr Val Ala
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 Ile Ala Gly Met Asn Glu Thr Gln Gln Lys Ala Leu Leu Asp Met Phe
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 Phe Ser Asn Ala Asp Ile Val Pro Gly Pro Leu Met Glu Asp Asn Thr
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 Arg Leu Met Ala Val Phe Glu Thr Phe Lys Lys Arg Asp Ala Leu Arg
 995 1000 1005
 Glu Val Leu Gln Thr Glu Gly Leu Ile Lys Thr Ala Val Glu Leu Leu
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 Arg Ala Met Arg Gly Thr Gln Arg Gln Leu Tyr Ser Ser Ala Arg Ile
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 1075 1080 1085
 Ser Ala Gly Trp Gly Arg Ile Ala Asp Leu Val Pro Asp Leu Val Thr
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<220>

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<222> (101)..(1258)

<223> RXA02102

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Ser	Phe	Ser	Val	Thr	Pro	Ile	Arg	Thr	Met	Ala	Asp	Gly	Thr	Ile	Lys	
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cag	att	cac	cct	ttc	aca	ggc	acc	gaa	gtg	tgg	acg	gtc	cct	ggg	cgt	211
Gln	Ile	His	Pro	Phe	Thr	Gly	Thr	Glu	Val	Trp	Thr	Val	Pro	Gly	Arg	
			25					30					35			

gga	aat	cga	cct	ctg	tca	cat	ccc	gct	tct	acg	atc	gtc	gaa	cta	tct	259
Gly	Asn	Arg	Pro	Leu	Ser	His	Pro	Ala	Ser	Thr	Ile	Val	Glu	Leu	Ser	
		40					45					50				

gca	cac	gat	cac	acc	tct	tac	tgt	gca	ttt	tgt	tcc	gac	aat	atg	ctc	307
Ala	His	Asp	His	Thr	Ser	Tyr	Cys	Ala	Phe	Cys	Ser	Asp	Asn	Met	Leu	
		55				60					65					

tcc	act	ccg	cct	gag	aaa	tgc	cgc	atc	atc	att	gat	agc	tcc	ggc	gac	355
Ser	Thr	Pro	Pro	Glu	Lys	Ser	Arg	Ile	Ile	Ile	Asp	Ser	Ser	Gly	Asp	
	70				75					80					85	

ttt	gac	atc	ctt	ccc	gga	gca	ttg	cct	ggg	gag	ctt	tca	gaa	acc	act	403
Phe	Asp	Ile	Leu	Pro	Gly	Ala	Leu	Pro	Gly	Glu	Leu	Ser	Glu	Thr	Thr	
			90						95					100		

ccg	gaa	ttt	cga	cga	gtc	ccc	aat	ctg	ttt	gag	att	gtc	tct	ttt	gac	451
Pro	Glu	Phe	Arg	Arg	Val	Pro	Asn	Leu	Phe	Glu	Ile	Val	Ser	Phe	Asp	
			105					110					115			

tac	tgg	cac	cag	aat	ttt	ggg	ttc	gat	atg	gat	tca	gaa	acc	gcc	atg	499
Tyr	Trp	His	Gln	Asn	Phe	Gly	Phe	Asp	Met	Asp	Ser	Glu	Thr	Ala	Met	
			120			125					130					

cgc	atg	gcg	caa	tac	ttg	gcg	att	cca	gaa	ggg	cgc	gaa	cat	gtt	tta	547
Arg	Met	Ala	Gln	Tyr	Leu	Ala	Ile	Pro	Glu	Gly	Arg	Glu	His	Val	Leu	
		135				140					145					

gcc	att	gtg	cgc	acc	cga	ctt	tct	gcc	gct	ggg	gaa	gat	ccc	gcg	cac	595
Ala	Ile	Val	Arg	Thr	Arg	Leu	Ser	Ala	Ala	Gly	Glu	Asp	Pro	Ala	His	
	150					155				160				165		

atg	acc	gat	ggc	gag	ttg	tta	gaa	aaa	gct	ccc	agc	tac	ttt	gct	ggg	643
Met	Thr	Asp	Gly	Glu	Leu	Leu	Glu	Lys	Ala	Pro	Ser	Tyr	Phe	Ala	Gly	
			170						175					180		

ggg	cat	gac	gtc	atc	atc	gga	cgc	cga	cac	ttt	gtc	gat	gac	gca	acc	691
Gly	His	Asp	Val	Ile	Ile	Gly	Arg	Arg	His	Phe	Val	Asp	Asp	Ala	Thr	

185	190	195	
acc agt gat caa ttg gcc tca tct gga aca ctg acc gtt aaa gag cat 739			
Thr Ser Asp Gln Leu Ala Ser Ser Gly Thr Leu Thr Val Lys Glu His			
200	205	210	
gag gcg ttc atc cgc ctg act gtc gat ggc atc agg gat ttg tac cac 787			
Glu Ala Phe Ile Arg Leu Thr Val Asp Gly Ile Arg Asp Leu Tyr His			
215	220	225	
cgc aac cgt tac gca cgc tat gta gtg cgc ttt caa aac tgg ttg aaa 835			
Arg Asn Arg Tyr Ala Pro Tyr Val Val Ala Phe Gln Asn Trp Leu Lys			
230	235	240	245
ccc gcc ggc gcg tct ttt gac cat ctt cat aaa cag ctc gtc gcc att 883			
Pro Ala Gly Ala Ser Phe Asp His Leu His Lys Gln Leu Val Ala Ile			
250	255	260	
gat gaa cgc ggc cga ctt att gcc gat gaa ctg cat cat cta cgt ggc 931			
Asp Glu Arg Gly Arg Leu Ile Ala Asp Glu Leu His His Leu Arg Gly			
265	270	275	
aat ccc aat atg tac aac gaa ctt gct gtt gat tac gcc gga tac cac 979			
Asn Pro Asn Met Tyr Asn Glu Leu Ala Val Asp Tyr Ala Gly Tyr His			
280	285	290	
aac ctg atc atc gcg gaa aac gat cac gcc gtg gcc ttc gca ggt ttc 1027			
Asn Leu Ile Ile Ala Glu Asn Asp His Ala Val Ala Phe Ala Gly Phe			
295	300	305	
ggt cac cgc tac ccc acc att gag att tac tct aag tcc gct att cct 1075			
Gly His Arg Tyr Pro Thr Ile Glu Ile Tyr Ser Lys Ser Ala Ile Pro			
310	315	320	325
gaa ccc tgg ctt caa agc gac gag gaa atc caa gcg atg agc aac ctc 1123			
Glu Pro Trp Leu Gln Ser Asp Glu Glu Ile Gln Ala Met Ser Asn Leu			
330	335	340	
atc cat gca tgc cat gct gca acc ggc gca gat gta ccc tgc aat gag 1171			
Ile His Ala Cys His Ala Thr Gly Ala Asp Val Pro Cys Asn Glu			
345	350	355	
gga tgg gta cac aaa cca atc gat gtt gat atg cca atg ccc tgg cat 1219			
Gly Trp Val His Lys Pro Ile Asp Val Asp Met Pro Met Pro Trp His			
360	365	370	
gtg atg atc aaa tgg cgt gtt tct acc ctg gca ggt ttt tgaaggtggc 1268			
Val Met Ile Lys Trp Arg Val Ser Thr Leu Ala Gly Phe			
375	380	385	
accaaggtgt atc 1281			
<210> 2578			
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<212> PRT			
<213> Corynebacterium glutamicum			
<400> 2578			
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 20 25 30
 Thr Val Pro Gly Arg Gly Asn Arg Pro Leu Ser His Pro Ala Ser Thr
 35 40 45
 Ile Val Glu Leu Ser Ala His Asp His Thr Ser Tyr Cys Ala Phe Cys
 50 55 60
 Ser Asp Asn Met Leu Ser Thr Pro Pro Glu Lys Ser Arg Ile Ile Ile
 65 70 75 80
 Asp Ser Ser Gly Asp Phe Asp Ile Leu Pro Gly Ala Leu Pro Gly Glu
 85 90 95
 Leu Ser Glu Thr Thr Pro Glu Phe Arg Arg Val Pro Asn Leu Phe Glu
 100 105 110
 Ile Val Ser Phe Asp Tyr Trp His Gln Asn Phe Gly Phe Asp Met Asp
 115 120 125
 Ser Glu Thr Ala Met Arg Met Ala Gln Tyr Leu Ala Ile Pro Glu Gly
 130 135 140
 Arg Glu His Val Leu Ala Ile Val Arg Thr Arg Leu Ser Ala Ala Gly
 145 150 155 160
 Glu Asp Pro Ala His Met Thr Asp Gly Glu Leu Leu Glu Lys Ala Pro
 165 170 175
 Ser Tyr Phe Ala Gly Gly His Asp Val Ile Ile Gly Arg Arg His Phe
 180 185 190
 Val Asp Asp Ala Thr Thr Ser Asp Gln Leu Ala Ser Ser Gly Thr Leu
 195 200 205
 Thr Val Lys Glu His Glu Ala Phe Ile Arg Leu Thr Val Asp Gly Ile
 210 215 220
 Arg Asp Leu Tyr His Arg Asn Arg Tyr Ala Pro Tyr Val Val Ala Phe
 225 230 235 240
 Gln Asn Trp Leu Lys Pro Ala Gly Ala Ser Phe Asp His Leu His Lys
 245 250 255
 Gln Leu Val Ala Ile Asp Glu Arg Gly Arg Leu Ile Ala Asp Glu Leu
 260 265 270
 His His Leu Arg Gly Asn Pro Asn Met Tyr Asn Glu Leu Ala Val Asp
 275 280 285
 Tyr Ala Gly Tyr His Asn Leu Ile Ile Ala Glu Asn Asp His Ala Val
 290 295 300
 Ala Phe Ala Gly Phe Gly His Arg Tyr Pro Thr Ile Glu Ile Tyr Ser
 305 310 315 320
 Lys Ser Ala Ile Pro Glu Pro Trp Leu Gln Ser Asp Glu Glu Ile Gln
 325 330 335

Ala Met Ser Asn Leu Ile His Ala Cys His Ala Thr Gly Ala Asp
 340 345 350

Val Pro Cys Asn Glu Gly Trp Val His Lys Pro Ile Asp Val Asp Met
 355 360 365

Pro Met Pro Trp His Val Met Ile Lys Trp Arg Val Ser Thr Leu Ala
 370 375 380

Gly Phe
 385

<210> 2579
 <211> 519
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(496)
 <223> RXA02103

<400> 2579
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 ggctagtcac aacaccaagg ctattgtcta ctgtgggtgtt atg ccg aag att cag 115
 Met Pro Lys Ile Gln
 1 5

ttt gat gtt tta gtc ccc gac aca gat tcc atc gca cta gcg gga cgt 163
 Phe Asp Val Leu Val Pro Asp Thr Asp Ser Ile Ala Leu Ala Gly Arg
 10 15 20

ttt acc gta gtc gcc aac ctt ttg atc gaa aaa ggc ctc atg gat cat 211
 Phe Thr Val Val Ala Asn Leu Leu Ile Glu Lys Gly Leu Met Asp His
 25 30 35

ggc gtt gtt gtc cat gat cca gca gcg aaa atc gca gaa gct gtg gaa 259
 Gly Val Val Val His Asp Pro Ala Ala Lys Ile Ala Glu Ala Val Glu
 40 45 50

gag cag ctt cgc cag act tac cgc gac gag cat gaa gat gca gac ttg 307
 Glu Gln Leu Arg Gln Thr Tyr Arg Asp Glu His Glu Asp Ala Asp Leu
 55 60 65

gaa gaa tcc tcg gtc aac cgt tac ctc att gaa gtt gat gga gtt aaa 355
 Glu Glu Ser Ser Val Asn Arg Tyr Leu Ile Glu Val Asp Gly Val Lys
 70 75 80 85

ggc tcc gtt aac caa gtg acc atg att ttt gcc cgt ttg ctc acc ccg 403
 Gly Ser Val Asn Gln Val Thr Met Ile Phe Ala Arg Leu Leu Thr Pro
 90 95 100

cca gca gag ttg cca aag gac gct ttc ctc ctg gag cag gaa ctt gcc 451
 Pro Ala Glu Leu Pro Lys Asp Ala Phe Leu Leu Glu Gln Glu Leu Ala
 105 110 115

tat gaa gtt cct gca gtc tac cca tgg act gtg gag atc ctt cgc 496
 Tyr Glu Val Pro Ala Val Tyr Pro Trp Thr Val Glu Ile Leu Arg
 120 125 130

tagttttgag ctacgtattc ttg

519

<210> 2580

<211> 132

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2580

Met Pro Lys Ile Gln Phe Asp Val Leu Val Pro Asp Thr Asp Ser Ile
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Ala Leu Ala Gly Arg Phe Thr Val Val Ala Asn Leu Leu Ile Glu Lys
 20 25 30

Gly Leu Met Asp His Gly Val Val Val His Asp Pro Ala Ala Lys Ile
 35 40 45

Ala Glu Ala Val Glu Glu Gln Leu Arg Gln Thr Tyr Arg Asp Glu His
 50 55 60

Glu Asp Ala Asp Leu Glu Glu Ser Ser Val Asn Arg Tyr Leu Ile Glu
 65 70 75 80

Val Asp Gly Val Lys Gly Ser Val Asn Gln Val Thr Met Ile Phe Ala
 85 90 95

Arg Leu Leu Thr Pro Pro Ala Glu Leu Pro Lys Asp Ala Phe Leu Leu
 100 105 110

Glu Gln Glu Leu Ala Tyr Glu Val Pro Ala Val Tyr Pro Trp Thr Val
 115 120 125

Glu Ile Leu Arg
 130

<210> 2581

<211> 1044

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1021)

<223> RXA02109

<400> 2581

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taaagctctt atataacctg tataggaaag cgaaaacctc atg ctt gca gtg cta 115
 Met Leu Ala Val Leu
 1 5

ttc ggg gtg gtg gcc ggt gcc atc atg cct ttc caa act tcg gtg aat 163
 Phe Gly Val Val Ala Gly Ala Ile Met Pro Phe Gln Thr Ser Val Asn
 10 15 20

aat aga ttg cgt cag tcc gtg gga gca cca ctg ctg gcg tct ttt att 211
 Asn Arg Leu Arg Gln Ser Val Gly Ala Pro Leu Leu Ala Ser Phe Ile

25	30	35	
tcc ttt ttg gta gga act ttt tca ctc ctg gtt gca acg tgg atc acc Ser Phe Leu Val Gly Thr Phe Ser Leu Leu Val Ala Thr Trp Ile Thr 40 45 50			259
agt ggg cac ccg tat cct gct cta gga aat aca act ggc caa ccg tgg Ser Gly His Pro Tyr Pro Ala Leu Gly Asn Thr Thr Gly Gln Pro Trp 55 60 65			307
tgg att ttc acc ggt ggc atg ttg ggt gtt gtg ctg ctg acg gga aac Trp Ile Phe Thr Gly Gly Met Leu Gly Val Val Leu Leu Thr Gly Asn 70 75 80 85			355
att ttg ctg ttt ccc cga gtc ggc agc gtg cag acc gtt att ttg ccc Ile Leu Leu Phe Pro Arg Val Gly Ser Val Gln Thr Val Ile Leu Pro 90 95 100			403
atc tcc gga cag atc atc atg ggc cta att atc gat aca act ggc ctg Ile Ser Gly Gln Ile Ile Met Gly Leu Ile Ile Asp Thr Gly Leu 105 110 115			451
gca cat tcg cct caa gca ccg tta acc ctg ttc aga gta ttg ggt gct Ala His Ser Pro Gln Ala Pro Leu Thr Leu Phe Arg Val Leu Gly Ala 120 125 130			499
gct gcg gta ctt gtt gga tcg ctg gcc gca gtg gga gtg ttc tct aag Ala Ala Val Leu Val Gly Ser Leu Ala Ala Val Gly Val Phe Ser Lys 135 140 145			547
aaa aac atc gga cag acc caa tcc caa ggt gcc tcc att tgg ttg tgg Lys Asn Ile Gly Gln Thr Gln Ser Gln Gly Ala Ser Ile Trp Leu Trp 150 155 160 165			595
cgc ctc ttc gga gtg gtg atg ggc atg tgc caa gca acc cag gtt gca Arg Leu Phe Gly Val Val Met Gly Met Cys Gln Ala Thr Gln Val Ala 170 175 180			643
gtc aat ggt tac ttg gga act gtc cta gga tcc ccc att gag tca gca Val Asn Gly Tyr Leu Gly Thr Val Leu Gly Ser Pro Ile Glu Ser Ala 185 190 195			691
ctg gtg tct ttc gct gtt ggc acc acc gcg ctg ttt att ctg ctg ttg Leu Val Ser Phe Ala Val Gly Thr Thr Ala Leu Phe Ile Leu Leu Leu 200 205 210			739
gtc acc cga acc aag tgg cgt gga atc aac ggc gct ggg aag aaa aac Val Thr Arg Thr Lys Trp Arg Gly Ile Asn Gly Ala Gly Lys Lys Asn 215 220 225			787
cca tgg tgg atg tgg atc ggt ggc gtc atc ggc gcg act gtt att ttc Pro Trp Trp Met Trp Ile Gly Gly Val Ile Gly Ala Thr Val Ile Phe 230 235 240 245			835
agt act gct tac ctg gga ccg atc att ggc act ggt gtt acc gtg gtg Ser Thr Ala Tyr Leu Gly Pro Ile Ile Gly Thr Gly Val Thr Val Val 250 255 260			883
gtt atg ttg ctg ggc atg atg ttg gcc agc ctg atg atc gac gct ttt Val Met Leu Leu Gly Met Met Leu Ala Ser Leu Met Ile Asp Ala Phe 265 270 275			931

gga atc ctt ggc agc ccg cgc cgc cac att cac atc gcg cag ctt ctc 979
 Gly Ile Leu Gly Ser Pro Arg Arg His Ile His Ile Ala Gln Leu Leu
 280 285 290

ggg ctc gtg gtg atc atc ctc ggc gta aca atg atc aga atc 1021
 Gly Leu Val Val Ile Ile Leu Gly Val Thr Met Ile Arg Ile
 295 300 305

taaaccaaga atctaaacca aga 1044

<210> 2582

<211> 307

<212> PRT

<213> Corynebacterium glutamicum

<400> 2582

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Gln Thr Ser Val Asn Asn Arg Leu Arg Gln Ser Val Gly Ala Pro Leu
 20 25 30

Leu Ala Ser Phe Ile Ser Phe Leu Val Gly Thr Phe Ser Leu Leu Val
 35 40 45

Ala Thr Trp Ile Thr Ser Gly His Pro Tyr Pro Ala Leu Gly Asn Thr
 50 55 60

Thr Gly Gln Pro Trp Trp Ile Phe Thr Gly Gly Met Leu Gly Val Val
 65 70 75 80

Leu Leu Thr Gly Asn Ile Leu Leu Phe Pro Arg Val Gly Ser Val Gln
 85 90 95

Thr Val Ile Leu Pro Ile Ser Gly Gln Ile Ile Met Gly Leu Ile Ile
 100 105 110

Asp Thr Thr Gly Leu Ala His Ser Pro Gln Ala Pro Leu Thr Leu Phe
 115 120 125

Arg Val Leu Gly Ala Ala Val Leu Val Gly Ser Leu Ala Ala Val
 130 135 140

Gly Val Phe Ser Lys Lys Asn Ile Gly Gln Thr Gln Ser Gln Gly Ala
 145 150 155 160

Ser Ile Trp Leu Trp Arg Leu Phe Gly Val Val Met Gly Met Cys Gln
 165 170 175

Ala Thr Gln Val Ala Val Asn Gly Tyr Leu Gly Thr Val Leu Gly Ser
 180 185 190

Pro Ile Glu Ser Ala Leu Val Ser Phe Ala Val Gly Thr Thr Ala Leu
 195 200 205

Phe Ile Leu Leu Leu Val Thr Arg Thr Lys Trp Arg Gly Ile Asn Gly
 210 215 220

Ala Gly Lys Lys Asn Pro Trp Trp Met Trp Ile Gly Gly Val Ile Gly

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<211> 597
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS															
<222> (101)..(574)															
<223> RXA02117															
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ctatgagtc															115
agacgttttt aaagggagcg aattaccata															
gtg tct aca gat cca															
Val Ser Thr Asp Pro															
1 5															
gaa gag ttc gac caa gct gaa acc ctc gat caa ctc gcg tat gag atc															163
Glu Glu Phe Asp Gln Ala Glu Thr Leu Asp Gln Leu Ala Tyr Glu Ile															
10 15 20															
atc ctg ctc acc cgg tat ggt gtc caa aac aca ccg acc aac aag cgc															211
Ile Leu Leu Thr Arg Tyr Gly Val Gln Asn Thr Pro Thr Asn Lys Arg															
25 30 35															
gaa gcc atc atg gat cgc agc gcc ctc atc ttg ctc acc cgc ctt gac															259
Glu Ala Ile Met Asp Arg Ser Ala Leu Ile Leu Leu Thr Arg Leu Asp															
40 45 50															
gct caa gga cct atg aca gtt aat gag cta gct gaa agc ttt gga ctt															307
Ala Gln Gly Pro Met Thr Val Asn Glu Leu Ala Glu Ser Phe Gly Leu															
55 60 65															
aac gtt tct acc gtg cac cgc caa ctc aaa gca gcc att gcc aat ggc															355
Asn Val Ser Thr Val His Arg Gln Leu Lys Ala Ala Ile Ala Asn Gly															
70 75 80 85															
tta att gaa gtc gtc gat gat caa gca tgc ccc gct aaa ctt cat cgt															403
Leu Ile Glu Val Val Asp Asp Gln Ala Cys Pro Ala Lys Leu His Arg															
90 95 100															
cca act gag ttg ggt aaa gaa aaa ctc cag cag gag ctt ctt gcc cgc															451
Pro Thr Glu Leu Gly Lys Glu Lys Leu Gln Gln Glu Leu Leu Ala Arg															

105	110	115	
cag cag gat ctc acc cgc att ctt cat gat tgg gat gag gaa gac att			499
Gln Gln Asp Leu Thr Arg Ile Leu His Asp Trp Asp Glu Glu Asp Ile			
120	125	130	
aaa acg cat gcc aag cta ttg cgg aag cac aat gaa agc ttg gaa gaa			547
Lys Thr His Ala Lys Leu Leu Arg Lys His Asn Glu Ser Leu Glu Glu			
135	140	145	
tac ctc gat atg aag tgg ccc cgc ccc taagtgccca taaacgcacc			594
Tyr Leu Asp Met Lys Trp Pro Arg Pro			
150	155		
tct			597

<210> 2584

<211> 158

<212> PRT

<213> Corynebacterium glutamicum

<400> 2584

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Pro Thr Asn Lys Arg Glu Ala Ile Met Asp Arg Ser Ala Leu Ile Leu			
35	40	45	
Leu Thr Arg Leu Asp Ala Gln Gly Pro Met Thr Val Asn Glu Leu Ala			
50	55	60	
Glu Ser Phe Gly Leu Asn Val Ser Thr Val His Arg Gln Leu Lys Ala			
65	70	75	80
Ala Ile Ala Asn Gly Leu Ile Glu Val Val Asp Asp Gln Ala Cys Pro			
85	90	95	
Ala Lys Leu His Arg Pro Thr Glu Leu Gly Lys Glu Lys Leu Gln Gln			
100	105	110	
Glu Leu Leu Ala Arg Gln Gln Asp Leu Thr Arg Ile Leu His Asp Trp			
115	120	125	
Asp Glu Glu Asp Ile Lys Thr His Ala Lys Leu Leu Arg Lys His Asn			
130	135	140	
Glu Ser Leu Glu Glu Tyr Leu Asp Met Lys Trp Pro Arg Pro			
145	150	155	

<210> 2585

<211> 1494

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1471)

<223> RXA02123

<400> 2585

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gcgaaaaatt cctgaccgcc cacttaaaaa aaggtctagg gtg tgg ggt gtg agt 115
 Val Trp Gly Val Ser
 1 5

ctt cca cca aat gta caa act gtc ggt gag ctg aag gcc gcc ggc cac 163
 Leu Pro Pro Asn Val Gln Thr Val Gly Glu Leu Lys Ala Ala Gly His
 10 15 20

atc tac cga cct ttg cgc gta gaa atc cgc gac aac ctc cta gcc aaa 211
 Ile Tyr Arg Pro Leu Arg Val Glu Ile Arg Asp Asn Leu Leu Ala Lys
 25 30 35

ctt cgc agc ggc gaa gat ccg tgg cca ggc ctg cac ggc ctg aac tac 259
 Leu Arg Ser Gly Glu Asp Pro Trp Pro Gly Leu His Gly Leu Asn Tyr
 40 45 50

acg gtc atc cgg cag ctt gaa cgc gcg ctc atc gcc ggc cac gac atc 307
 Thr Val Ile Arg Gln Leu Glu Arg Ala Leu Ile Ala Gly His Asp Ile
 55 60 65

gtg ctg ctc ggc gaa cgc ggc cag ggt aaa acc cgc ctg ctc cgc acg 355
 Val Leu Leu Gly Glu Arg Gly Gln Gly Lys Thr Arg Leu Leu Arg Thr
 70 75 80 85

tta ata acg ctt ctc gac gag tgg tcc ccg atc att ccc ggg cgc gac 403
 Leu Ile Thr Leu Leu Asp Glu Trp Ser Pro Ile Ile Pro Gly Arg Asp
 90 95 100

gtt cca gaa cac cct ctt gcg cca aac gta gag atc tcc gat gat cag 451
 Val Pro Glu His Pro Leu Ala Pro Asn Val Glu Ile Ser Asp Asp Gln
 105 110 115

ccc att gaa tgg gta cac cgc gat gcg cgc tat acc gag aaa ctt gcc 499
 Pro Ile Glu Trp Val His Arg Asp Ala Arg Tyr Thr Glu Lys Leu Ala
 120 125 130

acc cca gat act tcc gtg gct gat ctt atc ggt gat gtt gac cca atg 547
 Thr Pro Asp Thr Ser Val Ala Asp Leu Ile Gly Asp Val Asp Pro Met
 135 140 145

cgt gtt gct gaa ggc cgc agc ctc ggt gat cta gaa acc att cac tac 595
 Arg Val Ala Glu Gly Arg Ser Leu Gly Asp Leu Glu Thr Ile His Tyr
 150 155 160 165

ggt ctg att cct cgc gcc aac cgt ggc atc gtg gcg atc aac gag ctt 643
 Gly Leu Ile Pro Arg Ala Asn Arg Gly Ile Val Ala Ile Asn Glu Leu
 170 175 180

cct gac ctc gct gaa cgc atc cag gtt gcc atg ctc aac gtc atg gag 691
 Pro Asp Leu Ala Glu Arg Ile Gln Val Ala Met Leu Asn Val Met Glu
 185 190 195

gaa cgt gat gtg cag att cgt ggc tac aac att cgt ttg gac ttg gat 739
 Glu Arg Asp Val Gln Ile Arg Gly Tyr Asn Ile Arg Leu Asp Leu Asp
 200 205 210

gtg ctg gtt gtt gcc tca gcc aac cct gag gat tac acc aac cgt ggc	787
Val Leu Val Val Ala Ser Ala Asn Pro Glu Asp Tyr Thr Asn Arg Gly	
215 220 225	
cga att atc act ccg ctc aaa gac cgc ttc ggt gca gaa atc cgc acc	835
Arg Ile Ile Thr Pro Leu Lys Asp Arg Phe Gly Ala Glu Ile Arg Thr	
230 235 240 245	
cac tac cca ctt gag ttg gac gat gaa gtg gca att atc cgc cag gaa	883
His Tyr Pro Leu Glu Leu Asp Asp Glu Val Ala Ile Ile Arg Gln Glu	
250 255 260	
gca gag ctt gtt gcg caa gtc cct gat atc ttg gtt gaa att ctt gcc	931
Ala Glu Leu Val Ala Gln Val Pro Asp Ile Leu Val Glu Ile Leu Ala	
265 270 275	
cgc tac acc cga gcg ctt cgt gaa tcc tca tct gtg aat cag cgt tct	979
Arg Tyr Thr Arg Ala Leu Arg Glu Ser Ser Ser Val Asn Gln Arg Ser	
280 285 290	
ggg gtg tct gct cgt ttc tcc att gca ggt gca gaa act gtg gcc gca	1027
Gly Val Ser Ala Arg Phe Ser Ile Ala Gly Ala Glu Thr Val Ala Ala	
295 300 305	
gca gct ctt cga cgc gca gca gtg ttc ggc gaa gat gag gcc gtt gcc	1075
Ala Ala Leu Arg Arg Ala Ala Val Phe Gly Glu Asp Glu Ala Val Ala	
310 315 320 325	
cgc ctg gtt gat ttg gaa gca gcc gtg gaa gtc ctc ggc ggc aag att	1123
Arg Leu Val Asp Leu Glu Ala Ala Val Glu Val Leu Gly Gly Lys Ile	
330 335 340	
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Glu Phe Glu Ser Gly Glu Glu Gly Arg Glu Trp Glu Ile Leu Asp Tyr	
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Leu Leu Arg Thr Ala Thr Ala Glu Ala Leu Arg Ser Thr Leu Arg Ser	
360 365 370	
ctg gat ctc acc ccg ctc atc gca gca tta gac ggc agc atc acc gtt	1267
Leu Asp Leu Thr Pro Leu Ile Ala Ala Leu Asp Gly Ser Ile Thr Val	
375 380 385	
tcc act ggc acg aac atc acc gcg tca gaa ttt ttg gct tct ctc ccc	1315
Ser Thr Gly Thr Asn Ile Thr Ala Ser Glu Phe Leu Ala Ser Leu Pro	
390 395 400 405	
gaa ctc ggc gaa agc acg cta tat gac gac atc gct caa gct ttt ggt	1363
Glu Leu Gly Glu Ser Thr Leu Tyr Asp Asp Ile Ala Gln Ala Phe Gly	
410 415 420	
gcc acc aca cca agt act cgc gcg atg gcc att gag ctt gct ttg gaa	1411
Ala Thr Thr Pro Ser Thr Arg Ala Met Ala Ile Glu Leu Ala Leu Glu	
425 430 435	
ggg ctt tac ctt tcc cga aaa att gcc aag gat tct ggc gaa ggt gaa	1459
Gly Leu Tyr Leu Ser Arg Lys Ile Ala Lys Asp Ser Gly Glu Gly Glu	
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 Thr Ile Tyr Gly
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1494

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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2586
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 35 40 45
 His Gly Leu Asn Tyr Thr Val Ile Arg Gln Leu Glu Arg Ala Leu Ile
 50 55 60
 Ala Gly His Asp Ile Val Leu Leu Gly Glu Arg Gly Gln Gly Lys Thr
 65 70 75 80
 Arg Leu Leu Arg Thr Leu Ile Thr Leu Leu Asp Glu Trp Ser Pro Ile
 85 90 95
 Ile Pro Gly Arg Asp Val Pro Glu His Pro Leu Ala Pro Asn Val Glu
 100 105 110
 Ile Ser Asp Asp Gln Pro Ile Glu Trp Val His Arg Asp Ala Arg Tyr
 115 120 125
 Thr Glu Lys Leu Ala Thr Pro Asp Thr Ser Val Ala Asp Leu Ile Gly
 130 135 140
 Asp Val Asp Pro Met Arg Val Ala Glu Gly Arg Ser Leu Gly Asp Leu
 145 150 155 160
 Glu Thr Ile His Tyr Gly Leu Ile Pro Arg Ala Asn Arg Gly Ile Val
 165 170 175
 Ala Ile Asn Glu Leu Pro Asp Leu Ala Glu Arg Ile Gln Val Ala Met
 180 185 190
 Leu Asn Val Met Glu Glu Arg Asp Val Gln Ile Arg Gly Tyr Asn Ile
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 Arg Leu Asp Leu Asp Val Leu Val Val Ala Ser Ala Asn Pro Glu Asp
 210 215 220
 Tyr Thr Asn Arg Gly Arg Ile Ile Thr Pro Leu Lys Asp Arg Phe Gly
 225 230 235 240
 Ala Glu Ile Arg Thr His Tyr Pro Leu Glu Leu Asp Asp Glu Val Ala
 245 250 255
 Ile Ile Arg Gln Glu Ala Glu Leu Val Ala Gln Val Pro Asp Ile Leu
 260 265 270

Val Glu Ile Leu Ala Arg Tyr Thr Arg Ala Leu Arg Glu Ser Ser Ser
275 280 285

Val Asn Gln Arg Ser Gly Val Ser Ala Arg Phe Ser Ile Ala Gly Ala
290 295 300

Glu Thr Val Ala Ala Ala Leu Arg Arg Ala Val Phe Gly Glu
305 310 315 320

Asp Glu Ala Val Ala Arg Leu Val Asp Leu Glu Ala Ala Val Glu Val
325 330 335

Leu Gly Gly Lys Ile Glu Phe Glu Ser Gly Glu Glu Gly Arg Glu Trp
340 345 350

Glu Ile Leu Asp Tyr Leu Leu Arg Thr Ala Thr Ala Glu Ala Leu Arg
355 360 365

Ser Thr Leu Arg Ser Leu Asp Leu Thr Pro Leu Ile Ala Ala Leu Asp
370 375 380

Gly Ser Ile Thr Val Ser Thr Gly Thr Asn Ile Thr Ala Ser Glu Phe
385 390 395 400

Leu Ala Ser Leu Pro Glu Leu Gly Glu Ser Thr Leu Tyr Asp Asp Ile
405 410 415

Ala Gln Ala Phe Gly Ala Thr Thr Pro Ser Thr Arg Ala Met Ala Ile
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Glu Leu Ala Leu Glu Gly Leu Tyr Leu Ser Arg Lys Ile Ala Lys Asp
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Ser Gly Glu Gly Glu Thr Ile Tyr Gly
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<211> 2079

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

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<222> (101)..(2056)

<223> RXA02124

<400> 2587

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Met Ala Thr Ser His
1 5

tca cga ccc cgc cgc agc cgt tac gga cgc tac acc gga ggc cca gat 163
Ser Arg Pro Arg Arg Ser Arg Tyr Gly Arg Tyr Thr Gly Gly Pro Asp
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cgc ctg gca cct cca gtg gat ctc agc gat gcc ctg cgc gat att gct 211
Pro Leu Ala Pro Pro Val Asp Leu Ser Asp Ala Leu Arg Asp Ile Ala

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Ser	Lys	His	Arg	Glu	Gly	Thr	Asp	Thr	Pro	Thr	Asp	Phe	Ala	Asn	Phe															
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Glu	Leu	Ile	Asp	Ala	Leu	Ala	Ala	Arg	Ser	Ala	Ala	Ala	Ser	Arg	Met															
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Phe	Asn	Ser	Ile	Ser	Glu	Glu	Gln	Arg	Arg	Glu	Leu	Met	Lys	Leu	Ser															
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gct gga aac ctc caa ggt ctg cgc ccc gac ctc aac tgg gat ggc tcc 979
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gaa caa ttc tcc ggc gac gaa ggc atg gga ctt ggt gat ggc acc ggc 1027
 Glu Gln Phe Ser Gly Asp Glu Gly Met Gly Leu Gly Asp Gly Thr Gly
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gcc atg cag gac ctc gcc gaa ctc gac aac ctt gct gaa caa ctg agc 1075
 Ala Met Gln Asp Leu Ala Glu Leu Asp Asn Leu Ala Glu Gln Leu Ser
 310 315 320 325

aac tcc cac acc gac ctc gac att gat gcg att cgc cgc caa ctc ggc 1123
 Asn Ser His Thr Asp Leu Asp Ile Asp Ala Ile Arg Arg Gln Leu Gly
 330 335 340

gat gac gcc gct gtc tct gcc gaa act ttg gcc aaa ctg gag cgc gcg 1171
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 345 350 355

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ctc agc ccc cag gcc atg cgc cgt cta ggg aaa gcg ctt ctc gac gcc 1267
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 375 380 385

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 425 430 435

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 Asp Asp Val Glu Val Ile Glu Thr Glu Ala Arg Thr Leu Asn Ala Val
 455 460 465

gca ctg cta gta gac acc agt tat tcc atg gct gcc gaa ggc cgc tgg 1555
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 Val Pro Met Lys Gln Thr Ala Leu Ala Leu His His Leu Val Ser Thr
 490 495 500

cgg ttt aga gga gat gaa cta gca cta atc act ttt ggt cga cat gcc 1651
 Arg Phe Arg Gly Asp Glu Leu Ala Leu Ile Thr Phe Gly Arg His Ala
 505 510 515

caa aac atg gac atc gag gaa ctg act gca ctg cca ccg gtt cac gaa 1699
 Gln Asn Met Asp Ile Glu Leu Thr Ala Leu Pro Val His Glu
 520 525 530

caa gga act aat ctc cac cac gca tta ctg ctg gca gaa ccg ttc ttt 1747
 Gln Gly Thr Asn Leu His His Ala Leu Leu Leu Ala Glu Arg Phe Phe
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gct cgc cat ccc tcc atg aaa gca agc ctg ctc att gtc aca gat ggc 1795
 Ala Arg His Pro Ser Met Lys Ala Ser Leu Leu Ile Val Thr Asp Gly
 550 555 560

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 Glu Pro Thr Ala His Leu Glu Ala Asp Gly His Ala Trp Phe Asn Trp
 570 575 580

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 Pro Thr Asp Pro Glu Thr Met Phe Lys Thr Val Thr Gln Leu Asp Lys
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gta acc aag cga gga acc cac acc aca ctc ttc cga ctg gga cat gat 1939
 Val Thr Lys Arg Gly Thr His Thr Thr Leu Phe Arg Leu Gly His Asp
 600 605 610

caa gga tta gag cac ttt ctc aac caa cta gcc gac cgt gtt gcc ggc 1987
 Gln Gly Leu Glu His Phe Leu Asn Gln Leu Ala Asp Arg Val Gly Gly
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acc gtg gtg gct ccc gat ctg gac gga ctc ggc gcc gca gtc gtg ggc 2035
 Thr Val Val Ala Pro Asp Leu Asp Gly Leu Gly Ala Ala Val Val Gly
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gag tat tta cga cac cgc tac tgagcattgg acgttttgcg ctt 2079
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2588
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Leu Arg Asp Ile Ala Asp Asp Val Met Ala Gly Tyr Ser Pro Glu Gln
 35 40 45

Ala Leu Arg Glu Tyr Leu Arg Arg Gly Ala Arg Gly Gln Glu Gly Leu
 50 55 60

Asp Asp Leu Ala Trp Arg Ala Ala Glu Arg Arg Arg Glu Leu Leu Ser
 65 70 75 80

Arg Asn Asn Leu Gly Gly Thr Leu Ala Glu Val Arg Lys Leu Leu Asp
 85 90 95

Glu Gly Leu Lys Leu Glu Arg Ala Gln Leu Ala Arg Asp Ile Asp Met
 100 105 110
 Asp Asp Thr Asp Arg Ala Phe Arg Glu Met Gln Ile Ser Asn Leu Pro
 115 120 125
 Glu Ser Thr Ala Ala Ala Val Ser Glu Leu Asn Ser Tyr Asp Trp Gln
 130 135 140
 Ser Gln Glu Ala Arg Gln Lys Phe Glu Gln Ile Arg Asp Leu Leu Gly
 145 150 155 160
 Arg Glu Met Leu Asp Gln Gln Phe Ser Gly Met Lys Gln Ala Met Glu
 165 170 175
 Gly Ala Ser Asp Glu Asp Lys Ala Ala Ile Ala Glu Met Leu Arg Asp
 180 185 190
 Leu Asn Asp Leu Leu Ser Lys His Arg Glu Gly Thr Asp Thr Pro Thr
 195 200 205
 Asp Phe Ala Asn Phe Met Ala Lys His Gly Glu His Phe Pro Glu Gln
 210 215 220
 Pro Arg Asp Ile Asn Glu Leu Ile Asp Ala Leu Ala Ala Arg Ser Ala
 225 230 235 240
 Ala Ala Ser Arg Met Phe Asn Ser Ile Ser Glu Glu Gln Arg Arg Glu
 245 250 255
 Leu Met Lys Leu Ser Ala Gln Ala Phe Gly Ser Pro Glu Leu Gln Glu
 260 265 270
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 275 280 285
 Asn Trp Asp Gly Ser Glu Gln Phe Ser Gly Asp Glu Gly Met Gly Leu
 290 295 300
 Gly Asp Gly Thr Gly Ala Met Gln Asp Leu Ala Glu Leu Asp Asn Leu
 305 310 315 320
 Ala Glu Gln Leu Ser Asn Ser His Thr Asp Leu Asp Ile Asp Ala Ile
 325 330 335
 Arg Arg Gln Leu Gly Asp Asp Ala Ala Val Ser Ala Glu Thr Leu Ala
 340 345 350
 Lys Leu Glu Arg Ala Leu Arg Asp Ser Gly Leu Leu Arg Arg Asn Pro
 355 360 365
 Asp Gly Ser Leu Lys Leu Ser Pro Gln Ala Met Arg Arg Leu Gly Lys
 370 375 380
 Ala Leu Leu Asp Ala Ala Ser Glu Gln Leu Ser Ser Arg Pro Gly Ser
 385 390 395 400
 Arg Asp Ser Arg Leu Ala Gly Ala Asn Gly Glu Ala Thr Gly Ala Ser
 405 410 415
 Arg Pro Tyr Val Phe Gly Asp Thr Gln Pro Trp Asp Val Thr Arg Thr

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420                               425                               430

Ile Thr Asn Ala Leu Gln Arg Thr Ala Gly Thr Asp Thr Glu Gly Pro
435                               440                               445

Leu Arg Ile Asn Leu Asp Asp Val Glu Val Ile Glu Thr Glu Ala Arg
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Thr Leu Asn Ala Val Ala Leu Leu Val Asp Thr Ser Tyr Ser Met Ala
465                               470                               475                               480

Ala Glu Gly Arg Trp Val Pro Met Lys Gln Thr Ala Leu Ala Leu His
485                               490                               495

His Leu Val Ser Thr Arg Phe Arg Gly Asp Glu Leu Ala Leu Ile Thr
500                               505                               510

Phe Gly Arg His Ala Gln Asn Met Asp Ile Glu Glu Leu Thr Ala Leu
515                               520                               525

Pro Pro Val His Glu Gln Gly Thr Asn Leu His His Ala Leu Leu Leu
530                               535                               540

Ala Glu Arg Phe Phe Ala Arg His Pro Ser Met Lys Ala Ser Leu Leu
545                               550                               555                               560

Ile Val Thr Asp Gly Glu Pro Thr Ala His Leu Glu Ala Asp Gly His
565                               570                               575

Ala Trp Phe Asn Trp Pro Thr Asp Pro Glu Thr Met Phe Lys Thr Val
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Thr Gln Leu Asp Lys Val Thr Lys Arg Gly Thr His Thr Thr Leu Phe
595                               600                               605

Arg Leu Gly His Asp Gln Gly Leu Glu His Phe Leu Asn Gln Leu Ala
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Asp Arg Val Gly Gly Thr Val Val Ala Pro Asp Leu Asp Gly Leu Gly
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<222> (101)..(901)
<223> RXA02125

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Met Val Ala Thr Ser
1 5

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gtt gca gga tac cga aac att gat act gcc cta gcg tat gga aac gag Val Ala Gly Tyr Arg Asn Ile Asp Thr Ala Leu Ala Tyr Gly Asn Glu 25 30 35	211
cgc ggc gtt ggc gaa ggc att cgc acc gct gga gtg ccc cgc gag gag Arg Gly Val Gly Glu Gly Ile Arg Thr Ala Gly Val Pro Arg Glu Glu 40 45 50	259
ctc ttt att tcc acc aag cta gct gca gaa atc aaa gat tac gat gga Leu Phe Ile Ser Thr Lys Leu Ala Ala Glu Ile Lys Asp Tyr Asp Gly 55 60 65	307
gca gtc gcc gcg att gat gag tct ttg gcg aaa att ggc ttg gat tat Ala Val Ala Ala Ile Asp Glu Ser Leu Ala Lys Ile Gly Leu Asp Tyr 70 75 80 85	355
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cac gtt aat cag ctt ctt gtg cat gtt gga aac acc cca agc gag tta His Val Asn Gln Leu Leu Val His Val Gly Asn Thr Pro Ser Glu Leu 150 155 160 165	595
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atc gcc cac gga gag atg ctg aag aac cag cag gtc aag gcg att gct Ile Ala His Gly Glu Met Leu Lys Asn Gln Gln Val Lys Ala Ile Ala 185 190 195	691
gac aag tac aac gtg agc att ccg cag cta tgc att cgg tac aca att Asp Lys Tyr Asn Val Ser Ile Pro Gln Leu Cys Ile Arg Tyr Thr Ile 200 205 210	739
caa ctg gga acg gtg tct ttg cca aag act gcc aac cca gat cat atg Gln Leu Gly Thr Val Ser Leu Pro Lys Thr Ala Asn Pro Asp His Met 215 220 225	787
agc tcc aat gcg cag atc gac ttt gaa att tcc gag gaa gac atg gcg Ser Ser Asn Ala Gln Ile Asp Phe Glu Ile Ser Glu Glu Asp Met Ala 230 235 240 245	835

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<210> 2590

<211> 267

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2590

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Ala Tyr Gly Asn Glu Arg Gly Val Gly Glu Gly Ile Arg Thr Ala Gly
 35 40 45

Val Pro Arg Glu Glu Leu Phe Ile Ser Thr Lys Leu Ala Ala Glu Ile
 50 55 60

Lys Asp Tyr Asp Gly Ala Val Ala Ala Ile Asp Glu Ser Leu Ala Lys
 65 70 75 80

Ile Gly Leu Asp Tyr Val Asp Leu Met Leu Ile His Ser Pro Gln Pro
 85 90 95

Trp Ser Asp Phe Arg Gly Gly Asp Tyr Ser Glu Gly Asn Arg Glu Ala
 100 105 110

Trp Arg Ala Leu Glu Asp Ala Tyr Lys Ala Gly Lys Ile Arg Ser Ile
 115 120 125

Gly Val Ser Asn Phe Leu Glu Ala Asp Leu Glu Asn Ile Leu Asp Ser
 130 135 140

Ala Thr Val Ala Pro His Val Asn Gln Leu Leu Val His Val Gly Asn
 145 150 155 160

Thr Pro Ser Glu Leu Ile Ser Phe Cys Asp Ser Lys Gly Ile Leu Val
 165 170 175

Glu Ala Tyr Ser Pro Ile Ala His Gly Glu Met Leu Lys Asn Gln Gln
 180 185 190

Val Lys Ala Ile Ala Asp Lys Tyr Asn Val Ser Ile Pro Gln Leu Cys
 195 200 205

Ile Arg Tyr Thr Ile Gln Leu Gly Thr Val Ser Leu Pro Lys Thr Ala
 210 215 220

Asn Pro Asp His Met Ser Ser Asn Ala Gln Ile Asp Phe Glu Ile Ser
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Glu Glu Asp Met Ala Ala Leu Gln Glu Val Thr Ala Arg Asp Tyr Gly

245

250

255

Glu His Ser Gly Phe Pro Val Tyr Ser Gly Lys
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<210> 2591

<211> 357

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(334)

<223> RXA02129

<400> 2591

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 Met Lys Ile Ile Phe
 1 5

aaa atg gct agt aac aag ttc atc gac aac aaa aag ggg ctg gct atg 163
 Lys Met Ala Ser Asn Lys Phe Ile Asp Asn Lys Lys Gly Leu Ala Met
 10 15 20

cta gtt ttt gcc gaa ctt gtg atg gaa atg ctt gat cag cct gaa gaa 211
 Leu Val Phe Ala Glu Leu Val Met Glu Met Leu Asp Gln Pro Glu Glu
 25 30 35

caa ctt cat aat gtg cgt gga gtg gct att gag aag cgg gag ttc ctc 259
 Gln Leu His Asn Val Arg Gly Val Ala Ile Glu Lys Arg Glu Phe Leu
 40 45 50

aaa gct ctc acc gct gat ttc acc agc aga ctt aaa caa gct caa acc 307
 Lys Ala Leu Thr Ala Asp Phe Thr Ser Arg Leu Lys Gln Ala Gln Thr
 55 60 65

gat aag att ctt gtt tgg gat ttc gca tgactattat gtggcgacc 354
 Asp Lys Ile Leu Val Trp Asp Phe Ala
 70 75

cgt 357

<210> 2592

<211> 78

<212> PRT

<213> Corynebacterium glutamicum

<400> 2592

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Asp Gln Pro Glu Glu Gln Leu His Asn Val Arg Gly Val Ala Ile Glu
 35 40 45

Lys Arg Glu Phe Leu Lys Ala Leu Thr Ala Asp Phe Thr Ser Arg Leu
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Lys Gln Ala Gln Thr Asp Lys Ile Leu Val Trp Asp Phe Ala
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<211> 739

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(739)

<223> RXA02132

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Val His Asn Phe Ser
1 5

ttc gac gtg gac gaa tcc tac gcc aag aag aac aac gaa atc ctc cgc 163
Phe Asp Val Asp Glu Ser Tyr Ala Lys Lys Asn Asn Glu Ile Leu Arg
10 15 20

gac gca aag cga ctc cag atc tca gca ctg tgc ctt gga ctc atc ctc 211
Asp Ala Lys Arg Leu Gln Ile Ser Ala Leu Cys Leu Gly Leu Ile Leu
25 30 35

ggc ggc gga gcc gta gcc gtc tac ctg ttt tct aac gga gca gtg tgg 259
Gly Gly Gly Ala Val Ala Val Tyr Leu Phe Ser Asn Gly Ala Val Trp
40 45 50

atg tgg atg atc gcc atc gtc atg gtc ttc ctc gcc ctg ttg agc ttc 307
Met Trp Met Ile Ala Ile Val Met Val Phe Leu Ala Leu Leu Ser Phe
55 60 65

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Ile Met Ile Pro Val Ile Pro Arg Gln Met Gly Asn Ala Gln Thr Leu
70 75 80 85

tac gat gac tac gaa cta gcc ccc gcc atc atc gca gaa gta aac ccc 403
Tyr Asp Asp Tyr Glu Leu Ala Pro Ala Ile Ile Ala Glu Val Asn Pro
90 95 100

cgc gat gtg gtc ctc ctg gca ctc gtc aac cgc aat gtg aac ccc gaa 451
Arg Asp Val Val Leu Leu Ala Leu Val Asn Arg Asn Val Asn Pro Glu
105 110 115

gcc aaa cca gag tgg gca ttg gcc acc cgc acg atc gtt cgc gtc gga 499
Ala Lys Pro Glu Trp Ala Leu Ala Thr Arg Thr Ile Val Arg Val Gly
120 125 130

gca cac gaa cgt cgc ctc gcc gaa cgt atc cca tcc gtc gca atc acc 547
Ala His Glu Arg Arg Leu Gly Glu Arg Ile Pro Ser Val Ala Ile Thr
135 140 145

ggc cga cgc acc gtc aaa gac caa gac cac tgg gat gaa atc agc ccc 595

Gly Arg Arg Thr Val Lys Asp Gln Asp His Trp Asp Glu Ile Ser Pro
 150 155 160 165

atg cca att acc tgg ggc acc acg gac aaa gac atc atc cgt gaa gcc 643
 Met Pro Ile Thr Trp Gly Thr Thr Asp Lys Asp Ile Ile Arg Glu Ala
 170 175 180

gag aaa act atc ccc cac gaa ctc tgg gcc aaa cta gaa aag aac cgc 691
 Glu Lys Thr Ile Pro His Glu Leu Trp Ala Lys Leu Glu Lys Asn Arg
 185 190 195

ggc aag ttg gag gac gtt aaa aag acc ccc aac aac ctg ttc aaa cta 739
 Gly Lys Leu Glu Asp Val Lys Lys Thr Pro Asn Asn Leu Phe Lys Leu
 200 205 210

<210> 2594

<211> 213

<212> PRT

<213> Corynebacterium glutamicum

<400> 2594

Val His Asn Phe Ser Phe Asp Val Asp Glu Ser Tyr Ala Lys Lys Asn
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Asn Glu Ile Leu Arg Asp Ala Lys Arg Leu Gln Ile Ser Ala Leu Cys
 20 25 30

Leu Gly Leu Ile Leu Gly Gly Gly Ala Val Ala Val Tyr Leu Phe Ser
 35 40 45

Asn Gly Ala Val Trp Met Trp Met Ile Ala Ile Val Met Val Phe Leu
 50 55 60

Ala Leu Leu Ser Phe Ile Met Ile Pro Val Ile Pro Arg Gln Met Gly
 65 70 75 80

Asn Ala Gln Thr Leu Tyr Asp Asp Tyr Glu Leu Ala Pro Ala Ile Ile
 85 90 95

Ala Glu Val Asn Pro Arg Asp Val Val Leu Leu Ala Leu Val Asn Arg
 100 105 110

Asn Val Asn Pro Glu Ala Lys Pro Glu Trp Ala Leu Ala Thr Arg Thr
 115 120 125

Ile Val Arg Val Gly Ala His Glu Arg Arg Leu Gly Glu Arg Ile Pro
 130 135 140

Ser Val Ala Ile Thr Gly Arg Arg Thr Val Lys Asp Gln Asp His Trp
 145 150 155 160

Asp Glu Ile Ser Pro Met Pro Ile Thr Trp Gly Thr Thr Asp Lys Asp
 165 170 175

Ile Ile Arg Glu Ala Glu Lys Thr Ile Pro His Glu Leu Trp Ala Lys
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Leu Glu Lys Asn Arg Gly Lys Leu Glu Asp Val Lys Lys Thr Pro Asn
 195 200 205

Asn Leu Phe Lys Leu
210

<210> 2595

<211> 921

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(898)

<223> RXA02137

<400> 2595

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Met Val Val Leu Ile
1 5

cct ttc aac gat gaa gtg tgc acc cct att ccc gat ttg gga ggt ttt 163
Pro Phe Asn Asp Glu Val Cys Thr Pro Ile Pro Asp Leu Gly Gly Phe
10 15 20

cct tgt agc cta ttg agt gtg aaa ctt cct tgg gat aaa aat aag aac 211
Pro Cys Ser Leu Ser Val Lys Leu Pro Trp Asp Lys Asn Lys Asn
25 30 35

aac gaa ggg gct gac gct gca ggc caa gac gcc agc tcc acc cct gag 259
Asn Glu Gly Ala Asp Ala Ala Gly Gln Asp Ala Ser Ser Thr Pro Glu
40 45 50

acc gct acg cct gac gct act gag cag aaa ttg cca aag ggg cac acg 307
Thr Ala Thr Pro Asp Ala Thr Glu Gln Lys Leu Pro Lys Gly His Thr
55 60 65

gca ccg aag ggc cgt ccc act ccg aag cgt cgt gaa gtt gag tta gag 355
Ala Pro Lys Gly Arg Pro Thr Pro Lys Arg Arg Glu Val Glu Leu Glu
70 75 80 85

cga ggt gtc gtt ggc ggc cag tct ttg gcg cct act gat act tat gcg 403
Arg Gly Val Val Gly Gly Gln Ser Leu Ala Pro Thr Asp Thr Tyr Ala
90 95 100

cag cag cgc cag aag cgt aaa gaa ttt aaa gct tct atg acc aag gaa 451
Gln Gln Arg Gln Lys Arg Lys Glu Phe Lys Ala Ser Met Thr Lys Glu
105 110 115

gaa ttc aag gca tac aag cag aaa gag cgc gat gcc cga gtt aag cgt 499
Glu Phe Lys Ala Tyr Lys Lys Glu Arg Asp Ala Arg Val Lys Arg
120 125 130

cag cgc gaa acc caa gct gca atg gat cgc ggc gaa gat gct tat ttg 547
Gln Arg Glu Thr Gln Ala Ala Met Asp Arg Gly Glu Asp Ala Tyr Leu
135 140 145

atg gat cgc gat aag ggc gag gtt cgc cgt ttt gcg cgt gac tgg gtg 595
Met Asp Arg Asp Lys Gly Glu Val Arg Arg Phe Ala Arg Asp Trp Val
150 155 160 165

gat tcc cgc agg ttc ttg tct aac ttt gtg atg cca gta gct att gct 643
Asp Ser Arg Arg Phe Leu Ser Asn Phe Val Met Pro Val Ala Ile Ala
170 175 180

ttg ctg gtt gtc atg ctg atc ggt aac ttc aac cca tca ttc gct gcg 691
Leu Leu Val Val Met Leu Ile Gly Asn Phe Asn Pro Ser Phe Ala Ala
185 190 195

act tct tcc atg gtt gcc atg gtt ttg atg ttg ggc ttc ctg att gag 739
Thr Ser Ser Met Val Ala Met Val Leu Met Leu Gly Phe Leu Ile Glu
200 205 210

ggc atc acc act ggt cgt cgt gtg aac aag gct gct cgc acg agg ttc 787
Gly Ile Thr Thr Gly Arg Arg Val Asn Lys Ala Ala Arg Thr Arg Phe
215 220 225

cct ggt acc acc gag act ggt ttt ggt ctg ggt tac tac gcg tat tcc 835
Pro Gly Thr Thr Glu Thr Gly Phe Gly Leu Gly Tyr Tyr Ala Tyr Ser
230 235 240 245

cgc acc att cag cct cgt aag tgg cgt acc cct cgt gca cgc gtt gaa 883
Arg Thr Ile Gln Pro Arg Lys Trp Arg Thr Pro Arg Ala Arg Val Glu
250 255 260

att ggt gct gaa gtc tagcgcatgc gcacgttagt tct 921
Ile Gly Ala Glu Val
265

<210> 2596
<211> 266
<212> PRT
<213> Corynebacterium glutamicum

<400> 2596
Met Val Val Leu Ile Pro Phe Asn Asp Glu Val Cys Thr Pro Ile Pro
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Asp Leu Gly Gly Phe Pro Cys Ser Leu Ser Val Lys Leu Pro Trp
20 25 30

Asp Lys Asn Lys Asn Asn Glu Gly Ala Asp Ala Ala Gly Gln Asp Ala
35 40 45

Ser Ser Thr Pro Glu Thr Ala Thr Pro Asp Ala Thr Glu Gln Lys Leu
50 55 60

Pro Lys Gly His Thr Ala Pro Lys Gly Arg Pro Thr Pro Lys Arg Arg
65 70 75 80

Glu Val Glu Leu Glu Arg Gly Val Val Gly Gly Gln Ser Leu Ala Pro
85 90 95

Thr Asp Thr Tyr Ala Gln Gln Arg Gln Lys Arg Lys Glu Phe Lys Ala
100 105 110

Ser Met Thr Lys Glu Glu Phe Lys Ala Tyr Lys Gln Lys Glu Arg Asp
115 120 125

Ala Arg Val Lys Arg Gln Arg Glu Thr Gln Ala Ala Met Asp Arg Gly
130 135 140

Glu Asp Ala Tyr Leu Met Asp Arg Asp Lys Gly Glu Val Arg Arg Phe
145 150 155 160

Ala Arg Asp Trp Val Asp Ser Arg Arg Phe Leu Ser Asn Phe Val Met
165 170 175

Pro Val Ala Ile Ala Leu Leu Val Val Met Leu Ile Gly Asn Phe Asn
180 185 190

Pro Ser Phe Ala Ala Thr Ser Ser Met Val Ala Met Val Leu Met Leu
195 200 205

Gly Phe Leu Ile Glu Gly Ile Thr Thr Gly Arg Arg Val Asn Lys Ala
210 215 220

Ala Arg Thr Arg Phe Pro Gly Thr Thr Glu Thr Gly Phe Gly Leu Gly
225 230 235 240

Tyr Tyr Ala Tyr Ser Arg Thr Ile Gln Pro Arg Lys Trp Arg Thr Pro
245 250 255

Arg Ala Arg Val Glu Ile Gly Ala Glu Val
260 265

<210> 2597

<211> 531

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(508)

<223> RXA02141

<400> 2597

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aagaaggagt ggcgaaaaaa tgaagtcttc agcaaaactc atg tac ggc ccg acc 115
Met Tyr Gly Pro Thr
1 5

gta ttc atg gcc gca atg gct gtc atc tac atc ttc gca aca atg cac 163
Val Phe Met Ala Ala Met Ala Val Ile Tyr Ile Phe Ala Thr Met His
10 15 20

gtt agt gat ggc ggc agc gtt aaa ggt gtt gag tgg gtc ggt tct gtg 211
Val Ser Asp Gly Gly Ser Val Lys Gly Val Glu Trp Val Gly Ser Val
25 30 35

gcc ctg gtc ctg tca gca ggt ctg acg ctt atg ctc ggt gtc tac ctt 259
Ala Leu Val Leu Ser Ala Gly Leu Thr Leu Met Leu Gly Val Tyr Leu
40 45 50

cac ttc act gaa gtc cgc gta gat gtt ctt cca gag gac tgg gaa gag 307
His Phe Thr Glu Val Arg Val Asp Val Leu Pro Glu Asp Trp Glu Glu
55 60 65

gct gag gtt gcc gac aag gca gga acc ctc ggg ttc ttc agc cca agc 355
Ala Glu Val Ala Asp Lys Ala Gly Thr Leu Gly Phe Phe Ser Pro Ser

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70              75              80              85
tcc att tgg ccg gca gct atg tcc ggt gcg gtt gga ttc ctt gca ttc 403
Ser Ile Trp Pro Ala Ala Met Ser Gly Ala Val Gly Phe Leu Ala Phe
          90              95              100

ggc gtt gtg tac ttc cac tac tgg atg atc gca gtt ggt ctg atg etc 451
Gly Val Val Tyr Phe His Tyr Trp Met Ile Ala Val Gly Leu Met Leu
          105              110              115

ctg atc ttc acg atc acc aag ctc aac ctt cag tac ggc gtg cca aaa 499
Leu Ile Phe Thr Ile Thr Lys Leu Asn Leu Gln Tyr Gly Val Pro Lys
          120              125              130

gaa aag cac tagtactaaa accacatatg ctc 531
Glu Lys His
          135

<210> 2598
<211> 136
<212> PRT
<213> Corynebacterium glutamicum

<400> 2598
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Phe Ala Thr Met His Val Ser Asp Gly Gly Ser Val Lys Gly Val Glu
          20              25              30

Trp Val Gly Ser Val Ala Leu Val Leu Ser Ala Gly Leu Thr Leu Met
          35              40              45

Leu Gly Val Tyr Leu His Phe Thr Glu Val Arg Val Asp Val Leu Pro
          50              55              60

Glu Asp Trp Glu Glu Ala Glu Val Ala Asp Lys Ala Gly Thr Leu Gly
          65              70              75              80

Phe Phe Ser Pro Ser Ser Ile Trp Pro Ala Ala Met Ser Gly Ala Val
          85              90              95

Gly Phe Leu Ala Phe Gly Val Val Tyr Phe His Tyr Trp Met Ile Ala
          100              105              110

Val Gly Leu Met Leu Leu Ile Phe Thr Ile Thr Lys Leu Asn Leu Gln
          115              120              125

Tyr Gly Val Pro Lys Glu Lys His
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<210> 2599
<211> 750
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(727)

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<223> RXA02146

<400> 2599

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				Val	Gly	Lys	His	Arg	
				1				5	

cgc	aac	aat	tca	aac	gca	act	cgc	aag	gct	gta	gca	gca	tct	gca	gtt	163
Arg	Asn	Asn	Ser	Asn	Ala	Thr	Arg	Lys	Ala	Val	Ala	Ala	Ser	Ala	Val	
			10						15					20		

gcg	ctt	gga	gca	acc	gca	gct	atc	gcc	tcc	cca	gca	cag	gca	gct	gag	211
Ala	Leu	Gly	Ala	Thr	Ala	Ala	Ile	Ala	Ser	Pro	Ala	Gln	Ala	Ala	Glu	
			25					30					35			

gtt	gtt	gtt	cct	ggc	acc	gga	atc	agc	gtt	gac	atc	gct	ggc	atc	gag	259
Val	Val	Val	Pro	Gly	Thr	Gly	Ile	Ser	Val	Asp	Ile	Ala	Gly	Ile	Glu	
			40				45					50				

acc	act	cca	ggt	ctt	aac	aac	gtt	cca	gga	atc	gat	cag	tgg	atc	cct	307
Thr	Thr	Pro	Gly	Leu	Asn	Asn	Val	Pro	Gly	Ile	Asp	Gln	Trp	Ile	Pro	
			55			60					65					

tcc	ctt	agc	agc	cag	gca	gct	cct	act	gct	tac	gca	gcc	gtc	att	gat	355
Ser	Leu	Ser	Ser	Gln	Ala	Ala	Pro	Thr	Ala	Tyr	Ala	Ala	Val	Ile	Asp	
					75				80						85	

gca	cct	gca	gca	cag	gct	gca	cct	gca	gca	agc	acc	ggt	cag	gca	atc	403
Ala	Pro	Ala	Ala	Gln	Ala	Ala	Pro	Ala	Ala	Ser	Thr	Gly	Gln	Ala	Ile	
				90					95					100		

gtt	gat	gca	gcg	cgc	acc	aag	att	ggt	tcc	cca	tac	ggt	tgg	ggt	gct	451
Val	Asp	Ala	Ala	Arg	Thr	Lys	Ile	Gly	Ser	Pro	Tyr	Gly	Trp	Gly	Ala	
			105				110						115			

acc	ggt	cct	aac	gct	ttc	gac	tgc	tcc	ggc	ctt	acc	tca	tgg	gca	tac	499
Thr	Gly	Pro	Asn	Ala	Phe	Asp	Cys	Ser	Gly	Leu	Thr	Ser	Trp	Ala	Tyr	
		120				125						130				

agc	cag	gtt	ggc	aag	tcc	atc	cca	cgt	acc	tcc	cag	gct	cag	gct	gca	547
Ser	Gln	Val	Gly	Lys	Ser	Ile	Pro	Arg	Thr	Ser	Gln	Ala	Gln	Ala	Ala	
		135				140					145					

cag	ggc	acc	cct	gtt	gct	tac	tct	gac	ctt	cag	gct	ggc	gac	atc	gtt	595
Gln	Gly	Thr	Pro	Val	Ala	Tyr	Ser	Asp	Leu	Gln	Ala	Gly	Asp	Ile	Val	
		150			155				160					165		

gcg	ttc	tac	tcc	ggc	gct	acc	cac	gtt	ggt	atc	tac	tcc	ggc	cac	ggc	643
Ala	Phe	Tyr	Ser	Gly	Ala	Thr	His	Val	Gly	Ile	Tyr	Ser	Gly	His	Gly	
			170						175					180		

acc	gtt	atc	cac	gca	ctg	aac	agc	agc	acc	cct	ctg	tct	gag	cac	tcc	691
Thr	Val	Ile	His	Ala	Leu	Asn	Ser	Ser	Thr	Pro	Leu	Ser	Glu	His	Ser	
			185				190						195			

ttg	gat	tac	atg	cca	ttc	cac	tct	gca	gtt	cgt	ttc	taatctgcat	737
Leu	Asp	Tyr	Met	Pro	Phe	His	Ser	Ala	Val	Arg	Phe		
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750

<210> 2600

<211> 209

<212> PRT

<213> Corynebacterium glutamicum

<400> 2600

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Ala	Ala	Ser	Ala	Val	Ala	Leu	Gly	Ala	Thr	Ala	Ala	Ile	Ala	Ser	Pro
			20					25					30		

Ala	Gln	Ala	Ala	Glu	Val	Val	Val	Pro	Gly	Thr	Gly	Ile	Ser	Val	Asp
	35					40						45			

Ile	Ala	Gly	Ile	Glu	Thr	Thr	Pro	Gly	Leu	Asn	Asn	Val	Pro	Gly	Ile
	50					55					60				

Asp	Gln	Trp	Ile	Pro	Ser	Leu	Ser	Ser	Gln	Ala	Ala	Pro	Thr	Ala	Tyr
	65				70					75					80

Ala	Ala	Val	Ile	Asp	Ala	Pro	Ala	Ala	Gln	Ala	Ala	Pro	Ala	Ala	Ser
				85					90					95	

Thr	Gly	Gln	Ala	Ile	Val	Asp	Ala	Ala	Arg	Thr	Lys	Ile	Gly	Ser	Pro
		100						105					110		

Tyr	Gly	Trp	Gly	Ala	Thr	Gly	Pro	Asn	Ala	Phe	Asp	Cys	Ser	Gly	Leu
		115					120					125			

Thr	Ser	Trp	Ala	Tyr	Ser	Gln	Val	Gly	Lys	Ser	Ile	Pro	Arg	Thr	Ser
	130					135					140				

Gln	Ala	Gln	Ala	Ala	Gln	Gly	Thr	Pro	Val	Ala	Tyr	Ser	Asp	Leu	Gln
	145					150				155					160

Ala	Gly	Asp	Ile	Val	Ala	Phe	Tyr	Ser	Gly	Ala	Thr	His	Val	Gly	Ile
			165						170					175	

Tyr	Ser	Gly	His	Gly	Thr	Val	Ile	His	Ala	Leu	Asn	Ser	Ser	Thr	Pro
			180					185						190	

Leu	Ser	Glu	His	Ser	Leu	Asp	Tyr	Met	Pro	Phe	His	Ser	Ala	Val	Arg
		195					200						205		

Phe

<210> 2601

<211> 525

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(502)

<223> RXA02152

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Met Ala Ile Tyr Arg
1 5
aag ctt gcg gct tcc gct gca gca ctg gcc ctg tcc gca tca ctg gtc 163
Lys Leu Ala Ala Ser Ala Ala Ala Leu Ala Leu Ser Ala Ser Leu Val
10 15 20
gct tgt ggc gac tct gag gac acc acc gaa gaa acc tca acc acc tct 211
Ala Cys Gly Asp Ser Glu Asp Thr Thr Glu Glu Thr Ser Thr Thr Ser
25 30 35
tct tcg acc act tcc agc tcc tcc agc tct tct agc tcc agc acc gcg 259
Ser Ser Thr Thr Ser Ser Ser Ser Ser Ser Ser Ser Thr Ala
40 45 50
gct act tcc gag gaa tct tcc gca gtt gaa gag cca gca gtg gaa gct 307
Ala Thr Ser Glu Glu Ser Ser Ala Val Glu Glu Pro Ala Val Glu Ala
55 60 65
cct gtg gaa gag gct cca gtc gag gca cct gtt gag cag gca cct gtc 355
Pro Val Glu Glu Ala Pro Val Glu Ala Pro Val Glu Gln Ala Pro Val
70 75 80 85
gtg gag caa gct cca gtt gag cag gct ccg gca ccg gtt cag gaa gca 403
Val Glu Gln Ala Pro Val Glu Gln Ala Pro Ala Pro Val Gln Glu Ala
90 95 100
cct gca cca gtc gag cag gct cca gct cca gtt cag gaa gca cct gca 451
Pro Ala Pro Val Glu Gln Ala Pro Ala Pro Val Gln Glu Ala Pro Ala
105 110 115
gct gac gcg cca cct gca ctt cca ggt ggt ggc ggc gga cac gct ggc 499
Ala Asp Ala Pro Pro Ala Leu Pro Gly Gly Gly Gly His Ala Gly
120 125 130
tac taaaaattca tgcttttacc cac 525
Tyr

<210> 2602

<211> 134

<212> PRT

<213> Corynebacterium glutamicum

<400> 2602

Met Ala Ile Tyr Arg Lys Leu Ala Ala Ser Ala Ala Ala Leu Ala Leu
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20 25 30
Thr Ser Thr Thr Ser Ser Ser Thr Thr Ser Ser Ser Ser Ser Ser
35 40 45
Ser Ser Ser Thr Ala Ala Thr Ser Glu Glu Ser Ser Ala Val Glu Glu

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Pro Ala Val Glu Ala Pro Val Glu Glu Ala Pro Val Glu Ala Pro Val
65              70              75              80
Glu Gln Ala Pro Val Val Glu Gln Ala Pro Val Glu Gln Ala Pro Ala
85              90              95
Pro Val Gln Glu Ala Pro Ala Pro Val Glu Gln Ala Pro Ala Pro Val
100             105             110
Gln Glu Ala Pro Ala Ala Asp Ala Pro Pro Ala Leu Pro Gly Gly Gly
115             120             125
Gly Gly His Ala Gly Tyr
130

<210> 2603
<211> 876
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(853)
<223> RXA02163

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caacaccacg acggggccgat tcaccccatc ctattcgcct atg gcg gtg gca aca 115
                                     Met Ala Val Ala Thr
                                     1             5
ttc gga acc atc acc gac atg ttg gaa acc aag ggg atc gtg agc aat 163
Phe Gly Thr Ile Thr Asp Met Leu Glu Thr Lys Gly Ile Val Ser Asn
10             15             20
gta ggc ggc acc gac acc atc gat ttg ggc gcg ttg ttg aat gaa acc 211
Val Gly Gly Thr Asp Thr Ile Asp Leu Gly Ala Leu Leu Asn Glu Thr
25             30             35
caa gcc gga acc cgc tgg agc gaa ctt agc ccc aac tat cag tcc aac 259
Gln Ala Gly Thr Arg Trp Ser Glu Leu Ser Pro Asn Tyr Gln Ser Asn
40             45             50
cgc gtc gtg cag att tct acc acc gat gtg cgc acc tct aac tcg gcg 307
Arg Val Val Gln Ile Ser Thr Thr Asp Val Arg Thr Ser Asn Ser Ala
55             60             65
gcc atg tac cta tca atg atg tcc tgg gtg aaa aat ggc gga aaa acg 355
Ala Met Tyr Leu Ser Met Met Ser Trp Val Lys Asn Gly Gly Lys Thr
70             75             80             85
gtg agc agc act gcg gaa gcc gat gcc atc atc cca gag ctt agc caa 403
Val Ser Ser Thr Ala Glu Ala Asp Ala Ile Ile Pro Glu Leu Ser Gln
90             95             100
ctg ttc gtg ggc cag gcc tat acc gaa agc acc tcc gcc ggc cgg ttt 451
Leu Phe Val Gly Gln Gly Tyr Thr Glu Ser Thr Ser Ala Gly Pro Phe

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105              110              115

gat gaa tac ctc tcc caa gga atg ggt tct aaa cca atg gtg atg atc 499
Asp Glu Tyr Leu Ser Gln Gly Met Gly Ser Lys Pro Met Val Met Ile
      120              125              130

tac gaa gcc cag ttc ctc gcg gaa caa aac aag gaa aac tca cgg att 547
Tyr Glu Ala Gln Phe Leu Ala Glu Gln Asn Lys Glu Asn Ser Arg Ile
      135              140              145

tcc gcc gat atg gaa cta gtg tat cca agc ccc acc gtg tac agc acg 595
Ser Gly Asp Met Glu Leu Val Tyr Pro Ser Pro Thr Val Tyr Ser Thr
      150              155              160

cat acg gtg gtt agc ttg agt gac gtc gcc gcg gag atc gcc gaa ctc 643
His Thr Val Val Ser Leu Ser Asp Val Gly Ala Glu Ile Gly Glu Leu
      170              175              180

cta gaa acc gac gaa acc ctg cag cag ttg gca gtc aaa cac ggt ttt 691
Leu Glu Thr Asp Glu Thr Leu Gln Gln Leu Ala Val Lys His Gly Phe
      185              190              195

agg cca aag aac tcc gca atg atc gcc gat gct gcc atg acc gac cgc 739
Arg Pro Lys Asn Ser Ala Met Ile Ala Asp Ala Gly Met Thr Asp Arg
      200              205              210

atg ccc aac aac ctc aat gtc att gat ccg ccg gac tat gac ttc cta 787
Met Pro Asn Asn Leu Asn Val Ile Asp Pro Pro Asp Tyr Asp Phe Leu
      215              220              225

gaa cga ctc att gat gcc gtg gcc gca tcg tac agt gcc acc cca gca 835
Glu Arg Leu Ile Asp Gly Val Gly Ala Ser Tyr Ser Ala Thr Pro Ala
      230              235              240

gaa gag gac aca gat cta tgaaaaatct tgtaaaagggt aca 876
Glu Glu Asp Thr Asp Leu
      250

<210> 2604
<211> 251
<212> PRT
<213> Corynebacterium glutamicum

<400> 2604
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Gly Ile Val Ser Asn Val Gly Gly Thr Asp Thr Ile Asp Leu Gly Ala
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Leu Leu Asn Glu Thr Gln Ala Gly Thr Arg Trp Ser Glu Leu Ser Pro
      35              40              45

Asn Tyr Gln Ser Asn Arg Val Val Gln Ile Ser Thr Thr Asp Val Arg
      50              55              60

Thr Ser Asn Ser Ala Ala Met Tyr Leu Ser Met Met Ser Trp Val Lys
      65              70              75              80

Asn Gly Gly Lys Thr Val Ser Ser Thr Ala Glu Ala Asp Ala Ile Ile

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	85	90	95
Pro Glu Leu Ser Gln Leu Phe Val Gly Gln Gly Tyr Thr Glu Ser Thr	100	105	110
Ser Ala Gly Pro Phe Asp Glu Tyr Leu Ser Gln Gly Met Gly Ser Lys	115	120	125
Pro Met Val Met Ile Tyr Glu Ala Gln Phe Leu Ala Glu Gln Asn Lys	130	135	140
Glu Asn Ser Arg Ile Ser Gly Asp Met Glu Leu Val Tyr Pro Ser Pro	145	150	155
Thr Val Tyr Ser Thr His Thr Val Val Ser Leu Ser Asp Val Gly Ala	165	170	175
Glu Ile Gly Glu Leu Leu Glu Thr Asp Glu Thr Leu Gln Gln Leu Ala	180	185	190
Val Lys His Gly Phe Arg Pro Lys Asn Ser Ala Met Ile Ala Asp Ala	195	200	205
Gly Met Thr Asp Arg Met Pro Asn Asn Leu Asn Val Ile Asp Pro Pro	210	215	220
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Ser Ala Thr Pro Ala Glu Glu Asp Thr Asp Leu	245	250	
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Met Lys Asn Leu Val	5		
aaa ggt aca gcg ctg ggc ttg agc ttg gtg ctt ctg gca ggt tgt tca	163		
Lys Gly Thr Ala Leu Gly Leu Ser Leu Val Leu Leu Ala Gly Cys Ser	10	15	20
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Thr Val Ser Asp Ser Ile Asp Ser Leu Gly Gly Gly Leu Gly Gly Ser	25	30	35
tct gag act ttg aag att gtg gcc gcc aca gag ctg gaa gat ctg cag	259		
Ser Glu Thr Leu Lys Ile Val Ala Ala Thr Glu Leu Glu Asp Leu Gln	40	45	50

ccc gcg atc gag caa gcc tcc gac gac ttg ggt ttt gat att gaa ctg	307
Pro Ala Ile Glu Gln Ala Ser Asp Asp Leu Gly Phe Asp Ile Glu Leu	
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agc ttt cca ggc ggc aca ctc agc aac agc caa gcc ctc atg gat ggc	355
Ser Phe Pro Gly Gly Thr Leu Ser Asn Ser Gln Ala Leu Met Asp Gly	
70 75 80 85	
gct ttt gac cag gac tat gat gcc acc tgg ttt gcc acc aac cgt tac	403
Ala Phe Asp Gln Asp Tyr Asp Ala Thr Trp Phe Ala Thr Asn Arg Tyr	
90 95 100	
gtc gat ctg atc ggc gct tcc aac aag ctg ggg gag acc acc aaa atc	451
Val Asp Leu Ile Gly Ala Ser Asn Lys Leu Gly Glu Thr Thr Lys Ile	
105 110 115	
gcg acc tct ccc gtg gcg ttc ggt gtg aaa act tcc atg gcc cag gag	499
Ala Thr Ser Pro Val Ala Phe Gly Val Lys Thr Ser Met Ala Gln Glu	
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ctc ggc tgg gat cag cgc cag cca acc tgg gaa gag ctg ggc cag gcc	547
Leu Gly Trp Asp Gln Arg Gln Pro Thr Trp Glu Glu Leu Gly Gln Ala	
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Ser Gln Thr Gln Asp Phe Thr Phe Gly Met Thr Asp Pro Ala Thr Ser	
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Asn Ser Gly Phe Ser Ala Leu Val Ala Met Ala Thr Ala Tyr Ala Asp	
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acc ggc cag gcc tta aca acc aac gac atc ccc gcg atc gcc gag ccg	691
Thr Gly Gln Ala Leu Thr Thr Asn Asp Ile Pro Ala Ile Ala Glu Pro	
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Met Ser Thr Ser Leu Ser Gly Gln Thr Ile Thr Ser Gly Ser Ser Gly	
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Trp Leu Lys Asp Thr Phe Leu Glu Gln Pro Asp Arg Ala Asn Ala Ile	
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Ile Asn Tyr Glu Ser Val Leu His Thr Met Ile Ser Glu Asp Gly Ala	
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Asp Ile Thr Val Val Val Pro Ala Asp Gly Val Val Ser Ala Asp Tyr	
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Pro Leu Ser Thr Ile Thr Gly Ser Asp Gln Gly Glu His Val Ala Glu	
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Leu Ala Gly Trp Phe Ala Glu His Pro Asp Ala Leu Thr Asp Thr Tyr	
280 285 290	

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Arg Arg Pro Thr Thr Ala Asn Ala Thr Leu Pro Ala Glu Leu Ser Ser	
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Gln Thr Ile Ile Glu Ala Pro Phe Pro Gly Ser Lys Thr Val Thr Asp	
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Ala Leu Ile Asp Ala Tyr Thr Asn Gln Phe Arg Val Pro Gly Glu Thr	
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Thr Phe Val Leu Asp Val Ser Gly Ser Met Leu Gly Gln Arg Ile Thr	
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Leu Leu Lys Asp Thr Met Ser Asp Leu Ile Ser Gly Glu Ala Thr Thr	
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Asp Leu Ala Asn Val Ser Leu Arg Asp Arg Glu Lys Val Ser Ile Ile	
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Pro Phe Ser Phe Gly Pro His Glu Val Ile Ser Glu Thr Leu Gly Ala	
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Gln Ala Asp Gly Gly Thr Gly Ile Tyr Asp Ala Val Leu Ala Ala Tyr	
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Ala Glu Ser Ala Gly Gly Asp Tyr Ile Pro Ser Ile Val Leu Met Thr	
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Asp Gly Glu Leu Thr Ala Gly Arg Thr Tyr Asp Phe Leu Thr Glu	
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Trp Asn Ala Leu Pro Ser Asn Ile Arg Ser Ile Pro Val Phe Val Ile	
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Leu Tyr Gly Glu Ala Asn Val Ala Asp Met Glu Gln Leu Ala Ala Thr	
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Thr Gly Gly Glu Thr Phe Asp Ala Ile Asn Gly Asp Leu Asp Glu Ala	
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<211> 525

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2606

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50 55 60Phe Asp Ile Glu Leu Ser Phe Pro Gly Gly Thr Leu Ser Asn Ser Gln
65 70 75 80Ala Leu Met Asp Gly Ala Phe Asp Gln Asp Tyr Asp Ala Thr Trp Phe
85 90 95Ala Thr Asn Arg Tyr Val Asp Leu Ile Gly Ala Ser Asn Lys Leu Gly
100 105 110Glu Thr Thr Lys Ile Ala Thr Ser Pro Val Ala Phe Gly Val Lys Thr
115 120 125Ser Met Ala Gln Glu Leu Gly Trp Asp Gln Arg Gln Pro Thr Trp Glu
130 135 140Glu Leu Gly Gln Ala Ser Gln Thr Gln Asp Phe Thr Phe Gly Met Thr
145 150 155 160Asp Pro Ala Thr Ser Asn Ser Gly Phe Ser Ala Leu Val Ala Met Ala
165 170 175Thr Ala Tyr Ala Asp Thr Gly Gln Ala Leu Thr Thr Asn Asp Ile Pro
180 185 190Ala Ile Ala Glu Pro Met Ser Thr Ser Leu Ser Gly Gln Thr Ile Thr
195 200Ser Gly Ser Ser Gly Trp Leu Lys Asp Thr Phe Leu Glu Gln Pro Asp
210 215 220Arg Ala Asn Ala Ile Ile Asn Tyr Glu Ser Val Leu His Thr Met Ile
225 230 235 240Ser Glu Asp Gly Ala Asp Ile Thr Val Val Val Pro Ala Asp Gly Val
245 250 255Val Ser Ala Asp Tyr Pro Leu Ser Thr Ile Thr Gly Ser Asp Gln Gly
260 265 270Glu His Val Ala Glu Leu Ala Gly Trp Phe Ala Glu His Pro Asp Ala
275 280 285

Leu Thr Asp Thr Tyr Arg Arg Pro Thr Thr Ala Asn Ala Thr Leu Pro

290	295	300
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Lys Thr Val Thr Asp 325	Ala Leu Ile Asp 330	Ala Tyr Thr Asn Gln Phe Arg 335
Val Pro Gly Glu Thr Thr 340	Phe Val Leu Asp Val 345	Ser Gly Ser Met Leu 350
Gly Gln Arg Ile Thr 355	Leu Leu Lys Asp Thr 360	Met Ser Asp Leu Ile Ser 365
Gly Gly Ala Thr Thr 370	Asp Leu Ala Asn Val 375	Ser Leu Arg Asp Arg Glu 380
Lys Val Ser Ile Ile 385	Pro Phe Ser Phe 390	Gly Pro His Glu Val Ile Ser 395
Glu Thr Leu Gly Ala 405	Val Gly Ser Pro 410	Ser Arg Thr Asp Leu Gln 415
Arg Val Glu Ala Leu 420	Gln Ala Asp Gly 425	Gly Thr Gly Ile Tyr Asp Ala 430
Val Leu Ala Ala Tyr 435	Ala Glu Ser Ala 440	Gly Gly Asp Tyr Ile Pro Ser 445
Ile Val Leu Met Thr 450	Asp Gly Glu Leu 455	Thr Ala Gly Arg Thr Tyr Asp 460
Gln Phe Leu Thr Glu 465	Trp Asn Ala Leu 470	Pro Ser Asn Ile Arg Ser Ile 475
Pro Val Phe Val Ile 485	Leu Tyr Gly Glu 490	Ala Asn Val Ala Asp Met Glu 495
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Asp Leu Asp Glu Ala 515	Phe Lys Glu Ile 520	Arg Ala Tyr Gln 525

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<212> DNA

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Val Pro Thr Asn Asn
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 Gly Gly Ser Phe Phe Phe Ser Arg Lys Asn Leu Ala Gly Ile Ala Ile
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 Ala Thr Leu Ile Ile Ala Leu His Leu Val Ile Gly Leu Gly Ala Phe
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 Trp Pro Val Val Ala Ile Ala Gly Tyr Gly Ala Ala Val Ala Leu Thr
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 Pro Lys Asn Pro Pro Lys Lys Glu Leu Pro Pro Val Glu Ala Thr Pro
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 Glu Leu Asp Ser Pro Gly Leu Leu Ala Ala Arg Ser Gln Glu Leu Val
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 Arg Thr Met Tyr Ser His Gly Ala Ala Ala Pro Val Ile Glu Ala Ile
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aag agg cta gac agc tca ctg caa ttg gtc att ggt aac tgg aca agc 451
 Lys Arg Leu Asp Ser Ser Leu Gln Leu Val Ile Gly Asn Trp Thr Ser
 105 110 115

ctg acc aat ttt ccc gag cac caa gtc acc att cgc tca att atc aac 499
 Leu Thr Asn Phe Pro Glu His Gln Val Thr Ile Arg Ser Ile Ile Asn
 120 125 130

cag tac atc cca gcc att atc gac gct tac ctg aag atc ccc acc cgc 547
 Gln Tyr Ile Pro Gly Ile Ile Asp Ala Tyr Leu Lys Ile Pro Thr Arg
 135 140 145

aac gat cct cgg gca gtc gaa gac ctc att gaa tcc ttc gac ctc ctg 595
 Asn Asp Pro Arg Ala Val Glu Asp Leu Ile Glu Ser Phe Asp Leu Leu
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 Asn Ser Glu Thr Met Lys Ile Phe Asn Ala Ile Gln Glu Gln Gly Leu
 170 175 180

aat aac ctt gaa gat cac ggt cgc gca ctg cgc atg caa ttt ggt caa 691
 Asn Asn Leu Glu Asp His Gly Arg Ala Leu Arg Met Gln Phe Gly Gln
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<211> 204

<212> PRT

<213> Corynebacterium glutamicum

<400> 2608

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Gly Leu Gly Ala Phe Trp Pro Val Val Ala Ile Ala Gly Tyr Gly Ala
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Ala Val Ala Leu Thr Pro Lys Asn Pro Pro Lys Lys Glu Leu Pro Pro
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Val Gln Ala Thr Pro Glu Leu Asp Ser Pro Gly Leu Leu Ala Ala Arg
      65           70           75           80
Ser Gln Glu Leu Val Arg Thr Met Tyr Ser His Gly Ala Ala Ala Pro
      85           90           95
Val Ile Glu Ala Ile Lys Arg Leu Asp Ser Ser Leu Gln Leu Val Ile
      100          105          110
Gly Asn Trp Thr Ser Leu Thr Asn Phe Pro Glu His Gln Val Thr Ile
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Arg Ser Ile Ile Asn Gln Tyr Ile Pro Gly Ile Ile Asp Ala Tyr Leu
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Lys Ile Pro Thr Arg Asn Asp Pro Arg Ala Val Glu Asp Leu Ile Glu
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Ser Phe Asp Leu Leu Asn Ser Glu Thr Met Lys Ile Phe Asn Ala Ile
      165          170          175
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Met Ser Leu Asp Pro
1 5
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Gln Leu Leu Glu Val Leu Ala Cys Pro Lys Asp Lys Gly Pro Leu Arg
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tat ctg gag agc gaa cag ctc ttg gtc aac gaa cgc ctc aac ctg gcc 211

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Tyr Leu Glu Ser Glu Gln Leu Leu Val Asn Glu Arg Leu Asn Leu Ala
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Tyr Arg Ile Asp Asp Gly Ile Pro Val Leu Leu Ile Asp Glu Ala Thr
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Leu Thr Pro Leu His Ser Phe Lys Glu Pro Ala Ile Leu Tyr Ala Gly
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cag gct tct gcc tgg cag cag gtg atc gct gat tcc agc gaa gac cac 211
Gln Ala Ser Ala Trp Gln Gln Val Ile Ala Asp Ser Ser Glu Asp His
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atc acc gca acg cac ctg cgc gag ctc ctg tct cgc tcc cgt gca aag 259
Ile Thr Ala Thr His Leu Arg Glu Leu Leu Ser Arg Ser Arg Ala Lys
      40                      45                      50

act gca cct ttc gct cgc caa atc acc gcc atc gtg cct ggc tca ctt 307

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Asp	Asn	Glu	Glu	Asp	Val	Leu	Ala	Phe	Ala	Ile	Leu	Leu	Gly	Ala	Ala	
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Leu	Ser	Arg	Glu	Ile	Ile	Gln	Asp	Thr	Ile	Ala	Gly	Val	Asp	Gly	Val	
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Glu	Val	Ser	Leu	Arg	Asn	Ala	Arg	Ala	His	Phe	Val	Val	Ser	Gly	Lys	
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Pro	Glu	Ala	Leu	Lys	Lys	Ala	Ala	Ala	Leu	Gln	Arg	Ala	Ala	Asp		
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Met Ile Gly Gly Gly Ile Gly Thr Pro Ala Lys Ala Ala Tyr Tyr Leu	
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acc ggt gaa tgg tcc acc gat ttg ggc ttc cca gca atg cca gtg gac	1843
Thr Gly Glu Trp Ser Thr Asp Leu Gly Phe Pro Ala Met Pro Val Asp	
570 575 580	
ggc atc ctc gtg ggt acc gct gcc atg gca acc aag gaa gca acc act	1891
Gly Ile Leu Val Gly Thr Ala Ala Met Ala Thr Lys Glu Ala Thr Thr	
585 590 595	
tct cct cag gtc aag cag gca ctg gtc gac acc cca ggt gtt gat cca	1939
Ser Pro Gln Val Lys Gln Ala Leu Val Asp Thr Pro Gly Val Asp Pro	
600 605 610	
cac gac gct ggc ggc tgg gtt ggc cgt ggc gat gct cgt ggt ggc gtg	1987
His Asp Ala Gly Gly Trp Val Gly Arg Gly Asp Ala Arg Gly Gly Val	
615 620 625	
acc tct ggt ctg tca cac ctg cac gct gac atg tac gag ctg gac aac	2035
Thr Ser Gly Leu Ser His Leu His Ala Asp Met Tyr Glu Leu Asp Asn	
630 635 640 645	
gat tct gct gca gct tcc cgc ctg atc tct tcc atc gat tct gat gat	2083
Asp Ser Ala Ala Ala Ser Arg Leu Ile Ser Ser Ile Asp Ser Asp Asp	
650 655 660	
tac gca gat cac cgc gaa gag ctc atc gag gct atc aac aag acc gct	2131
Tyr Ala Asp His Arg Glu Leu Ile Glu Ala Ile Asn Lys Thr Ala	
665 670 675	
aag cct ttc ttc ggc gag gtc gaa gag atg act tac gca gag tgg atc	2179
Lys Pro Phe Phe Gly Glu Val Glu Glu Met Thr Tyr Ala Glu Trp Ile	
680 685 690	
cag cgt tgg gtt gag ctt gct tac cca act cag gac cca acc tgg gat	2227
Gln Arg Trp Val Glu Leu Ala Tyr Pro Thr Gln Asp Pro Thr Trp Asp	
695 700 705	
gat cgt ttc ctc gat ttg gtt cac cgc att gaa gct cgt ctc aac gag	2275
Asp Arg Phe Leu Asp Leu Val His Arg Ile Glu Ala Arg Leu Asn Glu	
710 715 720 725	
gca gag cac ggc gcc atc acc aca ctg ttc cca gac cat gcg tct gtg	2323
Ala Glu His Gly Ala Ile Thr Thr Leu Phe Pro Asp His Ala Ser Val	
730 735 740	
gaa aat gag gaa gag gcc gtc gaa aag ctt ctt gct gct tac ccg cag	2371
Glu Asn Glu Glu Glu Ala Val Glu Lys Leu Leu Ala Ala Tyr Pro Gln	
745 750 755	
gcc cgc gag atc cag gtc tct gcg cgc gac gcc gcg tgg ttt att ggt	2419
Ala Arg Glu Ile Gln Val Ser Ala Arg Asp Ala Ala Trp Phe Ile Gly	
760 765 770	
ctg tgc cgc aag cac cac aag cct atg cct tgg gtt cca gca atc gat	2467
Leu Cys Arg Lys His His Lys Pro Met Pro Trp Val Pro Ala Ile Asp	
775 780 785	

gct gac cta gca cgc tgg tgg ggc ctt gac acc ctg tgg cag tcc cag 2515
 Ala Asp Leu Ala Arg Trp Trp Gly Leu Asp Thr Leu Trp Gln Ser Gln
 790 795 800 805

aac gag cgc tac ggc gcg aac tca gtc cgc gtt atc cca gga cca gtc 2563
 Asn Glu Arg Tyr Gly Ala Asn Ser Val Arg Val Ile Pro Gly Pro Val
 810 815 820

tcc gtc gcc ggc atc gac cgt gtt gac gag cca gtt gca gag ctg ctc 2611
 Ser Val Ala Gly Ile Asp Arg Val Asp Glu Pro Val Ala Glu Leu Leu
 825 830 835

ggc cgc ttc gaa gct gcc tgc gtt gac gct ctc gac ggc gag cca gaa 2659
 Gly Arg Phe Glu Ala Ala Cys Val Asp Ala Leu Asp Gly Glu Pro Glu
 840 845 850

gag atc ttc gct cgc ctc aat gac tcc aag aac gag cgc gaa ttc ctg 2707
 Glu Ile Phe Ala Arg Leu Asn Glu Ser Lys Asn Glu Arg Glu Phe Leu
 855 860 865

ctg gct acc cca cac atc gtg tgg cac ggc aac ctg atc gac aac cca 2755
 Leu Ala Thr Pro His Ile Val Trp His Gly Asn Leu Ile Asp Asn Pro
 870 875 880 885

gct cac gtc ctc aac gag ggt gct ttc gag ctc atc gag gag gat ggc 2803
 Ala His Val Leu Asn Glu Gly Ala Phe Glu Leu Ile Glu Glu Asp Gly
 890 895 900

tac tgg gtc atc cgt atc ctg gct gat tcc tac ttc gac gat ctg cca 2851
 Tyr Trp Val Ile Arg Ile Leu Ala Asp Ser Tyr Phe Asp Asp Leu Pro
 905 910 915

gtt gag cag cgc cca tac ctg gtt cag cat gtt gac atc cca gtt gag 2899
 Val Glu Gln Arg Pro Tyr Leu Val Gln His Val Asp Ile Pro Val Glu
 920 925 930

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 Leu Gly Asp Ala Gly
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<210> 2612

<211> 938

<212> PRT

<213> Corynebacterium glutamicum

<400> 2612

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Ile Leu Tyr Ala Gly Gln Ala Ser Ala Trp Gln Gln Val Ile Ala Asp
 20 25 30

Ser Ser Glu Asp His Ile Thr Ala Thr His Leu Arg Glu Leu Leu Ser
 35 40 45

Arg Ser Arg Ala Lys Thr Ala Pro Phe Ala Arg Gln Ile Thr Ala Ile
 50 55 60

Val Pro Gly Ser Leu Ala Arg Leu Glu Glu Leu Thr Arg Glu Asp Ala
 65 70 75 80

Gln Ile Gly Ala Asp Ile Asp Ala Gln Pro Ala Val Ser Ile Pro Gly
 85 90 95
 Ile Leu Leu Gly Gln Ile Ala Ala Thr Arg Gln Leu Arg Asp Leu Gly
 100 105 110
 Leu Asp Val Ala Ala Ala Ser Arg Leu Gly His Ser Gln Gly Ile Leu
 115 120 125
 Gly Val Glu Ala Val Asp Asn Glu Glu Asp Val Leu Ala Phe Ala Ile
 130 135 140
 Leu Leu Gly Ala Ala Ala Ser Gln Phe Ala Gly Lys Gly Ala His Met
 145 150 155 160
 Leu Ser Val Arg Gly Leu Ser Arg Glu Ile Ile Gln Asp Thr Ile Ala
 165 170 175
 Gly Val Asp Gly Val Glu Val Ser Leu Arg Asn Ala Arg Ala His Phe
 180 185 190
 Val Val Ser Gly Lys Pro Glu Ala Leu Lys Lys Ala Ala Ala Ala Leu
 195 200 205
 Gln Arg Ala Ala Asp Val Tyr Asn Glu Asp Ile Asn Glu Lys Arg Lys
 210 215 220
 Gly Gly Ser Leu Ala Glu Pro Lys Phe Asp Tyr Leu Asp Val Ala Ile
 225 230 235 240
 Pro Phe His His Ser Ser Met Gln Asp Ala Ala Asp Leu Ala Val Glu
 245 250 255
 Trp Ala Thr Thr Cys Gly Leu Asn Val Asn Ala Arg Ala Leu Ala Glu
 260 265 270
 Ala Ile Leu Val Asn Pro Ala Asp Trp Val Glu Gln Ile Ala Asn Leu
 275 280 285
 Lys Ala Asp Tyr Val Leu Ser Leu Asp Ala Gly Val Ser Arg Phe Thr
 290 295 300
 Ala Pro Leu Leu Asp Gly Arg Gly Ile Ser Leu Val Pro Ala Phe Ser
 305 310 315 320
 Ala Ala Glu Arg Asp Asn Leu Ala Arg Pro Gly Phe His Val Pro Thr
 325 330 335
 Ala Glu Asp Trp Ser Glu Phe Ala Pro Lys Leu Val Lys Leu Pro Asn
 340 345 350
 Gly Glu His Lys Val Leu Thr Gly Phe Ser Arg Leu Thr Gly Tyr Ser
 355 360 365
 Pro Ile Val Leu Ala Gly Met Thr Pro Thr Thr Val Asp Pro Glu Ile
 370 375 380
 Val Ala Ala Ala Ala Asn Ala Gly His Trp Ala Glu Met Ala Gly Gly
 385 390 395 400

Gly Gln Tyr Ser Glu Glu Val Phe Thr Lys Asn Lys Glu Lys Leu Val
 405 410 415
 Ser Leu Leu Lys Val Gly Arg Ser Ala Gln Phe Asn Ser Met Phe Phe
 420 425 430
 Asp Arg Tyr Met Trp Asn Leu Gln Phe Gly Ala Gln Arg Ile Val Ser
 435 440 445
 Lys Ala Arg Ala Thr Gly Thr Ser Ile Asn Gly Val Val Val Ser Ala
 450 455 460
 Gly Ile Pro Glu Val Glu Glu Ala Thr Glu Leu Ile Asn Asp Leu Asn
 465 470 475 480
 Ala Asp Gly Phe Pro Tyr Val Ala Phe Lys Pro Gly Thr Val Asp Gln
 485 490 495
 Ile Arg Ala Thr Leu Lys Ile Ala Asp Ala Asn Pro Glu Thr Lys Ile
 500 505 510
 Ile Ile Gln Ile Glu Asp Gly His Ala Gly Gly His His Ser Trp Val
 515 520 525
 Asn Leu Asp Asp Leu Leu Leu Thr Thr Tyr Ala Glu Leu Arg Ser Arg
 530 535 540
 Lys Asn Val Val Val Met Ile Gly Gly Gly Ile Gly Thr Pro Ala Lys
 545 550 555 560
 Ala Ala Tyr Tyr Leu Thr Gly Glu Trp Ser Thr Asp Leu Gly Phe Pro
 565 570 575
 Ala Met Pro Val Asp Gly Ile Leu Val Gly Thr Ala Ala Met Ala Thr
 580 585 590
 Lys Glu Ala Thr Thr Ser Pro Gln Val Lys Gln Ala Leu Val Asp Thr
 595 600 605
 Pro Gly Val Asp Pro His Asp Ala Gly Gly Trp Val Gly Arg Gly Asp
 610 615 620
 Ala Arg Gly Gly Val Thr Ser Gly Leu Ser His Leu His Ala Asp Met
 625 630 635 640
 Tyr Glu Leu Asp Asn Asp Ser Ala Ala Ala Ser Arg Leu Ile Ser Ser
 645 650 655
 Ile Asp Ser Asp Asp Tyr Ala Asp His Arg Glu Glu Leu Ile Glu Ala
 660 665 670
 Ile Asn Lys Thr Ala Lys Pro Phe Phe Gly Glu Val Glu Glu Met Thr
 675 680 685
 Tyr Ala Glu Trp Ile Gln Arg Trp Val Glu Leu Ala Tyr Pro Thr Gln
 690 695 700
 Asp Pro Thr Trp Asp Asp Arg Phe Leu Asp Leu Val His Arg Ile Glu
 705 710 715 720
 Ala Arg Leu Asn Glu Ala Glu His Gly Ala Ile Thr Thr Leu Phe Pro

725 730 735
 Asp His Ala Ser Val Glu Asn Glu Glu Glu Ala Val Glu Lys Leu Leu
 740 745
 Ala Ala Tyr Pro Gln Ala Arg Glu Ile Gln Val Ser Ala Arg Asp Ala
 755 760 765
 Ala Trp Phe Ile Gly Leu Cys Arg Lys His His Lys Pro Met Pro Trp
 770 775 780
 Val Pro Ala Ile Asp Ala Asp Leu Ala Arg Trp Trp Gly Leu Asp Thr
 785 790 795 800
 Leu Trp Gln Ser Gln Asn Glu Arg Tyr Gly Ala Asn Ser Val Arg Val
 805 810 815
 Ile Pro Gly Pro Val Ser Val Ala Gly Ile Asp Arg Val Asp Glu Pro
 820 825 830
 Val Ala Glu Leu Leu Gly Arg Phe Glu Ala Ala Cys Val Asp Ala Leu
 835 840 845
 Asp Gly Glu Pro Glu Glu Ile Phe Ala Arg Leu Asn Glu Ser Lys Asn
 850 855 860
 Glu Arg Glu Phe Leu Leu Ala Thr Pro His Ile Val Trp His Gly Asn
 865 870 875 880
 Leu Ile Asp Asn Pro Ala His Val Leu Asn Glu Gly Ala Phe Glu Leu
 885 890 895
 Ile Glu Glu Asp Gly Tyr Trp Val Ile Arg Ile Leu Ala Asp Ser Tyr
 900 905 910
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 915 920 925
 Asp Ile Pro Val Glu Leu Gly Asp Ala Gly
 930 935

<210> 2613

<211> 897

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(874)

<223> RXA02170

<400> 2613

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 Val Ser Thr Val Leu
 1 5

 tta gca gga gta gtt att att ggc gga att ttt act ctc cct cag aag 163
 Leu Ala Gly Val Val Ile Ile Gly Gly Ile Phe Thr Leu Pro Gln Lys

	10	15	20	
	gag gaa gta aag gtt tcc	gaa ttg cag cca cag gcc agc gct gca tcc	211	
	Glu Glu Val Lys Val Ser	Glu Leu Gln Pro Gln Ala Ser		
	25	30	35	
	atc ccg tct tca tct tcc	aca gct ggg aaa gca gtg gaa gaa agc cct	259	
	Ile Pro Ser Ser Ser Ser	Thr Ala Gly Lys Ala Val Glu Glu Ser Pro		
	40	45	50	
	cta acg cag ttt gtg gaa aac tgg aca ggc tcc caa att acg tac atg	307		
	Leu Thr Gln Phe Val Glu Asn Ser Thr Gly Ser Gln Ile Thr Tyr Met			
	55	60	65	
	agc ctg aaa gac gat ttc cat act ggc acg tct acg gaa cgt ttt gcg	355		
	Ser Leu Lys Asp Asp Phe His Thr Gly Thr Ser Thr Glu Arg Phe Ala			
	70	75	80	85
	cgc cca gcg tta agt ttg tct aag ctg tac atc gct gaa tat gtg ctg	403		
	Arg Pro Ala Leu Ser Lys Leu Ser Lys Ile Ala Glu Tyr Val Leu			
	90	95	100	
	gag cac ggc acg aat aat gag aag tct ttg gcg atg gaa atg atc aaa	451		
	Glu His Gly Thr Asn Asn Glu Lys Ser Leu Ala Met Glu Met Ile Lys			
	105	110	115	
	gat tcc tcc gac gta tcc gcc gaa atc ttg tat gag gcg tac cca gaa	499		
	Asp Ser Ser Asp Val Ser Ala Glu Ile Leu Tyr Glu Ala Tyr Pro Glu			
	120	125	130	
	tca att gag gag att gcg gat caa tac gga ttg ctg tcc aca agg gga	547		
	Ser Ile Glu Glu Ile Ala Asp Gln Tyr Gly Leu Leu Ser Thr Arg Gly			
	135	140	145	
	gac gcg cac tgg gga tac tgg gtg aca tcc act tac gat ttg gtg aaa	595		
	Asp Ala His Trp Gly Tyr Ser Val Thr Ser Thr Tyr Asp Leu Val Lys			
	150	155	160	165
	ttt gtc agc gct ctg att atc gat gat cca gat tca ccg atc ctt gaa	643		
	Phe Val Ser Ala Leu Ile Ile Asp Asp Pro Asp Ser Pro Ile Leu Glu			
	170	175	180	
	gcg atg cgt aat gcc agc gca gtc gcg gct gac ggt tat ccg caa gac	691		
	Ala Met Arg Asn Ala Ser Ala Val Ala Ala Asp Gly Tyr Pro Gln Asp			
	185	190	195	
	tgg ggg aca gcg gtg ctt gat gag gca gaa gga tcc aaa tgg gga tgg	739		
	Trp Gly Thr Ala Val Leu Asp Glu Ala Glu Gly Ser Lys Trp Gly Trp			
	200	205	210	
	tct gat gat ctg atg ctg cac tcc tct gtg acc ttt ggc gaa gac tat	787		
	Ser Asp Asp Leu Met Leu His Ser Ser Val Thr Phe Gly Glu Asp Tyr			
	215	220	225	
	gtt gtg gca gct gct gtg act gga tca aaa gaa gac ctg acc caa ttg	835		
	Val Val Ala Ala Ala Val Thr Gly Ser Lys Glu Asp Leu Thr Gln Leu			
	230	235	240	245
	gtg gaa aac caa ttg ggt gag gtt gtg agt cag cac ggc tagtttagct	884		
	Val Glu Asn Gln Leu Gly Glu Val Val Ser Gln His Gly			
	250	255		

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897

<210> 2614

<211> 258

<212> PRT

<213> Corynebacterium glutamicum

<400> 2614

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			20					25					30		

Ala	Ser	Ala	Ala	Ser	Ile	Pro	Ser	Ser	Ser	Ser	Thr	Ala	Gly	Lys	Ala
		35					40					45			

Val	Glu	Glu	Ser	Pro	Leu	Thr	Gln	Phe	Val	Glu	Asn	Ser	Thr	Gly	Ser
	50					55					60				

Gln	Ile	Thr	Tyr	Met	Ser	Leu	Lys	Asp	Asp	Phe	His	Thr	Gly	Thr	Ser
65					70					75					80

Thr	Glu	Arg	Phe	Ala	Arg	Pro	Ala	Leu	Ser	Leu	Ser	Lys	Leu	Tyr	Ile
			85					90						95	

Ala	Glu	Tyr	Val	Leu	Glu	His	Gly	Thr	Asn	Asn	Glu	Lys	Ser	Leu	Ala
			100				105						110		

Met	Glu	Met	Ile	Lys	Asp	Ser	Ser	Asp	Val	Ser	Ala	Glu	Ile	Leu	Tyr
		115				120					125				

Glu	Ala	Tyr	Pro	Glu	Ser	Ile	Glu	Glu	Ile	Ala	Asp	Gln	Tyr	Gly	Leu
	130					135					140				

Leu	Ser	Thr	Arg	Gly	Asp	Ala	His	Trp	Gly	Tyr	Ser	Val	Thr	Ser	Thr
145				150					155					160	

Tyr	Asp	Leu	Val	Lys	Phe	Val	Ser	Ala	Leu	Ile	Ile	Asp	Asp	Pro	Asp
		165							170					175	

Ser	Pro	Ile	Leu	Glu	Ala	Met	Arg	Asn	Ala	Ser	Ala	Val	Ala	Ala	Asp
		180					185						190		

Gly	Tyr	Pro	Gln	Asp	Trp	Gly	Thr	Ala	Val	Leu	Asp	Glu	Ala	Glu	Gly
		195				200					205				

Ser	Lys	Trp	Gly	Trp	Ser	Asp	Asp	Leu	Met	Leu	His	Ser	Ser	Val	Thr
	210				215						220				

Phe	Gly	Glu	Asp	Tyr	Val	Val	Ala	Ala	Ala	Val	Thr	Gly	Ser	Lys	Glu
225					230					235					240

Asp	Leu	Thr	Gln	Leu	Val	Glu	Asn	Gln	Leu	Gly	Glu	Val	Val	Ser	Gln
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His Gly

<210> 2615
 <211> 462
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(439)
 <223> RXA02172

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 Val Asn Ala Glu Gln
 1 5
 atc acc cag ggg cgt cgc cag ccg acg gct caa gag ttt cgg gac atg 163
 Ile Thr Gln Gly Arg Arg Gln Pro Thr Ala Gln Glu Phe Arg Asp Met
 10 15 20
 cag cgc agc cca gaa ttt gga gag ctg cgc agc aag ttc cgt tcc ttt 211
 Gln Ala Ser Pro Glu Phe Gly Glu Leu Arg Ser Lys Phe Arg Ser Phe
 25 30 35
 gct ttc cca atg acc gtt gcc ttc ttc ttg tgg tac gtc gtc tac gtt 259
 Ala Phe Pro Met Thr Val Ala Phe Phe Leu Trp Tyr Val Val Tyr Val
 40 45 50
 ctg gtt gca tcc ttt gca tca gag tgg atg gca acc cca gtt ttc ggc 307
 Leu Val Ala Ser Phe Ala Ser Glu Trp Met Ala Thr Pro Val Phe Gly
 55 60 65
 gca atc aac att ggc cta atc ttc ggc ttc ctt cag ttc gta acc aca 355
 Ala Ile Asn Ile Gly Leu Ile Phe Gly Phe Leu Gln Phe Val Thr Thr
 70 75 80 85
 ttc gtc att act tac atc tat gtc atg ttt gcg aac aag aac ttg gag 403
 Phe Val Ile Thr Tyr Ile Tyr Val Met Phe Ala Asn Lys Asn Leu Glu
 90 95 100
 cct cgt cag gct gct att cgc cag aag atg gaa ggt taatcagata 449
 Pro Arg Gln Ala Ala Ile Arg Gln Lys Met Glu Gly
 105 110
 tgaattccac tat 462

<210> 2616
 <211> 113
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2616
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Lys Phe Arg Ser Phe Ala Phe Pro Met Thr Val Ala Phe Phe Leu Trp
 35 40 45
 Tyr Val Val Tyr Val Leu Val Ala Ser Phe Ala Ser Glu Trp Met Ala
 50 55 60
 Thr Pro Val Phe Gly Ala Ile Asn Ile Gly Leu Ile Phe Gly Phe Leu
 65 70 75 80
 Gln Phe Val Thr Thr Phe Val Ile Thr Tyr Ile Tyr Val Met Phe Ala
 85 90 95
 Asn Lys Asn Leu Glu Pro Arg Gln Ala Ala Ile Arg Gln Lys Met Glu
 100 105 110
 Gly

<210> 2617
 <211> 1056
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1033)
 <223> RXA02177

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 Met Arg Glu Ile Phe
 1 5
 ctg atc agc ggt gat tcc acc gaa tca tcc ttg gtt ttc aag acc tcc 163
 Leu Ile Ser Gly Asp Ser Thr Glu Ser Ser Leu Val Phe Lys Thr Ser
 10 15 20
 gaa gag gac ggc gct gag gaa ttt ttc att gct gta aca gat gaa ctc 211
 Glu Glu Asp Gly Ala Glu Glu Phe Phe Ile Ala Val Thr Asp Glu Leu
 25 30 35
 cac gcc att ctt gca ggt cat agc gag att aag agc gcc cca gaa ccc 259
 His Ala Ile Leu Ala Gly His Ser Glu Ile Lys Ser Ala Pro Glu Pro
 40 45 50
 gaa gaa cac aaa gag gtc cca cct cct gtt cta gag ccg gtc gct gcg 307
 Glu Glu His Lys Glu Val Pro Pro Pro Val Leu Glu Pro Val Ala Ala
 55 60 65
 gta gaa gag ccc cgt gag gaa aaa gaa att gac cct cgt atc agc gct 355
 Val Glu Glu Pro Arg Glu Glu Lys Glu Ile Asp Pro Arg Ile Ser Ala
 70 75 80 85
 ccc ctg acg atg tca ccc cgc gaa att cag att cgg gtt cgc tca ggc 403
 Pro Leu Thr Met Ser Pro Arg Glu Ile Gln Ile Arg Val Arg Ser Gly
 90 95 100
 gcc acc atc gaa gaa tta gcc gaa gaa atc ggc gtc acc gaa gcc cgc 451

Ala Thr Ile Glu Glu Leu Ala Glu Glu Ile Gly Val Thr Glu Ala Arg	
105 110 115	
gtt gag ccc tat gcc cac ccc gtt ttg ctg gaa cgt gcc cgc att gcc	499
Val Glu Pro Tyr Ala His Pro Val Leu Leu Glu Arg Ala Arg Ile Ala	
120 125 130	
gac ttg gct aag caa tca cac ccc atc agg gaa aat ggt cct gca aaa	547
Asp Leu Ala Lys Gln Ser His Pro Ile Arg Glu Asn Gly Pro Ala Lys	
135 140 145	
ctg act ctc tgg gaa att ctt gca acg gcg ttt gcc act cgc gcc cac	595
Leu Thr Leu Trp Glu Ile Leu Ala Thr Ala Phe Ala Thr Arg Gly His	
150 155 160 165	
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Asp Leu Thr Thr Ala Arg Trp Asp Ala Tyr Lys Asp Ala Thr Asn Gln	
170 175 180	
tgg atc gtg cga gtt gat tgg aaa gca gga ctc agc gac aac tac gcg	691
Trp Ile Val Arg Val Asp Trp Lys Ala Gly Leu Ser Asp Asn Tyr Ala	
185 190 195	
gag tgg acg tta aac ctg cac aac acc agc aat ccc acc gct gat ccg	739
Glu Trp Thr Leu Asn Leu His Asn Thr Ser Asn Pro Thr Ala Asp Pro	
200 205 210	
cgg acc cca gtc gca gcc gat ttg atc gat cct gaa ttc att cag ccg	787
Arg Thr Pro Val Ala Ala Asp Leu Ile Asp Pro Glu Phe Ile Gln Pro	
215 220 225	
gta cgt acc ttg acg tcc gta aac tcc acc cag gaa cag tac gac gac	835
Val Arg Thr Leu Thr Ser Val Asn Ser Thr Gln Glu Gln Tyr Asp Asp	
230 235 240 245	
gea acc gat gtt ttc gac acc gta cca agc cct gac gac gca cca gac	883
Glu Thr Asp Val Phe Asp Thr Val Pro Ser Pro Asp Asp Ala Pro Asp	
250 255 260	
tca gaa tcc gat gcc gtt gct gaa atc acc aac gac aac gaa cct gaa	931
Ser Glu Ser Asp Ala Val Ala Glu Ile Thr Asn Asp Asn Glu Pro Glu	
265 270 275	
gtc gat gcg gaa gcc cca cgc aac agg cgt cga aaa gca gta acc cca	979
Val Asp Ala Glu Gly Pro Arg Asn Arg Arg Arg Lys Ala Val Thr Pro	
280 285 290	
cac tgg gaa gat gtt ctt tta gga gtt cgc gca aac aca aag cgc ccg	1027
His Trp Glu Asp Val Leu Leu Gly Val Arg Ala Asn Thr Lys Arg Pro	
295 300 305	
aag aaa taggatgtgc tgatgccaaag tca	1056
Lys Lys	
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<210> 2618

<211> 311

<212> PRT

<213> Corynebacterium glutamicum

<400> 2618

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Val Thr Asp Glu Leu His Ala Ile Leu Ala Gly His Ser Glu Ile Lys
 35           40           45

Ser Ala Pro Glu Pro Glu Glu His Lys Glu Val Pro Pro Pro Val Leu
 50           55           60

Glu Pro Val Ala Ala Val Glu Glu Pro Arg Glu Glu Lys Glu Ile Asp
 65           70           75           80

Pro Arg Ile Ser Ala Pro Leu Thr Met Ser Pro Arg Glu Ile Gln Ile
 85           90           95

Arg Val Arg Ser Gly Ala Thr Ile Glu Glu Leu Ala Glu Glu Ile Gly
100          105          110

Val Thr Glu Ala Arg Val Glu Pro Tyr Ala His Pro Val Leu Leu Glu
115          120          125

Arg Ala Arg Ile Ala Asp Leu Ala Lys Gln Ser His Pro Ile Arg Glu
130          135          140

Asn Gly Pro Ala Lys Leu Thr Leu Trp Glu Ile Leu Ala Thr Ala Phe
145          150          155          160

Ala Thr Arg Gly His Asp Leu Thr Thr Ala Arg Trp Asp Ala Tyr Lys
165          170          175

Asp Ala Thr Asn Gln Trp Ile Val Arg Val Asp Trp Lys Ala Gly Leu
180          185          190

Ser Asp Asn Tyr Ala Glu Trp Thr Leu Asn Leu His Asn Thr Ser Asn
195          200          205

Pro Thr Ala Asp Pro Arg Thr Pro Val Ala Ala Asp Leu Ile Asp Pro
210          215          220

Glu Phe Ile Gln Pro Val Arg Thr Leu Thr Ser Val Asn Ser Thr Gln
225          230          235          240

Glu Gln Tyr Asp Asp Glu Thr Asp Val Phe Asp Thr Val Pro Ser Pro
245          250          255

Asp Asp Ala Pro Asp Ser Glu Ser Asp Ala Val Ala Glu Ile Thr Asn
260          265          270

Asp Asn Glu Pro Glu Val Asp Ala Glu Gly Pro Arg Asn Arg Arg Arg
275          280          285

Lys Ala Val Thr Pro His Trp Glu Asp Val Leu Leu Gly Val Arg Ala
290          295          300

Asn Thr Lys Arg Pro Lys Lys
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<210> 2619
<211> 993
<212> DNA
<213> *Corynebacterium glutamicum*

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<222> (101)..(970)
<223> RYA02178
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<400> 2619																	
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				Met	Pro	Ser	Gln	Leu									
				1				5									
gga	gaa	aac	gcg	gcg	atc	gtc	acc	ctc	tgg	ttt	ggt	agc	gca	tcc	gat	163	
Gly	Glu	Asn	Ala	Ala	Ile	Val	Thr	Leu	Trp	Phe	Val	Ser	Ala	Ser	Asp		
				10					15					20			
ccc	caa	tcc	atc	atc	cgc	tcg	gaa	cct	cgg	gcg	gat	cgt	gga	tat	ggc	211	
Pro	Gln	Ser	Ile	Ile	Arg	Ser	Glu	Pro	Arg	Ala	Asp	Arg	Gly	Tyr	Gly		
			25					30					35				
cga	aaa	ctg	ttg	gca	cag	ctc	aac	cca	acg	tgg	cca	att	acc	ccc	atc	259	
Arg	Lys	Leu	Leu	Ala	Gln	Leu	Asn	Pro	Thr	Trp	Pro	Ile	Thr	Pro	Ile		
		40					45					50					
ggg	cag	ttc	gcc	ctc	aac	aga	tcc	gtt	cct	gct	agt	gcc	aac	gag	ttc	307	
Gly	Gln	Phe	Ala	Leu	Asn	Arg	Ser	Val	Pro	Ala	Ser	Ala	Asn	Glu	Phe		
	55					60					65						
tac	atc	gct	ggt	ttt	ccc	ggc	atc	acc	atc	att	caa	acc	gtg	ttg	gaa	355	
Tyr	Ile	Ala	Gly	Phe	Pro	Gly	Ile	Thr	Ile	Ile	Gln	Thr	Val	Leu	Glu		
	70				75					80				85			
gat	gtc	acc	tct	tta	tcc	aag	ctg	aat	cct	cgg	tta	ctg	cgc	agc	gtc	403	
Asp	Val	Thr	Ser	Leu	Ser	Lys	Leu	Asn	Pro	Arg	Leu	Leu	Arg	Ser	Val		
				90					95					100			
cgg	gca	aca	gat	gtc	tac	att	ttc	gcc	gtc	aat	gaa	gaa	acc	acc	ctt	451	
Pro	Ala	Thr	Asp	Val	Tyr	Ile	Phe	Ala	Val	Asn	Glu	Glu	Thr	Thr	Leu		
			105					110					115				
ggt	ggc	ttc	gca	cac	atc	tac	aac	ggt	gag	atc	aaa	cga	tcc	ttc	atc	499	
Gly	Gly	Phe	Ala	His	Ile	Tyr	Asn	Gly	Glu	Ile	Lys	Arg	Ser	Phe	Ile		
		120					125					130					
gcc	tat	gaa	gag	cgc	gtc	ttc	gaa	gac	aac	ggc	atc	ccc	ggc	ggc	ttt	547	
Ala	Tyr	Glu	Glu	Arg	Val	Phe	Glu	Asp	Asn	Gly	Ile	Pro	Gly	Gly	Phe		
		135				140					145						
gaa	acc	ccc	tac	tgg	gca	ggc	aaa	aaa	ggc	acc	cgg	aaa	act	gcg	ctg	595	
Glu	Thr	Pro	Tyr	Trp	Ala	Gly	Lys	Lys	Gly	Thr	Arg	Lys	Thr	Ala	Leu		
		150			155					160					165		
tcg	ttg	ccc	ttc	aac													

tgg ctc gga ttc gac gcc acc acc tcc cct gac atc aac gtc gtt gcc 691
 Trp Leu Gly Phe Asp Ala Thr Thr Ser Pro Asp Ile Asn Val Val Ala
 185 190 195

tat gcc acc gat ggt cgc ccc gag ccg cgc atc gct gca ccc cgc ata 739
 Tyr Ala Thr Asp Gly Arg Pro Glu Pro Arg Ile Ala Ala Pro Arg Ile
 200 205 210

att aac agc gag gaa gtg aca agg tcc gcc gtc gaa aag cta gga ctg 787
 Ile Asn Ser Glu Glu Val Thr Arg Ser Ala Val Glu Lys Leu Gly Leu
 215 220 225

cgc gaa tcc gcc ttc tac gac gac tac gaa gaa tac gag gca ccc gat 835
 Arg Glu Ser Ala Phe Tyr Asp Asp Tyr Glu Glu Tyr Glu Ala Pro Asp
 230 235 240 245

cga gtg gtg tcc aag cgc att acc tca aac gcg aaa aaa gcg gcc agc 883
 Arg Val Val Ser Lys Arg Ile Thr Ser Asn Ala Lys Lys Ala Ala Ser
 250 255 260

tca gca cag aaa ttt ggt aaa tct ctg tgg cga gcc agc cgc gaa ttc 931
 Ser Ala Gln Lys Phe Gly Lys Ser Leu Trp Arg Ala Ser Arg Glu Phe
 265 270 275

ggg tca aac atg gcg gaa aga ctc cgc cac act gac cgc tagcgctact 980
 Gly Ser Asn Met Ala Glu Arg Leu Arg His Thr Asp Arg
 280 285 290

acttagcgct gtt 993

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 <211> 290
 <212> PRT
 <213> *Corynebacterium glutamicum*

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Val Ser Ala Ser Asp Pro Gln Ser Ile Ile Arg Ser Glu Pro Arg Ala
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Asp Arg Gly Tyr Gly Arg Lys Leu Leu Ala Gln Leu Asn Pro Thr Trp
 35 40 45

Pro Ile Thr Pro Ile Gly Gln Phe Ala Leu Asn Arg Ser Val Pro Ala
 50 55 60

Ser Ala Asn Glu Phe Tyr Ile Ala Gly Phe Pro Gly Ile Thr Ile Ile
 65 70 75 80

Gln Thr Val Leu Glu Asp Val Thr Ser Leu Ser Lys Leu Asn Pro Arg
 85 90 95

Leu Leu Arg Ser Val Pro Ala Thr Asp Val Tyr Ile Phe Ala Val Asn
 100 105 110

Glu Glu Thr Thr Leu Gly Gly Phe Ala His Ile Tyr Asn Gly Glu Ile
 115 120 125

Lys Arg Ser Phe Ile Ala Tyr Glu Glu Arg Val Phe Glu Asp Asn Gly
 130 135 140
 Ile Pro Gly Gly Phe Glu Thr Pro Tyr Trp Ala Gly Lys Lys Gly Thr
 145 150 155 160
 Arg Lys Thr Ala Leu Ser Leu Pro Phe Asn Pro Ile Glu Leu Val His
 165 170 175
 Glu Ala Gln Arg Ala Trp Leu Gly Phe Asp Ala Thr Thr Ser Pro Asp
 180 185 190
 Ile Asn Val Val Ala Tyr Ala Thr Asp Gly Arg Pro Glu Pro Arg Ile
 195 200 205
 Ala Ala Pro Arg Ile Ile Asn Ser Glu Glu Val Thr Arg Ser Ala Val
 210 215 220
 Glu Lys Leu Gly Leu Arg Glu Ser Ala Phe Tyr Asp Asp Tyr Glu Glu
 225 230 235 240
 Tyr Glu Ala Pro Asp Arg Val Val Ser Lys Arg Ile Thr Ser Asn Ala
 245 250 255
 Lys Lys Ala Ala Ser Ser Ala Gln Lys Phe Gly Lys Ser Leu Trp Arg
 260 265 270
 Ala Ser Arg Glu Phe Gly Ser Asn Met Ala Glu Arg Leu Arg His Thr
 275 280 285
 Asp Arg
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 <211> 801
 <212> DNA
 <213> Corynebacterium glutamicum
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 <222> (101)..(778)
 <223> RXA02181
 <400> 2621
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 Met Val Asp Gly His
 1 5
 atc cgc aat ctt cag ggc cac atc gat cgc ctc gag gcg gca gcc cct 163
 Ile Arg Asn Leu Gln Gly His Ile Asp Arg Leu Glu Ala Ala Ala Pro
 10 15 20
 act gct tca cag ttc cat gat cgc atc atc act caa ttg cgt gaa gct 211
 Thr Ala Ser Gln Phe His Asp Arg Ile Ile Thr Gln Leu Arg Glu Ala
 25 30 35
 ccg ggc agt gtt cag gca gct gtc acg att gaa aat aac cac tat aac 259


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Pro Gly Ser Val Gln Ala Ala Val Thr Ile Glu Asn Asn His Tyr Asn
    40                      45                      50

gtc gag ctg cgc ccg ccc cgc aag tta aat tca ctg gtc acc ctt gat 307
Val Glu Leu Arg Pro Pro Arg Lys Leu Asn Ser Leu Val Thr Leu Asp
    55                      60                      65

acc cac ggc cac cgc gat gag cgc cta cat cca aag att aaa ggc cac 355
Thr His Gly His Arg Asp Glu Arg Leu His Pro Lys Ile Lys Gly His
    70                      75                      80                      85

gat atc gcg tgg cag aac acg gcc acc gca aac agc cgc cgc cag ggc 403
Asp Ile Ala Trp Gln Asn Thr Ala Thr Ala Asn Ser Arg Arg Gln Gly
    90                      95                      100

gcc gat gat gga ttg ctt gtc gac gag tcc ggc cag gtg atc atg gct 451
Ala Asp Asp Gly Leu Leu Val Asp Glu Ser Gly Gln Val Ile Met Ala
    105                      110                      115

atc aat gcc tct ctc ttg gcg att aag ggc gac acc gtg ttt cat tcc 499
Ile Asn Ala Ser Leu Leu Ala Ile Lys Gly Asp Thr Val Phe His Ser
    120                      125                      130

acg cac ccc agg tcg ctg cgc tct gtt ctg gaa tca acg gtc att gcc 547
Thr His Pro Arg Ser Leu Pro Ser Val Leu Glu Ser Thr Val Ile Ala
    135                      140                      145

tac ctg cag gaa caa ggc tgt aat gca aag cct cga gag caa ggc ttc 595
Tyr Leu Gln Glu Gln Gly Cys Asn Ala Lys Pro Arg Glu Gln Gly Phe
    150                      155                      160                      165

aac atc aat gat ttg cgc tct tcg gaa gtg tgg ctg gtg gat tct ttg 643
Asn Ile Asn Asp Leu Arg Ser Ser Glu Val Trp Leu Val Asp Ser Leu
    170                      175                      180

tcc ggc atc cgt cgc gtc gct gca tgg ctc gaa tac ggt tcc aaa ttc 691
Ser Gly Ile Arg Arg Val Ala Ala Trp Leu Glu Tyr Gly Ser Lys Phe
    185                      190                      195

cca gtc tca gaa acg cga cct gtg gca gct ttc gtg ccg acg ttt tct 739
Pro Val Ser Glu Thr Arg Pro Val Ala Ala Phe Val Pro Thr Phe Ser
    200                      205                      210

gaa gtc aat gac tac cta tgg agc act gca cag caa gtg taggtgcgtc 788
Glu Val Asn Asp Tyr Leu Trp Ser Thr Ala Gln Gln Val
    215                      220                      225

gactgttatt ctc 801

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<210> 2622

<211> 226

<212> PRT

<213> Corynebacterium glutamicum

<400> 2622

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Glu Ala Ala Ala Pro Thr Ala Ser Gln Phe His Asp Arg Ile Ile Thr
    20                      25                      30

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Gln Leu Arg Glu Ala Pro Gly Ser Val Gln Ala Ala Val Thr Ile Glu
35 40 45

Asn Asn His Tyr Asn Val Glu Leu Arg Pro Pro Arg Lys Leu Asn Ser
50 55 60

Leu Val Thr Leu Asp Thr His Gly His Arg Asp Glu Arg Leu His Pro
65 70 75 80

Lys Ile Lys Gly His Asp Ile Ala Trp Gln Asn Thr Ala Thr Ala Asn
85 90 95

Ser Arg Arg Gln Gly Ala Asp Asp Gly Leu Leu Val Asp Glu Ser Gly
100 105 110

Gln Val Ile Met Ala Ile Asn Ala Ser Leu Leu Ala Ile Lys Gly Asp
115 120 125

Thr Val Phe His Ser Thr His Pro Arg Ser Leu Pro Ser Val Leu Glu
130 135 140

Ser Thr Val Ile Ala Tyr Leu Gln Glu Gln Gly Cys Asn Ala Lys Pro
145 150 155 160

Arg Glu Gln Gly Phe Asn Ile Asn Asp Leu Arg Ser Ser Glu Val Trp
165 170 175

Leu Val Asp Ser Leu Ser Gly Ile Arg Arg Val Ala Ala Trp Leu Glu
180 185 190

Tyr Gly Ser Lys Phe Pro Val Ser Glu Thr Arg Pro Val Ala Ala Phe
195 200 205

Val Pro Thr Phe Ser Glu Val Asn Asp Tyr Leu Trp Ser Thr Ala Gln
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Gln Val
225

<210> 2623

<211> 648

<212> DNA

<213> *Corynebacterium glutamicum*

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<222> (101) . . (625)

<223> RXA02183

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atgagggttag attcgccct gctgactaga atcaagactc atg gca agc cgg aag 115
Met Ala Ser Arg Lys
1 5

acc aag cgt aaa aac ctc att cag att ctc agc ctt atc gtt gct gtg 163
Thr Lys Arg Lys Asn Leu Ile Gln Ile Leu Ser Leu Ile Val Ala Val
10 15 20

tta ttg gtg gtg att ttg tct gtg gtg ttc cag caa tgg tgg aac aat 211
 Leu Leu Val Val Ile Leu Ser Val Val Phe Gln Gln Trp Trp Asn Asn
 25 30 35
 cgc cca gag cca ctc ccc caa gag atc tct atc tca gca tct tct ccc 259
 Arg Pro Glu Pro Leu Pro Gln Glu Ile Ser Ile Ser Ala Ser Ser Pro
 40 45 50
 gct ggt gaa atc gag gta ttc cca ttc agc atg tgt gaa cca ggt gtt 307
 Ala Gly Glu Ile Glu Val Phe Pro Phe Ser Met Cys Glu Pro Gly Val
 55 60 65
 gaa tgc gaa gag aac gag gtg cca acg ctg gaa gtt ggt gct gat gaa 355
 Glu Cys Glu Glu Asn Glu Val Pro Thr Leu Glu Val Gly Ala Asp Glu
 70 75 80 85
 gag ttg cac ctg acg att cca gag gca att cat gat cat gac tgg tac 403
 Glu Leu His Leu Thr Ile Pro Glu Ala Ile His Asp His Asp Trp Tyr
 90 95 100
 ttg ttg acc att tat gat gat ccg gct gca aat gac gag ttc tac cac 451
 Leu Leu Thr Ile Tyr Asp Asp Pro Ala Ala Asn Asp Glu Phe Tyr His
 105 110 115
 acc agt tac gac gcc acc gag gca acc gtt cct ggt tct gtg gat cca 499
 Thr Ser Tyr Asp Ala Thr Glu Ala Thr Val Pro Gly Ser Val Asp Pro
 120 125 130
 acc gaa gag ggt gcg gag cgc cca cgt ctg gtc gta gtg gaa gtg tcc 547
 Thr Glu Glu Gly Ala Glu Arg Pro Arg Leu Val Val Val Glu Val Ser
 135 140 145
 gct gtg atg atc ggt gag gat gaa aat ggt gag gaa agc cct tac acc 595
 Ala Val Met Ile Gly Glu Asp Glu Asn Gly Glu Glu Ser Pro Tyr Thr
 150 155 160 165
 gtc acg tgg tgg cta tcc acg atg aac gag taactcactc acaacaata 645
 Val Thr Trp Ser Leu Ser Thr Met Asn Glu
 170 175
 agg 648

<210> 2624

<211> 175

<212> PRT

<213> Corynebacterium glutamicum

<400> 2624

Met Ala Ser Arg Lys Thr Lys Arg Lys Asn Leu Ile Gln Ile Leu Ser
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 Gln Trp Trp Asn Asn Arg Pro Glu Pro Leu Pro Gln Glu Ile Ser Ile
 35 40 45
 Ser Ala Ser Ser Pro Ala Gly Glu Ile Glu Val Phe Pro Phe Ser Met
 50 55 60

Cys Glu Pro Gly Val Glu Cys Glu Glu Asn Glu Val Pro Thr Leu Glu
 65 70 75 80
 Val Gly Ala Asp Glu Glu Leu His Leu Thr Ile Pro Glu Ala Ile His
 85 90 95
 Asp His Asp Trp Tyr Leu Leu Thr Ile Tyr Asp Asp Pro Ala Ala Asn
 100 105 110
 Asp Glu Phe Tyr His Thr Ser Tyr Asp Ala Thr Glu Ala Thr Val Pro
 115 120 125
 Gly Ser Val Asp Pro Thr Glu Glu Gly Ala Glu Arg Pro Arg Leu Val
 130 135 140
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 Glu Ser Pro Tyr Thr Val Thr Trp Ser Leu Ser Thr Met Asn Glu
 165 170 175

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 <211> 2322
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(2299)
 <223> RXA02187

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 Met Lys Lys Asp Ser 5
 ccc atc ccc acc ctc aag ggg tgg ttg gat act caa agt gat gat cag 163
 Pro Ile Pro Thr Leu Lys Gly Trp Leu Asp Thr Gln Ser Asp Asp Gln 20
 ctc tcc aca atc ctt aga aat cga ccc gat acg gtt ctc cct tta cca 211
 Leu Ser Thr Ile Leu Arg Asn Arg Pro Asp Thr Val Leu Pro Leu Pro 35
 cct aat ttg gcc tct ctt gct gcg cgt tta cag ctg agg gcg tct gcg 259
 Pro Asn Leu Ala Ser Leu Ala Ala Arg Leu Gln Leu Arg Ala Ser Ala 40 45 50
 att cgc gcg gtg ttg aaa ctc aat gcg ttg gaa ctt ggt gtg ttg gag 307
 Ile Arg Ala Val Leu Lys Leu Asn Ala Leu Glu Leu Gly Val Leu Glu 55 60 65
 gcc gtg gcc aac ctt ggt ggt gaa ctc cac ccg gtt act gcc ccc gaa 355
 Ala Val Ala Asn Leu Gly Gly Glu Leu His Pro Val Thr Ala Pro Glu 70 75 80 85
 gtg gtg gaa tat ttg cat gtg gcg ttg gca gag gat ctt cca gcg caa 403

Val	Val	Glu	Tyr	Leu	His	Val	Ala	Leu	Ala	Glu	Asp	Leu	Pro	Ala	Gln	
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gac	acg	att	ggc	gcg	gct	ctt	gcc	acg	ctg	aaa	aat	ttc	gcg	ttg	gtt	451
Asp	Thr	Ile	Gly	Ala	Ala	Leu	Ala	Thr	Leu	Lys	Asn	Phe	Ala	Leu	Val	
			105					110					115			
tat	ggc	gat	gac	cag	ttg	atg	att	gct	cag	gag	acg	atg	gct	gcg	ttg	499
Tyr	Gly	Asp	Asp	Gln	Leu	Met	Ile	Ala	Gln	Glu	Thr	Met	Ala	Ala	Leu	
			120					125				130				
cct	gtt	cat	tgg	cgg	ttg	ctt	ccg	gag	gta	agt	gat	cgc	ggg	cag	agt	547
Pro	Val	His	Trp	Arg	Leu	Leu	Pro	Glu	Val	Ser	Asp	Arg	Gly	Gln	Ser	
			135			140					145					
gag	gaa	cag	gtg	agg	gaa	agc	gtc	gat	aag	ctt	tct	gat	agg	cac	cgc	595
Glu	Glu	Gln	Val	Arg	Glu	Ser	Val	Asp	Lys	Leu	Ser	Asp	Arg	His	Arg	
			150			155					160				165	
aaa	ctt	ttg	cac	acg	ctt	gcg	gcc	tgc	ggc	gtc	ttc	ggc	ctg	acg	cgc	643
Lys	Leu	Leu	His	Thr	Leu	Ala	Ala	Ser	Gly	Gly	Phe	Gly	Leu	Thr	Arg	
			170						175					180		
gat	gcg	gcg	cct	gat	gcg	gat	ccg	tgc	cgg	ccg	att	ccg	cag	ttg	ctg	691
Asp	Ala	Ala	Pro	Asp	Ala	Asp	Pro	Ser	Arg	Pro	Ile	Pro	Gln	Leu	Leu	
			185					190					195			
gcg	tgc	ggg	ttg	ttg	gcg	cgc	gtg	gat	gag	cag	acc	gtg	cgc	ctg	ccg	739
Ala	Ser	Gly	Leu	Leu	Ala	Arg	Val	Asp	Glu	Gln	Thr	Val	Arg	Leu	Pro	
			200					205				210				
gcg	atg	gtg	cgg	cgt	gtg	att	gag	ggc	cgc	gag	cag	ctg	ccc	gct	cag	787
Ala	Met	Val	Arg	Arg	Val	Ile	Glu	Gly	Arg	Glu	Gln	Leu	Pro	Ala	Gln	
			215			220					225					
gtg	cgc	cca	att	ccg	cgc	acg	gcg	gcg	cca	ggt	tgc	aat	gat	ggc	ggc	835
Val	Arg	Pro	Ile	Pro	Arg	Thr	Ala	Ala	Pro	Gly	Ser	Asn	Asp	Gly	Gly	
			230			235				240				245		
att	gca	gcc	ggc	ctt	gag	gtg	gtg	cgg	cac	atg	cga	ttg	ctt	atc	gac	883
Ile	Ala	Ala	Gly	Leu	Glu	Val	Val	Arg	His	Met	Arg	Leu	Leu	Ile	Asp	
			250						255					260		
gcc	ctc	agc	cac	gtt	ccc	gcc	ccc	acg	ctg	aaa	gtc	gga	gcc	ctc	ggc	931
Ala	Leu	Ser	His	Val	Pro	Ala	Pro	Thr	Leu	Lys	Val	Gly	Ala	Leu	Gly	
			265					270					275			
gtg	cgc	gtg	gtg	act	cgc	ctg	agc	aag	gaa	tta	gac	ctt	gat	gag	acc	979
Val	Arg	Val	Val	Thr	Arg	Leu	Ser	Lys	Glu	Leu	Asp	Leu	Asp	Glu	Thr	
			280					285				290				
gag	ctg	gca	cgt	cta	ctg	agt	ttg	ggc	atg	ggc	agc	ggc	cta	atc	cgt	1027
Glu	Leu	Ala	Arg	Leu	Leu	Ser	Leu	Gly	Met	Ala	Ser	Gly	Leu	Ile	Arg	
			295			300					305					
aaa	ggc	gtg	ccc	gat	cca	ttg	ccc	atg	gat	gat	gat	ggc	ggc	gat	tac	1075
Lys	Gly	Val	Pro	Asp	Pro	Leu	Pro	Met	Asp	Asp	Asp	Gly	Gly	Asp	Tyr	
			310			315				320				325		
gtc	gct	ccc	acc	ccg	ctg	gct	gac	gaa	tgg	atg	gaa	tat	gat	ctg	gcg	1123
Val	Ala	Pro	Thr	Pro	Leu	Ala	Asp	Glu	Trp	Met	Glu	Tyr	Asp	Leu	Ala	

330	335	340	
cac caa ttg ggc acg ttg atg tct ggt tgg tgg aag caa act tac gcg His Gln Leu Gly Thr Leu Met Ser Gly Trp Trp Lys Gln Thr Tyr Ala 345 350 355			1171
ccg tgg ttg gtg ggt cgg gct gat gat aag gac aag ccg atc cat gtt Pro Trp Leu Val Gly Arg Ala Asp Asp Lys Asp Lys Pro Ile His Val 360 365 370			1219
ctc agt aaa aca agc atc att gat tgg ctt cct gat gct cgt gcg aag Leu Ser Lys Thr Ser Ile Ile Asp Ser Leu Pro Asp Ala Arg Ala Lys 375 380 385			1267
atc ctg tcc tct tta tct agg gtt tta gtg gac aat ctg cac gcg gat Ile Leu Ser Ser Leu Ser Arg Val Leu Val Asp Asn Leu His Ala Asp 390 395 400 405			1315
tta gca ttc cat tat ccc ctt gcg gcg agt cgg atg aat cct gac acc Leu Ala Phe His Tyr Pro Leu Ala Ala Ser Arg Met Asn Pro Asp Thr 410 415 420			1363
atc aca cag ctg gta cag gaa gcc cag tgg atc gga gca tat tct caa Ile Thr Gln Leu Val Gln Glu Ala Gln Trp Ile Gly Ala Tyr Ser Gln 425 430 435			1411
ggc gtg acc gca gcg ggt cag gcc tta att gat ggc gaa aac cct acg Gly Val Thr Ala Ala Gly Gln Ala Leu Ile Asp Gly Glu Asn Pro Thr 440 445 450			1459
gag gta atc aag gct cct gcg ccg gtg gag aat ttc atc gtg caa ggc Glu Val Ile Lys Ala Pro Ala Pro Val Glu Asn Phe Ile Val Gln Gly 455 460 465			1507
gat ttc acc atc atg gtt cca gga cca cta acc cct gcg atg caa aaa Asp Phe Thr Ile Met Val Pro Gly Pro Leu Thr Pro Ala Met Gln Lys 470 475 480 485			1555
acc atg gat tgg atc gca tgg ttg gaa tca cct ggt ttg gcc tgg gtg Thr Met Asp Ser Ile Ala Ser Leu Glu Ser Pro Gly Leu Ala Ser Val 490 495 500			1603
tat cga ctc agc gag aaa tcc atc agg cat gct ctg gat ctt ggg ctc Tyr Arg Leu Ser Glu Lys Ser Ile Arg His Ala Leu Asp Leu Gly Leu 505 510 515			1651
acc acc ccg gaa atc ttg gag ttt ctc aaa gaa cat tcc atg aca gat Thr Thr Pro Glu Ile Leu Glu Phe Leu Lys Glu His Ser Met Thr Asp 520 525 530			1699
ctg ccc caa tct gtg ggc tat ttg ctc agc gat atc gcc aga aag cac Leu Pro Gln Ser Val Gly Tyr Leu Leu Ser Asp Ile Ala Arg Lys His 535 540 545			1747
ggc acc ctc cga ggc ggc cct gca ctg tcc tat atc cgt agc gac gat Gly Thr Leu Arg Gly Gly Pro Ala Leu Ser Tyr Ile Arg Ser Asp Asp 550 555 560 565			1795
ccc gct ttg ctg cat tcc gca gtg gag gcg gcc gat gtg gcg ctt Pro Ala Leu Leu His Ser Ala Val Glu Ala Gly Ala Asp Val Ala Leu 570 575 580			1843

cgg cag atc gct ccc acc gtt gcg att gct caa gca ccc ctg ctt cag 1891
 Arg Gln Ile Ala Pro Thr Val Ala Ile Ala Gln Ala Pro Leu Leu Gln
 585 590 595

gtg atc act gtg ctg cgt gct gcc ggg ttc caa cct gtg gca gaa gac 1939
 Val Ile Thr Val Leu Arg Ala Ala Gly Phe Gln Pro Val Ala Glu Asp
 600 605 610

ggc gaa ggc gca agt ctg aat atc tcg cca tcc cct gca cgt gtg ccc 1987
 Gly Glu Gly Ala Ser Leu Asn Ile Ser Pro Ser Pro Ala Arg Val Pro
 615 620 625

gca gct tcc cca cca cca gtt gtt ccg gca ctg gat gaa agc cgg gta 2035
 Ala Ala Ser Pro Pro Pro Val Val Pro Ala Leu Asp Glu Ser Arg Val
 630 635 640 645

cag gca gca gtc aaa gca atc cga cgg gaa aat tca gca tct caa gga 2083
 Gln Ala Ala Val Lys Ala Ile Arg Arg Glu Asn Ser Ala Ser Gln Gly
 650 655 660

act gtt tcc aca cag cca act ctt tcg gtg ctg cag gct gca gtg cga 2131
 Thr Val Ser Thr Gln Pro Thr Leu Ser Val Leu Gln Ala Ala Val Arg
 665 670 675

ggg cag cgc acg gtg acg ttg ggg ttc gtc gat aag caa ggc gtg gcc 2179
 Gly Gln Arg Thr Val Thr Leu Gly Phe Val Asp Lys Gln Gly Val Ala
 680 685 690

gtg cac cgc gtc gtc aag cct tta acc gtc aac gcc ggg cag gtg gac 2227
 Val His Arg Val Val Lys Pro Leu Thr Val Asn Ala Gly Gln Val Asp
 695 700 705

gct gtg gat gaa gcc aca ggt gcg gtg cat cgt ttc atg ttg cac agg 2275
 Ala Val Asp Glu Ala Thr Gly Ala Val His Arg Phe Met Leu His Arg
 710 715 720 725

atc aca gaa gta ata gtg gat aac tagcctagaa gtgacataat gga 2322
 Ile Thr Glu Val Ile Val Asp Asn
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<210> 2626

<211> 733

<212> PRT

<213> Corynebacterium glutamicum

<400> 2626

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Gln Ser Asp Asp Gln Leu Ser Thr Ile Leu Arg Asn Arg Pro Asp Thr
 20 25 30

Val Leu Pro Leu Pro Pro Asn Leu Ala Ser Leu Ala Ala Arg Leu Gln
 35 40 45

Leu Arg Ala Ser Ala Ile Arg Ala Val Leu Lys Leu Asn Ala Leu Glu
 50 55 60

Leu Gly Val Leu Glu Ala Val Ala Asn Leu Gly Gly Glu Leu His Pro

65	70	75	80
Val Thr Ala Pro	Glu Val Val Glu Tyr	Leu His Val Ala Leu	Ala Glu
	85	90	95
Asp Leu Pro Ala	Gln Asp Thr Ile Gly	Ala Ala Leu Ala Thr	Leu Lys
	100	105	110
Asn Phe Ala Leu	Val Tyr Gly Asp Asp	Gln Leu Met Ile Ala	Gln Glu
	115	120	125
Thr Met Ala Ala	Leu Pro Val His Trp Arg	Leu Leu Pro Glu	Val Ser
	130	135	140
Asp Arg Gly Gln	Ser Glu Glu Gln Val Arg	Glu Ser Val Asp	Lys Leu
	145	150	155
Ser Asp Arg His	Arg Lys Leu Leu His Thr	Leu Ala Ala Ser	Gly Gly
	165	170	175
Phe Gly Leu Thr	Arg Asp Ala Ala Pro	Asp Ala Asp Pro	Ser Arg Pro
	180	185	190
Ile Pro Gln Leu	Leu Ala Ser Gly Leu	Leu Ala Arg Val	Asp Glu Gln
	195	200	205
Thr Val Arg Leu	Pro Ala Met Val Arg	Arg Val Ile Glu	Gly Arg Glu
	210	215	220
Gln Leu Pro Ala	Gln Val Arg Pro Ile Pro	Arg Thr Ala Ala	Pro Gly
	225	230	235
Ser Asn Asp Gly	Gly Ile Ala Ala Gly Leu	Glu Val Val Arg	His Met
	245	250	255
Arg Leu Leu Ile	Asp Ala Leu Ser His Val	Pro Ala Pro Thr	Leu Lys
	260	265	270
Val Gly Ala Leu	Gly Val Arg Val Val Thr	Arg Leu Ser Lys	Glu Leu
	275	280	285
Asp Leu Asp Glu	Thr Glu Leu Ala Arg Leu	Leu Ser Leu Gly	Met Ala
	290	295	300
Ser Gly Leu Ile	Arg Lys Gly Val Pro Asp	Pro Leu Pro Met	Asp Asp
	305	310	315
Asp Gly Gly Asp	Tyr Val Ala Pro Thr Pro	Leu Ala Asp Glu	Trp Met
	325	330	335
Glu Tyr Asp Leu	Ala His Gln Leu Gly Thr	Leu Met Ser Gly	Trp Trp
	340	345	350
Lys Gln Thr Tyr	Ala Pro Trp Leu Val Gly	Arg Ala Asp Asp	Lys Asp
	355	360	365
Lys Pro Ile His	Val Leu Ser Lys Thr Ser	Ile Ile Asp Ser	Leu Pro
	370	375	380
Asp Ala Arg Ala	Lys Ile Leu Ser Ser Leu	Ser Arg Val Leu	Val Asp
	385	390	395
			400

Asn Leu His Ala Asp Leu Ala Phe His Tyr Pro Leu Ala Ala Ser Arg
 405 410 415
 Met Asn Pro Asp Thr Ile Thr Gln Leu Val Gln Glu Ala Gln Trp Ile
 420 425 430
 Gly Ala Tyr Ser Gln Gly Val Thr Ala Ala Gly Gln Ala Leu Ile Asp
 435 440 445
 Gly Glu Asn Pro Thr Glu Val Ile Lys Ala Pro Ala Pro Val Glu Asn
 450 455 460
 Phe Ile Val Gln Gly Asp Phe Thr Ile Met Val Pro Gly Pro Leu Thr
 465 470 475 480
 Pro Ala Met Gln Lys Thr Met Asp Ser Ile Ala Ser Leu Glu Ser Pro
 485 490 495
 Gly Leu Ala Ser Val Tyr Arg Leu Ser Glu Lys Ser Ile Arg His Ala
 500 505 510
 Leu Asp Leu Gly Leu Thr Thr Pro Glu Ile Leu Glu Phe Leu Lys Glu
 515 520 525
 His Ser Met Thr Asp Leu Pro Gln Ser Val Gly Tyr Leu Leu Ser Asp
 530 535 540
 Ile Ala Arg Lys His Gly Thr Leu Arg Gly Gly Pro Ala Leu Ser Tyr
 545 550 555 560
 Ile Arg Ser Asp Asp Pro Ala Leu Leu His Ser Ala Val Glu Ala Gly
 565 570 575
 Ala Asp Val Ala Leu Arg Gln Ile Ala Pro Thr Val Ala Ile Ala Gln
 580 585 590
 Ala Pro Leu Leu Gln Val Ile Thr Val Leu Arg Ala Ala Gly Phe Gln
 595 600 605
 Pro Val Ala Glu Asp Gly Glu Gly Ala Ser Leu Asn Ile Ser Pro Ser
 610 615 620
 Pro Ala Arg Val Pro Ala Ala Ser Pro Pro Pro Val Val Pro Ala Leu
 625 630 635 640
 Asp Glu Ser Arg Val Gln Ala Ala Val Lys Ala Ile Arg Arg Glu Asn
 645 650 655
 Ser Ala Ser Gln Gly Thr Val Ser Thr Gln Pro Thr Leu Ser Val Leu
 660 665 670
 Gln Ala Ala Val Arg Gly Gln Arg Thr Val Thr Leu Gly Phe Val Asp
 675 680 685
 Lys Gln Gly Val Ala Val His Arg Val Val Lys Pro Leu Thr Val Asn
 690 695 700
 Ala Gly Gln Val Asp Ala Val Asp Glu Ala Thr Gly Ala Val His Arg
 705 710 715 720

Phe Met Leu His Arg Ile Thr Glu Val Ile Val Asp Asn
725 730

<210> 2627

<211> 693

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(670)

<223> RXA02199

<400> 2627

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gcctaagcaa cacaggcaaa gcgccactag tctcggtcgc atg act gac tcc act 115
Met Thr Asp Ser Thr
1 5

ccg caa ggc tca aca cca ggc atg tcc cct gaa gct atc ctc aac ggc 163
Pro Gln Gly Ser Thr Pro Gly Met Ser Pro Glu Ala Ile Leu Asn Gly
10 15 20

acc gga aag ccg tgg gaa gag tgg cta aaa ttg ctt gac gac gta aaa 211
Thr Gly Lys Pro Trp Glu Glu Trp Leu Lys Leu Leu Asp Asp Val Lys
25 30 35

gcc acc tct tgg act cac acc cac atc gca aag cac atc gtg gac aac 259
Ala Thr Ser Trp Thr His Thr His Ile Ala Lys His Ile Val Asp Asn
40 45 50

ttt gat gtc agt ggc tgg tgg gct caa ggc atc gcg att ggt tat gaa 307
Phe Asp Val Ser Gly Trp Trp Ala Gln Gly Ile Ala Ile Gly Tyr Glu
55 60 65

tac gaa cgt ggc atg cgc aaa ccc ggg atg acc agc gat ggg ttc gcg 355
Tyr Glu Arg Gly Met Arg Lys Pro Gly Met Thr Ser Asp Gly Phe Ala
70 75 80 85

gcc aat gcc tcc aaa acc ctt aac ctg ccg gtc gaa aaa gtg tgg aag 403
Ala Asn Ala Ser Lys Thr Leu Asn Leu Pro Val Glu Lys Val Trp Lys
90 95 100

ctc ttc gga gac gat gac ctg cgg gcg cag tgg ctc gat ccc gca cta 451
Leu Phe Gly Asp Asp Asp Leu Arg Ala Gln Trp Leu Asp Pro Ala Leu
105 110 115

att gag aaa acc tcc gcc tcc gaa cct aga aca ttc aat gcc aaa tgg 499
Ile Glu Lys Thr Ser Ala Ser Glu Pro Arg Thr Phe Asn Ala Lys Trp
120 125 130

ttg gcc gat gat tct cga gtg agc gtc aac ttc acc tcc aaa ggc gac 547
Leu Ala Asp Asp Ser Arg Val Ser Val Asn Phe Thr Ser Lys Gly Asp
135 140 145

aat aaa tcc agc ttc ggc atc cag cac aga cgc ctg cct gat caa gac 595
Asn Lys Ser Ser Phe Gly Ile Gln His Arg Arg Leu Pro Asp Gln Asp
150 155 160 165

agc atc cct gtc atg aaa gca ttc tgg aaa gaa cgc atc gct gca tta 643
 Ser Ile Pro Val Met Lys Ala Phe Trp Lys Glu Arg Ile Ala Ala Leu
 170 175 180

gtt gag gtg tca aaa caa ttt tcg ctt taacattaag ttcttagcct 690
 Val Glu Val Ser Lys Gln Phe Ser Leu
 185 190

tca 693

<210> 2628

<211> 190

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2628

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 20 25 30

Leu Asp Asp Val Lys Ala Thr Ser Trp Thr His Thr His Ile Ala Lys
 35 40 45

His Ile Val Asp Asn Phe Asp Val Ser Gly Trp Trp Ala Gln Gly Ile
 50 55 60

Ala Ile Gly Tyr Glu Tyr Glu Arg Gly Met Arg Lys Pro Gly Met Thr
 65 70 75 80

Ser Asp Gly Phe Ala Ala Asn Ala Ser Lys Thr Leu Asn Leu Pro Val
 85 90 95

Glu Lys Val Trp Lys Leu Phe Gly Asp Asp Asp Leu Arg Ala Gln Trp
 100 105 110

Leu Asp Pro Ala Leu Ile Glu Lys Thr Ser Ala Ser Glu Pro Arg Thr
 115 120 125

Phe Asn Ala Lys Trp Leu Ala Asp Asp Ser Arg Val Ser Val Asn Phe
 130 135 140

Thr Ser Lys Gly Asp Asn Lys Ser Ser Phe Gly Ile Gln His Arg Arg
 145 150 155 160

Leu Pro Asp Gln Asp Ser Ile Pro Val Met Lys Ala Phe Trp Lys Glu
 165 170 175

Arg Ile Ala Ala Leu Val Glu Val Ser Lys Gln Phe Ser Leu
 180 185 190

<210> 2629

<211> 501

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(478)

<223> RXA02203

<400> 2629

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gggcgtgcag ctctaggaaa tttcaggaac aatacatctc atg acc att cgc gcc 115
 Met Thr Ile Arg Ala
 1 5

act ttc cag cct tcc gta gat gaa ttc atc tcc act ctc gaa gag ttt 163
 Thr Phe Gln Pro Ser Val Asp Glu Phe Ile Ser Thr Leu Glu Glu Phe
 10 15 20

gca aca ggt tca tac ctt aaa gag gac gaa aag gaa ttc tgg gac gaa 211
 Ala Thr Gly Ser Tyr Leu Lys Glu Asp Glu Lys Glu Phe Trp Asp Glu
 25 30 35

cct ttc gat gtc aag gca ctt cca gat ctt cgt ttc atc ttg gaa aac 259
 Pro Phe Asp Val Lys Ala Leu Pro Asp Leu Arg Phe Ile Leu Glu Asn
 40 45 50

tac ctt gat tcc cta gat aag ctc ggt gaa gca cca gac ctt gat gct 307
 Tyr Leu Asp Ser Leu Asp Lys Leu Gly Glu Ala Pro Asp Leu Asp Ala
 55 60 65

gtt aac gcc tcc gct cag tcc acc ctt gat gag ctg gag aag ttc aac 355
 Val Asn Ala Ser Ala Gln Ser Thr Leu Asp Glu Leu Glu Lys Phe Asn
 70 75 80 85

aca aag cac cac ggt gct gtt gtt gag cct gaa gaa aaa gaa gag atc 403
 Thr Lys His His Gly Ala Val Val Glu Pro Glu Glu Lys Glu Glu Ile
 90 95 100

act aaa ttg atg ttt gat gct gca aag cag act ggt gca gat gat ctt 451
 Thr Lys Leu Met Phe Asp Ala Ala Lys Gln Thr Gly Ala Asp Asp Leu
 105 110 115

tct gca gag gct ttc cct gag ttt gag taaatttcag tagaagtttt 498
 Ser Ala Glu Ala Phe Pro Glu Phe Glu
 120 125

tta 501

<210> 2630

<211> 126

<212> PRT

<213> Corynebacterium glutamicum

<400> 2630

Met Thr Ile Arg Ala Thr Phe Gln Pro Ser Val Asp Glu Phe Ile Ser
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Thr Leu Glu Glu Phe Ala Thr Gly Ser Tyr Leu Lys Glu Asp Glu Lys
 20 25 30

Glu Phe Trp Asp Glu Pro Phe Asp Val Lys Ala Leu Pro Asp Leu Arg
 35 40 45

Phe Ile Leu Glu Asn Tyr Leu Asp Ser Leu Asp Lys Leu Gly Glu Ala

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50              55              60
Pro Asp Leu Asp Ala Val Asn Ala Ser Ala Gln Ser Thr Leu Asp Glu
65              70              75
Leu Glu Lys Phe Asn Thr Lys His His Gly Ala Val Val Glu Pro Glu
85              90              95
Glu Lys Glu Glu Ile Thr Lys Leu Met Phe Asp Ala Ala Lys Gln Thr
100             105             110
Gly Ala Asp Asp Leu Ser Ala Glu Ala Phe Pro Glu Phe Glu
115             120             125

<210> 2631
<211> 1059
<212> DNA
<213> Corynebacterium glutamicum

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<221> CDS
<222> (101)..(1036)
<223> RXA02206

<400> 2631
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Met Val Gly Ser Ser
1 5
ggt ttg cgg gta tcc agg ctc ggt ttg ggc acc tca aca tgg ggc tcg 163
Gly Leu Arg Val Ser Arg Leu Gly Leu Gly Thr Ser Thr Trp Gly Ser
10 15 20
ggc acc gag ctg gct gag gca ggc gat atc ttt aag gcg ttc atc aat 211
Gly Thr Glu Leu Ala Glu Ala Gly Asp Ile Phe Lys Ala Phe Ile Asn
25 30 35
tct ggt ggc acg ctt atc gac gtc tcc ccc aac tac acc acc ggc gtc 259
Ser Gly Gly Thr Leu Ile Asp Val Ser Pro Asn Tyr Thr Thr Gly Val
40 45 50
gcg gaa gaa atg ctc ggc acg atg ttg gat gcg gaa gtc tct cgt tcg 307
Ala Glu Glu Met Leu Gly Thr Met Leu Asp Ala Glu Val Ser Arg Ser
55 60 65
gct gtc gtc att tcc tcc agc gca ggt gtc aac ccc gct ctg ccg ctc 355
Ala Val Val Ile Ser Ser Ser Ala Gly Val Asn Pro Ala Leu Pro Leu
70 75 80 85
ggc cga cgt gtg gat tgc tcc cgc cgc aat ttg att gcc caa tta gat 403
Gly Arg Arg Val Asp Cys Ser Arg Arg Asn Leu Ile Ala Gln Leu Asp
90 95 100
gtc acc ctg cgg gca tta aac act gac tat ttg gat ttg tgg tct gtg 451
Val Thr Leu Arg Ala Leu Asn Thr Asp Tyr Leu Asp Leu Trp Ser Val
105 110 115
ggc tat tgg gat gag ggc acc cca ccg cat gag gtg gcc gat act ttg 499

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Gly	Tyr	Trp	Asp	Glu	Gly	Thr	Pro	His	Glu	Val	Ala	Asp	Thr	Leu	
		120					125				130				
gat	tac	gcc	gtg	cgc	acc	ggc	cga	gtc	cga	tat	gcc	ggt	gtc	cga	gga
Asp	Tyr	Ala	Val	Arg	Thr	Gly	Arg	Val	Arg	Tyr	Ala	Gly	Val	Arg	Gly
		135				140					145				547
tat	tcc	ggt	tgg	cag	tta	gcg	gtc	acc	cac	gct	gca	tcc	aat	cat	gca
Tyr	Ser	Gly	Trp	Gln	Leu	Ala	Val	Thr	His	Ala	Ala	Ser	Asn	His	Ala
		150				155				160				165	595
gcg	gcc	tcc	gcc	cgc	ccc	gtg	gtc	gtt	gca	caa	aat	gaa	tac	agc	ctg
Ala	Ala	Ser	Ala	Arg	Pro	Val	Val	Val	Ala	Gln	Asn	Glu	Tyr	Ser	Leu
				170					175					180	643
ctg	gaa	cgc	cgc	gca	gaa	caa	gaa	ctc	ctc	cct	gcc	acc	caa	cac	cta
Leu	Glu	Arg	Arg	Ala	Glu	Gln	Glu	Leu	Leu	Pro	Ala	Thr	Gln	His	Leu
				185				190					195		691
ggt	gtc	gga	ttc	ttt	gct	ggc	gct	ccg	ctg	ggg	caa	ggc	gtg	ctg	act
Gly	Val	Gly	Phe	Phe	Ala	Gly	Ala	Pro	Leu	Gly	Gln	Gly	Val	Leu	Thr
		200					205					210			739
gct	aaa	tac	cgc	tcc	gaa	att	ccc	cat	gat	tcc	aga	gct	gca	tcc	aca
Ala	Lys	Tyr	Arg	Ser	Glu	Ile	Pro	His	Asp	Ser	Arg	Ala	Ala	Ser	Thr
		215				220					225				787
gga	cgc	gac	gca	gaa	gtc	caa	agc	tac	cta	gat	aat	cga	ggc	cgc	atc
Gly	Arg	Asp	Ala	Glu	Val	Gln	Ser	Tyr	Leu	Asp	Asn	Arg	Gly	Arg	Ile
		230				235				240				245	835
att	gtc	gat	gct	ctt	gat	act	gca	gcc	aaa	gga	tta	ggc	att	agc	ccc
Ile	Val	Asp	Ala	Leu	Asp	Thr	Ala	Ala	Lys	Gly	Leu	Gly	Ile	Ser	Pro
				250					255					260	883
gct	gtc	aca	gcc	acc	acc	tgg	gtg	cgt	gat	cgt	ccc	gga	gtg	aca	gct
Ala	Val	Thr	Ala	Thr	Thr	Trp	Val	Arg	Asp	Arg	Pro	Gly	Val	Thr	Ala
			265					270					275		931
gtc	atc	gtg	ggc	gct	cgc	aca	cat	gaa	cag	ctg	tca	cat	ctt	ctc	aag
Val	Ile	Val	Gly	Ala	Arg	Thr	His	Glu	Gln	Leu	Ser	His	Leu	Leu	Lys
		280					285					290			979
gcg	gaa	tcg	gtg	act	ttg	cca	aca	cca	atc	aca	caa	gcc	ctt	gat	gat
Ala	Glu	Ser	Val	Thr	Leu	Pro	Thr	Pro	Ile	Thr	Gln	Ala	Leu	Asp	Asp
		295				300					305				1027
gtc	tcc	ctg	tgacttgg	gtc	caattacatt	cac									
Val	Ser	Leu													1059
		310													

<210> 2632

<211> 312

<212> PRT

<213> Corynebacterium glutamicum

<400> 2632

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Ser Thr Trp Gly Ser Gly Thr Glu Leu Ala Glu Ala Gly Asp Ile Phe
 20 25 30
 Lys Ala Phe Ile Asn Ser Gly Gly Thr Leu Ile Asp Val Ser Pro Asn
 35 40 45
 Tyr Thr Thr Gly Val Ala Glu Glu Met Leu Gly Thr Met Leu Asp Ala
 50 55 60
 Glu Val Ser Arg Ser Ala Val Val Ile Ser Ser Ala Gly Val Asn
 65 70 75 80
 Pro Ala Leu Pro Leu Gly Arg Arg Val Asp Cys Ser Arg Arg Asn Leu
 85 90 95
 Ile Ala Gln Leu Asp Val Thr Leu Arg Ala Leu Asn Thr Asp Tyr Leu
 100 105 110
 Asp Leu Trp Ser Val Gly Tyr Trp Asp Glu Gly Thr Pro His Glu
 115 120 125
 Val Ala Asp Thr Leu Asp Tyr Ala Val Arg Thr Gly Arg Val Arg Tyr
 130 135 140
 Ala Gly Val Arg Gly Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala
 145 150 155 160
 Ala Ser Asn His Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln
 165 170 175
 Asn Glu Tyr Ser Leu Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro
 180 185 190
 Ala Thr Gln His Leu Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly
 195 200 205
 Gln Gly Val Leu Thr Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser
 210 215 220
 Arg Ala Ala Ser Thr Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp
 225 230 235 240
 Asn Arg Gly Arg Ile Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly
 245 250 255
 Leu Gly Ile Ser Pro Ala Val Thr Ala Thr Thr Trp Val Arg Asp Arg
 260 265 270
 Pro Gly Val Thr Ala Val Ile Val Gly Ala Arg Thr His Glu Gln Leu
 275 280 285
 Ser His Leu Leu Lys Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr
 290 295 300
 Gln Ala Leu Asp Asp Val Ser Leu
 305 310

<210> 2633

<211> 553

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(553)

<223> RXA02211

<400> 2633

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				Met Val Ser Val Leu	
				1 5	

tta att cag	ccc cgt	cag gga	gaa gca	gtc gcc	gca gct	gag cga	cgt	163
Leu Ile Gln	Pro Arg	Gln Gly	Glu Ala	Val Ala	Ala Ala	Glu Arg	Arg	
	10			15		20		

gac ttt ttg	cag gcc	acc ggt	ctt aag	cct caa	gaa ctg	acc tcc	cga	211
Asp Phe Leu	Gln Ala	Thr Gly	Leu Lys	Pro Gln	Glu Leu	Thr Ser	Arg	
	25		30			35		

atg ttg gat	acc acc	act tct	cga att	ggc agt	ctg gaa	ggg ttc	gac	259
Met Leu Asp	Thr Thr	Thr Ser	Arg Ile	Gly Ser	Leu Thr	Gly Phe	Asp	
	40		45		50			

ggc gtg att	gtg ggc	gga agc	cca ctg	aat gcc	acc aac	ttt gag	tac	307
Gly Val Ile	Val Gly	Gly Ser	Pro Leu	Asn Ala	Thr Asn	Phe Glu	Tyr	
	55		60		65			

agc gat tgg	caa cgc	cac gtc	cac cgc	gaa ttg	tcc ttg	ctg atc	aat	355
Ser Asp Trp	Gln Arg	His Val	His Arg	Glu Leu	Ser Leu	Leu Ile	Asn	
	70		75		80		85	

cac cca ctg	cca aca	atc ttt	gtc tgc	tac ggc	aat acc	ttt ttg	acc	403
His Pro Leu	Pro Thr	Ile Phe	Val Cys	Tyr Gly	Asn Thr	Phe Leu	Thr	
	90			95		100		

ttc ttc tct	ggc gga	cag att	ggg cgc	aca cac	ccc gaa	gat tcc	ggc	451
Phe Phe Ser	Gly Gly	Gln Ile	Gly Arg	Thr His	Pro Glu	Asp Ser	Gly	
	105		110			115		

gcc acc aca	gtg ttg	cta act	gac gcc	ggc aaa	cga gac	gta ctc	act	499
Ala Thr Thr	Val Leu	Leu Thr	Asp Ala	Gly Lys	Arg Asp	Val Leu	Thr	
	120		125		130			

caa gac cta	ccg gat	agc ttt	acg tcc	ttt act	ggg cac	acg gaa	aac	547
Gln Asp Leu	Pro Asp	Ser Phe	Thr Ser	Phe Thr	Gly His	Thr Glu	Asn	
	135		140		145			

tcc gta								553
Ser Val								
150								

<210> 2634

<211> 151

<212> PRT

<213> Corynebacterium glutamicum

<400> 2634


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Met Val Ser Val Leu Leu Ile Gln Pro Arg Gln Gly Glu Ala Val Ala
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             20             25             30

Glu Leu Thr Ser Arg Met Leu Asp Thr Thr Thr Ser Arg Ile Gly Ser
  35             40             45

Leu Glu Gly Phe Asp Gly Val Ile Val Gly Gly Ser Pro Leu Asn Ala
  50             55             60

Thr Asn Phe Glu Tyr Ser Asp Trp Gln Arg His Val His Arg Glu Leu
  65             70             75             80

Ser Leu Leu Ile Asn His Pro Leu Pro Thr Ile Phe Val Cys Tyr Gly
             85             90             95

Asn Thr Phe Leu Thr Phe Phe Ser Gly Gln Ile Gly Arg Thr His
             100            105            110

Pro Glu Asp Ser Gly Ala Thr Thr Val Leu Leu Thr Asp Ala Gly Lys
             115            120            125

Arg Asp Val Leu Thr Gln Asp Leu Pro Asp Ser Phe Thr Ser Phe Thr
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Gly His Thr Glu Asn Ser Val
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<210> 2635

<211> 621

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(598)

<223> RXA02212

<400> 2635

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              Met Ile Pro Glu Asn
              1             5

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att gat ctc aag cag ctc gct tcg gag ctt ggt gat gat gcc gtg gca 163
Ile Asp Leu Lys Gln Leu Ala Ser Glu Leu Gly Asp Asp Ala Val Ala
             10             15             20

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atg ggg gag cac aca ggc aac cag ttt cgg act ttg gaa aaa gac ctt 211
Met Gly Glu His Thr Gly Asn Gln Phe Pro Thr Leu Glu Lys Asp Leu
             25             30             35

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att aat gtt gtg aca gat gca aag gaa tca gat ttt gga tct tta ggg 259
Ile Asn Val Val Thr Asp Ala Lys Glu Ser Asp Phe Gly Ser Leu Gly
             40             45             50

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gtc gtg att ctt gat gaa act cca gtg atg act tcc aac ctg agg gat 307

Val	Val	Ile	Leu	Asp	Glu	Thr	Pro	Val	Met	Thr	Ser	Asn	Leu	Arg	Asp	
55						60					65					
att	gcg	cag	gag	ctg	ttg	att	caa	acg	gat	ctg	gac	acc	gtt	gtg	gtg	355
Ile	Ala	Gln	Glu	Leu	Leu	Ile	Gln	Thr	Asp	Leu	Asp	Thr	Val	Val	Val	
70				75					80					85		
cgg	gct	cca	atg	tgc	gct	gcg	gtg	gtg	agt	gat	gtt	cat	tgc	agg	gcg	403
Arg	Ala	Pro	Met	Ser	Ala	Ala	Val	Val	Ser	Asp	Val	His	Ser	Arg	Ala	
				90					95				100			
gcg	ctt	gag	tca	ggg	cag	cat	gat	ttg	ctt	ggg	acc	act	gat	tac	gtg	451
Ala	Leu	Glu	Ser	Gly	Gln	His	Asp	Leu	Leu	Gly	Thr	Thr	Asp	Tyr	Val	
			105				110						115			
ctg	gga	acg	gag	ctt	ttg	gta	cag	gat	gta	acg	gaa	tgc	acg	gtg	ggg	499
Leu	Gly	Thr	Glu	Leu	Leu	Val	Gln	Asp	Val	Thr	Glu	Ser	Thr	Val	Gly	
			120			125						130				
aat	att	gat	tgg	ggt	caa	ttg	ctg	att	tgg	ggg	ttg	gtt	gct	ttg	gca	547
Asn	Ile	Asp	Trp	Gly	Gln	Leu	Leu	Ile	Trp	Gly	Leu	Val	Ala	Leu	Ala	
			135			140					145					
atc	gcc	gtg	gtt	gtt	gcg	ggt	gcg	tct	gtg	cgt	cga	aaa	gca	ata	tct	595
Ile	Ala	Val	Val	Val	Ala	Gly	Ala	Ser	Val	Arg	Arg	Lys	Ala	Ile	Ser	
150				155					160					165		
tta	taagtaaagt	tctaaagctt	tac													621
Leu																

<210> 2636
 <211> 166
 <212> PRT
 <213> *Corynebacterium glutamicum*
 <400> 2636
 Met Ile Pro Glu Asn Ile Asp Leu Lys Gln Leu Ala Ser Glu Leu Gly
 1 5 10 15
 Asp Asp Ala Val Ala Met Gly Glu His Thr Gly Asn Gln Phe Pro Thr
 20 25 30
 Leu Glu Lys Asp Leu Ile Asn Val Val Thr Asp Ala Lys Glu Ser Asp
 35 40 45
 Phe Gly Ser Leu Gly Val Val Ile Leu Asp Glu Thr Pro Val Met Thr
 50 55 60
 Ser Asn Leu Arg Asp Ile Ala Gln Glu Leu Leu Ile Gln Thr Asp Leu
 65 70 75 80
 Asp Thr Val Val Val Arg Ala Pro Met Ser Ala Ala Val Val Ser Asp
 85 90 95
 Val His Ser Arg Ala Ala Leu Glu Ser Gly Gln His Asp Leu Leu Gly
 100 105 110
 Thr Thr Asp Tyr Val Leu Gly Thr Glu Leu Leu Val Gln Asp Val Thr
 115 120 125

Glu Ser Thr Val Gly Asn Ile Asp Trp Gly Gln Leu Leu Ile Trp Gly
 130 135 140

Leu Val Ala Leu Ala Ile Ala Val Val Val Ala Gly Ala Ser Val Arg
 145 150 155 160

Arg Lys Ala Ile Ser Leu
 165

<210> 2637

<211> 329

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(306)

<223> RXA02216

<400> 2637

gta gcg ccc gcc cct gga cac gtg gtg ttg gca acg gga cca acc tgc 48
 Val Ala Pro Ala Pro Gly His Val Val Leu Ala Thr Gly Pro Thr Cys
 1 5 10 15

ccc atc cag atg ctg cgc gcc aac aag aac acc tgg tca gtt caa ttc 96
 Pro Ile Gln Met Leu Arg Ala Asn Lys Asn Thr Trp Ser Val Gln Phe
 20 25 30

cat gcg gat atg gat gcc gta ggc atg aaa aac cgc atg gat ttt tac 144
 His Ala Asp Met Asp Ala Val Gly Met Lys Asn Arg Met Asp Phe Tyr
 35 40 45

tcc aac tac cgg ttc ttc tcc cca gaa gat tat gac cgc atc att gca 192
 Ser Asn Tyr Arg Phe Phe Ser Pro Glu Asp Tyr Asp Arg Ile Ile Ala
 50 55 60

gag cta ccc tct gtt gac tcc att tat gcc aac agg gtg ctc cgc aac 240
 Glu Leu Pro Ser Val Asp Ser Ile Tyr Ala Asn Arg Val Leu Arg Asn
 65 70 75 80

ttc gtg gag gtc tgc gaa gga att cgt gtt gct gat ggt gct gag cac 288
 Phe Val Glu Val Cys Glu Gly Ile Arg Val Ala Asp Gly Ala Glu His
 85 90 95

caa ctc cca aag ctt aac taatcgagga gactgggtgat tgc 329
 Gln Leu Pro Lys Leu Asn
 100

<210> 2638

<211> 102

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2638

Val Ala Pro Ala Pro Gly His Val Val Leu Ala Thr Gly Pro Thr Cys
 1 5 10 15

Pro Ile Gln Met Leu Arg Ala Asn Lys Asn Thr Trp Ser Val Gln Phe

20 25 30
 His Ala Asp Met Asp Ala Val Gly Met Lys Asn Arg Met Asp Phe Tyr
 35 40 45
 Ser Asn Tyr Arg Phe Phe Ser Pro Glu Asp Tyr Asp Arg Ile Ile Ala
 50 55 60
 Glu Leu Pro Ser Val Asp Ser Ile Tyr Ala Asn Arg Val Leu Arg Asn
 65 70 75 80
 Phe Val Glu Val Cys Glu Gly Ile Arg Val Ala Asp Gly Ala Glu His
 85 90 95
 Gln Leu Pro Lys Leu Asn
 100

 <210> 2639
 <211> 786
 <212> DNA
 <213> *Corynebacterium glutamicum*

 <220>
 <221> CDS
 <222> (101)..(763)
 <223> RXA02217

 <400> 2639
 ccaaatgggt atgggcgctt ttgaccatcg tcaatgggtg ttgccccgct gcctactggg 60

 ctttcggcag gaaaaactaa gagttgttag ggtggcgctc atg act aat aaa aca 115
 Met Thr Asn Lys Thr
 1 5

 cga gct cta ctc att ggt ggc cac ggc aag gtg gcc ctc cta gca acc 163
 Arg Ala Leu Leu Ile Gly Gly His Gly Lys Val Ala Leu Leu Ala Thr
 10 15 20

 ccc atg ctt atc gac gcc tcg gtg cag gtc act tcc atg tac cgc aat 211
 Pro Met Leu Ile Asp Ala Ser Val Gln Val Thr Ser Met Tyr Arg Asn
 25 30 35

 ccg gac cac agg tcc gaa att gag gcg ctg ggc gcc aca act tta gag 259
 Pro Asp His Arg Ser Glu Ile Glu Ala Leu Gly Ala Thr Thr Leu Glu
 40 45 50

 cgt gac gtc acc aca ctc agc gtg gag gat tgg gca gat ctg ctc aag 307
 Arg Asp Val Thr Thr Leu Ser Val Glu Asp Trp Ala Asp Leu Leu Lys
 55 60 65

 gac ttc gac gta gtg gtg tgg agc gcc gga aac ggt ggc aag aac ggc 355
 Asp Phe Asp Val Val Val Trp Ser Ala Gly Asn Gly Gly Lys Asn Gly
 70 75 80 85

 gcg gat gca act tat gcc att gat cgt gat gcc gcg atc gca tcc att 403
 Ala Asp Ala Thr Tyr Ala Ile Asp Arg Asp Ala Ala Ile Ala Ser Ile
 90 95 100

 gat ggt gca gct agc cta ggg gag aag gca cct cgc tac atc atg gtg 451
 Asp Gly Ala Ala Ser Leu Gly Glu Lys Ala Pro Arg Tyr Ile Met Val

105	110	115	
agc tac att gga tcc tcc acg cac acc att gat cct tca gca tcc ttc			499
Ser Tyr Ile Gly Ser Ser Thr His Thr Ile Asp Pro Ser Ala Ser Phe			
120	125	130	
tac cca tat gca gaa tcc aaa aag gcc gct gat gag cac cta agc tcc			547
Tyr Pro Tyr Ala Glu Ser Lys Lys Ala Ala Asp Glu His Leu Ser Ser			
135	140	145	
acc aac ctg gat tac ctt atc ctc gca cca gca gcc tta act ctg gat			595
Thr Asn Leu Asp Tyr Leu Ile Leu Ala Pro Ala Leu Thr Leu Asp			
150	155	160	165
gaa gtc aat ggc gtt gag gtg atc gcc gat acc aac gaa gca gcc gca			643
Glu Val Asn Gly Val Glu Val Ile Ala Asp Thr Asn Glu Ala Ala			
170	175	180	
ggc cgc acc aca tca aga gtc ctc gtt gcg gaa gtt atc acc gag ttg			691
Gly Arg Thr Thr Ser Arg Val Leu Val Ala Glu Val Ile Thr Glu Leu			
185	190	195	
gtg gtt cgc gac ttc cca caa acc cgt gtg ctg cct ttc gtg gat ggc			739
Val Val Arg Asp Phe Pro Gln Thr Arg Val Leu Pro Phe Val Asp Gly			
200	205	210	
gaa tca cca gtc tcc tcg att agt taagctttgg gagttggtgc tca			786
Glu Ser Pro Val Ser Ser Ile Ser			
215	220		
<210> 2640			
<211> 221			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 2640			
Met Thr Asn Lys Thr Arg Ala Leu Leu Ile Gly Gly His Gly Lys Val			
1	5	10	15
Ala Leu Leu Ala Thr Pro Met Leu Ile Asp Ala Ser Val Gln Val Thr			
20	25	30	
Ser Met Tyr Arg Asn Pro Asp His Arg Ser Glu Ile Glu Ala Leu Gly			
35	40	45	
Ala Thr Thr Leu Glu Arg Asp Val Thr Thr Leu Ser Val Glu Asp Trp			
50	55	60	
Ala Asp Leu Leu Lys Asp Phe Asp Val Val Val Trp Ser Ala Gly Asn			
65	70	75	80
Gly Gly Lys Asn Gly Ala Asp Ala Thr Tyr Ala Ile Asp Arg Asp Ala			
85	90	95	
Ala Ile Ala Ser Ile Asp Gly Ala Ala Ser Leu Gly Glu Lys Ala Pro			
100	105	110	
Arg Tyr Ile Met Val Ser Tyr Ile Gly Ser Ser Thr His Thr Ile Asp			
115	120	125	

Pro Ser Ala Ser Phe Tyr Pro Tyr Ala Glu Ser Lys Lys Ala Ala Asp
130 135 140

Glu His Leu Ser Ser Thr Asn Leu Asp Tyr Leu Ile Leu Ala Pro Ala
145 150 155 160

Ala Leu Thr Leu Asp Glu Val Asn Gly Val Glu Val Ile Ala Asp Thr
165 170 175

Asn Glu Ala Ala Ala Gly Arg Thr Thr Ser Arg Val Leu Val Ala Glu
180 185 190

Val Ile Thr Glu Leu Val Val Arg Asp Phe Pro Gln Thr Arg Val Leu
195 200 205

Pro Phe Val Asp Gly Glu Ser Pro Val Ser Ser Ile Ser
210 215 220

<210> 2641

<211> 390

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(367)

<223> RXA02218

<400> 2641

caatgatttta tatgtcttgg acgagcgatt aaatagagtt ggcatacccc aaatgataga 60

cccaaagtgt cgtgtccacc gctcgttgta gcatgaaccc atg ttt gca atc atg 115
Met Phe Ala Ile Met
1 5

act gtc aca ggg cag gac cac acc gga att atc gcc gca gtt tcc acc 163
Thr Val Thr Gly Gln Asp His Thr Gly Ile Ile Ala Ala Val Ser Thr
10 15 20

gcg ttg gct gag cta gat gtc aat att cac aac gtt tcc caa acc atc 211
Ala Leu Ala Glu Leu Asp Val Asn Ile His Asn Val Ser Gln Thr Ile
25 30 35

atg gat caa tgg ttc acc atg atc ttg cac gtt ggt ttc gat gaa tcg 259
Met Asp Gln Trp Phe Thr Met Ile Leu His Val Gly Phe Asp Glu Ser
40 45 50

gtc ttg gat atc gcc aca gtt cag gaa cgc atg aag cca gtg gaa aag 307
Val Leu Asp Ile Ala Thr Val Gln Glu Arg Met Lys Pro Val Glu Lys
55 60 65

gaa cag gcc ttg gtt att cgt atc cag tct gaa gcc ttg ttc aac gcg 355
Glu Gln Gly Leu Val Ile Arg Ile Gln Ser Glu Ala Leu Phe Asn Ala
70 75 80 85

gtt aat gag atc tagggggtgc acatggatga ttt 390
Val Asn Glu Ile

<210> 2642
 <211> 89
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2642
 Met Phe Ala Ile Met Thr Val Thr Gly Gln Asp His Thr Gly Ile Ile
 1 5 10 15
 Ala Ala Val Ser Thr Ala Leu Ala Glu Leu Asp Val Asn Ile His Asn
 20 25 30
 Val Ser Gln Thr Ile Met Asp Gln Trp Phe Thr Met Ile Leu His Val
 35 40 45
 Gly Phe Asp Glu Ser Val Leu Asp Ile Ala Thr Val Gln Glu Arg Met
 50 55 60
 Lys Pro Val Glu Lys Glu Gln Gly Leu Val Ile Arg Ile Gln Ser Glu
 65 70 75 80
 Ala Leu Phe Asn Ala Val Asn Glu Ile
 85

<210> 2643
 <211> 1509
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1486)
 <223> RXA02219

<400> 2643
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 agccttggtc aacgcgggta atgagatcta ggggggtgcac atg gat gat ttt tct 115
 Met Asp Asp Phe Ser
 1 5
 gca tcg cta ggt ttt act gac cgt tcc tcg agg gga att ctg gac acc 163
 Ala Ser Leu Gly Phe Thr Asp Arg Ser Ser Arg Gly Ile Leu Asp Thr
 10 15 20
 atc gag atg att gag aag tat cgt ctt gat att cgc acc gtg acc atg 211
 Ile Glu Met Ile Glu Lys Tyr Arg Leu Asp Ile Arg Thr Val Thr Met
 25 30 35
 gga atc agc ctg ttg gaa tgc gcg cgt ggc tcg atg gaa gag acc gcg 259
 Gly Ile Ser Leu Leu Glu Cys Ala Arg Gly Ser Met Glu Glu Thr Ala
 40 45 50
 acg gct gtt tat gat cgc gtg acg tca cag gct gca cgt ctg gtt gag 307
 Thr Ala Val Tyr Asp Arg Val Thr Ser Gln Ala Ala Arg Leu Val Glu
 55 60 65
 gtt tgt gaa ggc att gag cgt gaa ttg ggc att ccc att gtg aat aag 355
 Val Cys Glu Gly Ile Glu Arg Glu Leu Gly Ile Pro Ile Val Asn Lys
 70 75 80 85

cgc atc tcg gtg act cca att gcc ctg gtg act gct ggt tgc agt ggc	403
Arg Ile Ser Val Thr Pro Ile Ala Leu Val Thr Ala Gly Cys Ser Gly	
90 95 100	
gat ccc gtt gac gtt gct cga gcc tta gat aag gca gca aaa gat gtc	451
Asp Pro Val Asp Val Ala Arg Ala Leu Asp Lys Ala Ala Lys Asp Val	
105 110 115	
gga gtg aac ttc atc ggc ggg tat tca gca ctg gtt gaa aaa ggt gga	499
Gly Val Asn Phe Ile Gly Gly Tyr Ser Ala Leu Val Gly Lys Gly Gly	
120 125 130	
acc acc tcc gat att cgg ctg atc cgc tcc att ccc gag gca ttg agc	547
Thr Thr Ser Asp Ile Arg Leu Ile Arg Ser Ile Pro Glu Ala Leu Ser	
135 140 145	
aca acc gat gtg gtg tgt gga tcc gtc aat gtg gcg tcg tct cgc gcg	595
Thr Thr Asp Val Val Cys Gly Ser Val Asn Val Ala Ser Ser Arg Ala	
150 155 160 165	
ggt atc aac atg aac gca gtc aat gag atg ggc aag gtg gtc aag caa	643
Gly Ile Asn Met Asn Ala Val Asn Glu Met Gly Lys Val Val Lys Gln	
170 175 180	
gca gct gaa ttg acc aaa gat cgc tcc gcc atc gca tgt gca aag cta	691
Ala Ala Glu Leu Thr Lys Asp Arg Ser Ala Ile Ala Cys Ala Lys Leu	
185 190 195	
gtg gtc ttt gcc aat tct gtg ggc gat aat cca ttc atg gct ggc gct	739
Val Val Phe Ala Asn Ser Val Gly Asp Asn Pro Phe Met Ala Gly Ala	
200 205 210	
ttc cac ggc att gag gag cgc gat tgt gtg gtc agc gtt ggt gtc tca	787
Phe His Gly Ile Glu Glu Pro Asp Cys Val Val Ser Val Gly Val Ser	
215 220 225	
gga cca ggc gtg gtt agt cgc gcg ctg ggc aat ctt caa ggt gcc acc	835
Gly Pro Gly Val Val Ser Arg Ala Leu Gly Asn Leu Gln Gly Ala Thr	
230 235 240 245	
ctt gat caa gtc gca gaa gag atc aag aaa gcg gcc ttc aag atc act	883
Leu Asp Gln Val Ala Glu Glu Ile Lys Lys Ala Ala Phe Lys Ile Thr	
250 255 260	
cgt act gga caa ctg gtt ggt gcg atg gcc tca gaa cgc cta gga gtt	931
Arg Thr Gly Gln Leu Val Gly Ala Met Ala Ser Glu Arg Leu Gly Val	
265 270 275	
cct ttc ggc atc gtt gat ctt tcg ctc gct ccc act gct gaa gtg ggc	979
Pro Phe Gly Ile Val Asp Leu Ser Leu Ala Pro Thr Ala Glu Val Gly	
280 285 290	
gat tcc gtg gca aat atc ctt gag gtc atg ggt ctt gac cag gtg ggc	1027
Asp Ser Val Ala Asn Ile Leu Glu Val Met Gly Leu Asp Gln Val Gly	
295 300 305	
aca cat ggc acc acc gcg gca ctc gca ctg ctc aac gac gcg gtg aaa	1075
Thr His Gly Thr Thr Ala Ala Leu Ala Leu Leu Asn Asp Ala Val Lys	
310 315 320 325	

Pro Ile Val Asn Lys Arg Ile Ser Val Thr Pro Ile Ala Leu Val Thr

85										90					95				
Ala	Gly	Cys	Ser	Gly	Asp	Pro	Val	Asp	Val	Ala	Arg	Ala	Leu	Asp	Lys				
			100						105						110				
Ala	Ala	Lys	Asp	Val	Gly	Val	Asn	Phe	Ile	Gly	Gly	Tyr	Ser	Ala	Leu				
		115					120					125							
Val	Glu	Lys	Gly	Gly	Thr	Thr	Ser	Asp	Ile	Arg	Leu	Ile	Arg	Ser	Ile				
	130					135					140								
Pro	Glu	Ala	Leu	Ser	Thr	Thr	Asp	Val	Val	Cys	Gly	Ser	Val	Asn	Val				
	145				150						155				160				
Ala	Ser	Ser	Arg	Ala	Gly	Ile	Asn	Met	Asn	Ala	Val	Asn	Glu	Met	Gly				
			165					170						175					
Lys	Val	Val	Lys	Gln	Ala	Ala	Glu	Leu	Thr	Lys	Asp	Arg	Ser	Ala	Ile				
			180					185					190						
Ala	Cys	Ala	Lys	Leu	Val	Val	Phe	Ala	Asn	Ser	Val	Gly	Asp	Asn	Pro				
			195				200						205						
Phe	Met	Ala	Gly	Ala	Phe	His	Gly	Ile	Glu	Glu	Pro	Asp	Cys	Val	Val				
			210			215					220								
Ser	Val	Gly	Val	Ser	Gly	Pro	Gly	Val	Val	Ser	Arg	Ala	Leu	Gly	Asn				
				230							235				240				
Leu	Gln	Gly	Ala	Thr	Leu	Asp	Gln	Val	Ala	Glu	Glu	Ile	Lys	Lys	Ala				
				245				250						255					
Ala	Phe	Lys	Ile	Thr	Arg	Thr	Gly	Gln	Leu	Val	Gly	Ala	Met	Ala	Ser				
			260				265					270							
Glu	Arg	Leu	Gly	Val	Pro	Phe	Gly	Ile	Val	Asp	Leu	Ser	Leu	Ala	Pro				
			275				280					285							
Thr	Ala	Glu	Val	Gly	Asp	Ser	Val	Ala	Asn	Ile	Leu	Glu	Val	Met	Gly				
			290			295					300								
Leu	Asp	Gln	Val	Gly	Thr	His	Gly	Thr	Thr	Ala	Ala	Leu	Ala	Leu	Leu				
				310					315					320					
Asn	Asp	Ala	Val	Lys	Lys	Gly	Gly	Met	Met	Ala	Cys	Ser	Arg	Val	Gly				
				325				330						335					
Gly	Leu	Ser	Gly	Ser	Phe	Ile	Pro	Val	Ser	Glu	Asp	Lys	Gly	Met	Ile				
			340					345					350						
Asp	Ala	Val	Arg	Thr	Gly	Ala	Ile	Ser	Ile	Asp	Lys	Leu	Glu	Ala	Met				
			355			360						365							
Thr	Ala	Ile	Cys	Ser	Val	Gly	Leu	Asp	Met	Ile	Ala	Ile	Pro	Gly	Asp				
			370			375					380								
Thr	Pro	Ala	Glu	Thr	Ile	Ser	Gly	Met	Ile	Ala	Asp	Glu	Ala	Ala	Ile				
			385		390				395					400					
Gly	Val	Met	Asn	His	Lys	Thr	Thr	Ala	Val	Arg	Val	Ile	Pro	Val	Pro				
				405				410						415					

Gly Thr Val Pro Gly Asp Glu Val Asp Phe Gly Gly Leu Leu Gly Tyr
 420 425 430

Ala Pro Val Ile Pro Val Asn Thr Val Gly Asn Ser Glu Phe Ile His
 435 440 445

Arg Gly Gly Phe Ile Pro Ala Pro Val His Gly Phe Arg Asn
 450 455 460

<210> 2645

<211> 1485

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1462)

<223> RXA02221

<400> 2645

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ccatcacgac ttcataccca ccaattgaaa gtaaagtcca atg ttt acc gca tcc 115
 Met Phe Thr Ala Ser
 1 5

att cct act tat gaa tta ggg tct ttc agc aag ggc tcc tac gtt gag 163
 Ile Pro Thr Tyr Glu Leu Gly Ser Phe Ser Lys Gly Ser Tyr Val Glu
 10 15 20

atc aaa gga act tac ttc tac cct gac acg cta aat act tta ttt aga 211
 Ile Lys Gly Thr Tyr Phe Tyr Pro Asp Thr Leu Asn Thr Leu Phe Arg
 25 30 35

aat tct ggg gca aaa gac aac gaa gag ttc ttt gta gac gta act ctt 259
 Asn Ser Gly Ala Lys Asp Asn Glu Glu Phe Phe Val Asp Val Thr Leu
 40 45 50

gtt cca gaa cca gat aat ccg cat agc act cga ggc cat gcc att tca 307
 Val Pro Glu Pro Asp Asn Pro His Ser Thr Arg Gly His Ala Ile Ser
 55 60 65

gtc cgc tgg aat gat ctg gta ata gga cat att gcc tcg gat atg act 355
 Val Arg Trp Asn Asp Leu Val Ile Gly His Ile Ala Ser Asp Met Thr
 70 75 80 85

gaa aaa ttc caa caa gtg cga cga gtt gca gct agt ggc tac gat gct 403
 Glu Lys Phe Gln Gln Val Arg Arg Val Ala Ala Ser Gly Tyr Asp Ala
 90 95 100

cga gtc tct gct cgg att tgg acg aat aca aac tat aag aat gaa cga 451
 Arg Val Ser Ala Arg Ile Trp Thr Asn Thr Asn Tyr Lys Asn Glu Arg
 105 110 115

gat ttt tgg gta tct gtt aag ctg ccc gat cca gat ttc ctt gtt cct 499
 Asp Phe Trp Val Ser Val Lys Leu Pro Asp Pro Asp Phe Leu Val Pro
 120 125 130

ctt aat gat cct ccc cat gac ggg ttt acc ctg ctg cct tat gga aca 547

Leu Asn Asp Pro Pro His Asp Gly Phe Thr Leu Leu Pro Tyr Gly Thr	
135 140 145	
gca atc caa gtc acc aag gaa tct gat cac atg gac gtg ctc tca gaa	595
Ala Ile Gln Val Thr Lys Glu Ser Asp His Met Asp Val Leu Ser Glu	
150 155 160 165	
ttc gtg cct cca tct gga caa ggt cag att ctc gta tcg cta cac atc	643
Phe Val Pro Pro Ser Gly Gln Gly Gln Ile Leu Val Ser Leu His Ile	
170 175 180	
att aac gca ggc gtg aga aaa gaa tgg gat ggc att gaa gtt cgg ctc	691
Ile Asn Ala Gly Val Arg Lys Glu Trp Asp Gly Ile Glu Val Arg Leu	
185 190 195	
gat aat caa cgg atc gga gag ctt aca aag gcc agt tca gaa aaa ttc	739
Asp Asn Gln Arg Ile Gly Glu Leu Thr Lys Ala Ser Ser Glu Lys Phe	
200 205 210	
gca ccc gta gtg cga cat ttc gat gac cta gga ctt agt aca cta tgt	787
Ala Pro Val Val Arg His Phe Asp Asp Leu Gly Leu Ser Thr Leu Cys	
215 220 225	
cgt gcg ctc atc aag ggg tca tca cta gct gct gaa gta act cta tat	835
Arg Ala Leu Ile Lys Gly Ser Ser Leu Ala Ala Glu Val Thr Leu Tyr	
230 235 240 245	
gga gct cgt gca cat gag ctt tcc gaa gaa gac tta gaa cct aaa agc	883
Gly Ala Arg Ala His Glu Leu Ser Glu Glu Asp Leu Glu Pro Lys Ser	
250 255 260	
tct tcc cca ttg ccc agg ttg gtt gaa tac cag tca aat ccg ttt aat	931
Ser Ser Pro Leu Pro Arg Leu Val Glu Tyr Gln Ser Asn Pro Phe Asn	
265 270 275	
tat caa gtc ccc aac agg tgg ccc ggc gag cag aat caa cgt gct cct	979
Tyr Gln Val Pro Asn Arg Trp Pro Gly Glu Gln Asn Gln Arg Ala Pro	
280 285 290	
aag tcg caa aag tct tct tca tca cct ttc gca gcg tat cgc ggg cca	1027
Lys Ser Gln Lys Ser Ser Ser Ser Pro Phe Ala Ala Tyr Arg Gly Pro	
295 300 305	
tcg caa cct agt aaa tca ctc aca ccg ttt gta gcg cag aca cct gcg	1075
Ser Gln Pro Ser Lys Ser Leu Thr Pro Phe Val Ala Gln Thr Pro Ala	
310 315 320 325	
cct cag cct agt gat cga ttt att gat tgg gat tca ttg ctt caa ccg	1123
Pro Gln Pro Ser Asp Arg Phe Ile Asp Trp Asp Ser Leu Leu Gln Pro	
330 335 340	
gac gga act cca aga gct acg cca ttc caa aga gga gta acc cgc ggg	1171
Asp Gly Thr Pro Arg Ala Thr Pro Phe Gln Arg Gly Val Thr Arg Gly	
345 350 355	
tta att ggc aag cat ttt tcg aat caa aaa tct cca aga att gac ttt	1219
Leu Ile Gly Lys His Phe Ser Asn Gln Lys Ser Pro Arg Ile Asp Phe	
360 365 370	
gca acg gtg ggg caa tgt gat gca att ctc cga act ttc gga gag ccg	1267
Ala Thr Val Gly Gln Cys Asp Ala Ile Leu Arg Thr Phe Gly Glu Pro	

375	380	385	
acc gac aag ctt tat aaa gac ggc agg act tct tgg cct ttg tgg tgg			1315
Thr Asp Lys Leu Tyr Lys Asp Gly Arg Thr Ser Trp Pro Leu Trp Trp			
390	395	400	405
gcg ctc atg gcg ata gtc acc ctt ctc gtc atg ttg ctg aac ttt att			1363
Ala Leu Met Ala Ile Val Thr Leu Leu Val Met Leu Leu Asn Phe Ile			
	410	415	420
cca gga att ggt ccg atc ttc cca ctt atc gga ttg atc gta ctt ggt			1411
Pro Gly Ile Gly Pro Ile Phe Pro Leu Ile Gly Leu Ile Val Leu Gly			
	425	430	435
cat cac ttt tgg act cgc cga aaa ctt aac cca cca ttc ggt aga tca			1459
His His Phe Trp Thr Arg Arg Lys Leu Asn Pro Pro Phe Gly Arg Ser			
	440	445	450
aaa tagatattct catcaaatat cgc			1485
Lys			

<210> 2646

<211> 454

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2646

Met Phe Thr Ala Ser Ile Pro Thr Tyr Glu Leu Gly Ser Phe Ser Lys

1

5

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Gly Ser Tyr Val Glu Ile Lys Gly Thr Tyr Phe Tyr Pro Asp Thr Leu

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25

30

Asn Thr Leu Phe Arg Asn Ser Gly Ala Lys Asp Asn Glu Glu Phe Phe

35

40

45

Val Asp Val Thr Leu Val Pro Glu Pro Asp Asn Pro His Ser Thr Arg

50

55

60

Gly His Ala Ile Ser Val Arg Trp Asn Asp Leu Val Ile Gly His Ile

65

70

75

80

Ala Ser Asp Met Thr Glu Lys Phe Gln Gln Val Arg Arg Val Ala Ala

85

90

95

Ser Gly Tyr Asp Ala Arg Val Ser Ala Arg Ile Trp Thr Asn Thr Asn

100

105

110

Tyr Lys Asn Glu Arg Asp Phe Trp Val Ser Val Lys Leu Pro Asp Pro

115

120

125

Asp Phe Leu Val Pro Leu Asn Asp Pro Pro His Asp Gly Phe Thr Leu

130

135

140

Leu Pro Tyr Gly Thr Ala Ile Gln Val Thr Lys Glu Ser Asp His Met

145

150

155

160

Asp Val Leu Ser Glu Phe Val Pro Pro Ser Gly Gln Gly Gln Ile Leu

165

170

175

Val Ser Leu His Ile Ile Asn Ala Gly Val Arg Lys Glu Trp Asp Gly
 180 185 190
 Ile Glu Val Arg Leu Asp Asn Gln Arg Ile Gly Glu Leu Thr Lys Ala
 195 200 205
 Ser Ser Glu Lys Phe Ala Pro Val Val Arg His Phe Asp Asp Leu Gly
 210 215 220
 Leu Ser Thr Leu Cys Arg Ala Leu Ile Lys Gly Ser Ser Leu Ala Ala
 225 230 235 240
 Glu Val Thr Leu Tyr Gly Ala Arg Ala His Glu Leu Ser Glu Glu Asp
 245 250 255
 Leu Glu Pro Lys Ser Ser Ser Pro Leu Pro Arg Leu Val Glu Tyr Gln
 260 265 270
 Ser Asn Pro Phe Asn Tyr Gln Val Pro Asn Arg Trp Pro Gly Glu Gln
 275 280 285
 Asn Gln Arg Ala Pro Lys Ser Gln Lys Ser Ser Ser Pro Phe Ala
 290 295 300
 Ala Tyr Arg Gly Pro Ser Gln Pro Ser Lys Ser Leu Thr Pro Phe Val
 305 310 315 320
 Ala Gln Thr Pro Ala Pro Gln Pro Ser Asp Arg Phe Ile Asp Trp Asp
 325 330 335
 Ser Leu Leu Gln Pro Asp Gly Thr Pro Arg Ala Thr Pro Phe Gln Arg
 340 345 350
 Gly Val Thr Arg Gly Leu Ile Gly Lys His Phe Ser Asn Gln Lys Ser
 355 360 365
 Pro Arg Ile Asp Phe Ala Thr Val Gly Gln Cys Asp Ala Ile Leu Arg
 370 375 380
 Thr Phe Gly Glu Pro Thr Asp Lys Leu Tyr Lys Asp Gly Arg Thr Ser
 385 390 395 400
 Trp Pro Leu Trp Trp Ala Leu Met Ala Ile Val Thr Leu Leu Val Met
 405 410 415
 Leu Leu Asn Phe Ile Pro Gly Ile Gly Pro Ile Phe Pro Leu Ile Gly
 420 425 430
 Leu Ile Val Leu Gly His His Phe Trp Thr Arg Arg Lys Leu Asn Pro
 435 440 445
 Pro Phe Gly Arg Ser Lys
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<210> 2647

<211> 741

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(718)

<223> RXA02227

<400> 2647

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ggagagggtgt ttgccacga atttcggtgg gcaggatagg gtg gaa gac gtg aat 115
 Val Glu Asp Val Asn
 1 5

gca acg ctg att atc atg cct gga agt ccg gcg ctg gta cct gaa ctg 163
 Ala Thr Leu Ile Ile Met Pro Gly Ser Pro Ala Leu Val Pro Glu Leu
 10 15 20

gca cca gcg gat gct gcg ggg gcg cgc ttg ttg gcg tcg tta cgt gca 211
 Ala Pro Ala Asp Ala Ala Gly Ala Arg Leu Leu Ala Ser Leu Arg Ala
 25 30 35

gtt ttt gat gcg gaa ctg gct aat gat gat cgc ccg atc gag ttg gtt 259
 Val Phe Asp Ala Glu Leu Ala Asn Asp Asp Arg Pro Ile Glu Leu Val
 40 45 50

ggc tcc cgg gat gag gcg tgg ttt acc aag cat gcg gga aat ctg cgg 307
 Gly Ser Arg Asp Glu Ala Trp Phe Thr Lys His Ala Gly Asn Leu Arg
 55 60 65

gcc tgg ggt gca ccg agc gtg cag gtt tct gac gga cat tat ttg ccg 355
 Ala Trp Gly Ala Pro Ser Val Gln Val Ser Asp Gly His Tyr Leu Pro
 70 75 80 85

gaa att ttg cag cgt gtc gcg ctg ggt ggt ttc gaa tcg cgt gta act 403
 Glu Ile Leu Gln Arg Val Ala Leu Gly Gly Phe Glu Ser Arg Val Thr
 90 95 100

cat gtg cgc gat cgg ttg ggt agc gtc aac gac aac acg gtt acg gtg 451
 His Val Arg Asp Arg Leu Gly Ser Val Asn Asp Asn Thr Val Thr Val
 105 110 115

ctt gcc ctt gac ggc ccc acg ggc ttg acc acc cgc gcg ccg tcc gca 499
 Leu Ala Leu Asp Gly Pro Thr Gly Leu Thr Thr Arg Ala Pro Ser Ala
 120 125 130

ctc gtg ccc ggc gcg tcc aac atc gac gcc tgg tgc cgc tca ttg ctg 547
 Leu Val Pro Gly Ala Ser Asn Ile Asp Ala Trp Cys Arg Ser Leu Leu
 135 140 145

tct gga aag ccc ggg gaa gtg ccc agc acc agc acg ctt atc gac gcc 595
 Ser Gly Lys Pro Gly Glu Val Pro Ser Thr Ser Thr Leu Ile Asp Ala
 150 155 160 165

tcc ctc cgc gaa cca cag ctc tgg ctc gac tta tcc gcc gtg gca aca 643
 Ser Leu Arg Glu Pro Gln Leu Trp Leu Asp Leu Ser Ala Val Ala Thr
 170 175 180

gaa gcg tca act gct caa ctt ctc gac agc gac gac aca cac ggc gtg 691
 Glu Ala Ser Thr Ala Gln Leu Leu Asp Ser Asp Asp Thr His Gly Val
 185 190 195

gga cgc tac gtt gct cgc tgg act ttt taacttaag gagatctaga 738

Gly Arg Tyr Val Ala Arg Trp Thr Phe
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tcg

741

<210> 2648

<211> 206

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2648

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Leu Val Pro Glu Leu Ala Pro Ala Asp Ala Ala Gly Ala Arg Leu Leu
20 25 30

Ala Ser Leu Arg Ala Val Phe Asp Ala Glu Leu Ala Asn Asp Asp Arg
35 40 45

Pro Ile Glu Leu Val Gly Ser Arg Asp Glu Ala Trp Phe Thr Lys His
50 55 60

Ala Gly Asn Leu Arg Ala Trp Gly Ala Pro Ser Val Gln Val Ser Asp
65 70 75 80

Gly His Tyr Leu Pro Glu Ile Leu Gln Arg Val Ala Leu Gly Gly Phe
85 90 95

Glu Ser Arg Val Thr His Val Arg Asp Arg Leu Gly Ser Val Asn Asp
100 105 110

Asn Thr Val Thr Val Leu Ala Leu Asp Gly Pro Thr Gly Leu Thr Thr
115 120 125

Arg Ala Pro Ser Ala Leu Val Pro Gly Ala Ser Asn Ile Asp Ala Trp
130 135 140

Cys Arg Ser Leu Leu Ser Gly Lys Pro Gly Glu Val Pro Ser Thr Ser
145 150 155 160

Thr Leu Ile Asp Ala Ser Leu Arg Glu Pro Gln Leu Trp Leu Asp Leu
165 170 175

Ser Ala Val Ala Thr Glu Ala Ser Thr Ala Gln Leu Leu Asp Ser Asp
180 185 190

Asp Thr His Gly Val Gly Arg Tyr Val Ala Arg Trp Thr Phe
195 200 205

<210> 2649

<211> 660

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(637)

<223> RXA02230

$$\begin{array}{ccccccc} \mathcal{G}^{\text{top}}(\mathcal{H}) & \mathcal{H}^{\text{top}}(\mathcal{H}) & \mathcal{H}^{\text{top}}(\mathcal{H}) & \mathcal{H}^{\text{top}}(\mathcal{H}) & \mathcal{H}^{\text{top}}(\mathcal{H}) & \mathcal{H}^{\text{top}}(\mathcal{H}) & \mathcal{H}^{\text{top}}(\mathcal{H}) \\ \text{Top} & \text{Top} & \text{Top} & \text{Top} & \text{Top} & \text{Top} & \text{Top} \end{array}$$

<211> 179

<213> Cor

<400> 2650

Met Gly Glu Gln Leu Pro Phe Ala Asn Gly Ser Arg Ser Asn Lys Leu
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Pro Leu Ile Val Ile Gly Leu Cys Cys Ile Met Leu Ile Leu Trp Leu
20 25 30

Lys Leu Pro Gly Val Leu Leu Ala Thr Ile Ile Gly Val Ala Thr Met
35 40 45

Ser Val Met Arg Met Arg Thr Ser Thr Pro Glu Thr Ala Ser Leu Val
50 55 60

Thr Ser Ile Arg Leu Ser Ala Glu Asp Ile Ser Asp Val Gln His Glu
65 70 75 80

Trp Gln Gln Phe Leu Thr Ser Pro Glu Ala Asp Ala Leu Ala Asp Arg
85 90 95

Thr Leu Val Arg Pro Ala Leu Ala Asp Pro Asp Cys Gly Asp Lys Ala
100 105 110

Ile Glu Lys Phe His Tyr Glu Ile Ser Asn Ala Asn Arg Phe Leu Gly
115 120 125

Arg Leu Asp Ala Arg Leu Gln Gln Asn Leu Val Val Ser Glu Leu Glu
130 135 140

Thr Leu Leu Lys Val Thr Asp Glu Arg Ala Leu Glu Leu Arg Glu Thr
145 150 155 160

Trp Leu Asp Ala Arg Lys Ala Ala Gln Lys Leu Gly Pro Asn Tyr Asn
165 170 175

Arg Glu Ser

<210> 2651

<211> 879

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(856)

<223> RXA02231

<400> 2651

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aaagtgacta ttgectgtta agggagtttag actaatcgcc atg act agc gat ctg 115
Met Thr Ser Asp Leu
1 5

aag aca atc ggt atg gat ttc gcc aag tgg caa gat gca gtg gaa gca 163
Lys Thr Ile Gly Met Asp Phe Ala Lys Trp Gln Asp Ala Val Glu Ala
10 15 20

gca att gct tca cag cgt ctc gag gta aca ggc gag gtc cgt ggc ggc 211
Ala Ile Ala Ser Gln Arg Leu Glu Val Thr Gly Glu Val Arg Gly Gly
25 30 35

cag ctc atc cag ttc tcg gat gat tcc ggc gcc caa att aac att ctg 259
 Gln Leu Ile Gln Phe Ser Asp Asp Ser Gly Ala Gln Ile Asn Ile Leu
 40 45 50
 gct gtc gag cct ttt gcc acc ttc gcc ggc ttt aac tcc gca aca gtc 307
 Ala Val Glu Pro Phe Ala Thr Phe Ala Gly Phe Asn Ser Ala Thr Val
 55 60 65
 gct tac ggc cac gtc agc atg atc aat gat gtg ctg tcc ctg gtc gat 355
 Ala Tyr Gly His Val Ser Met Ile Asn Asp Val Leu Ser Leu Val Asp
 70 75 80 85
 atc atc gat cct ttc ggc acc cct gtt gcc acc att acc tgc aac ctt 403
 Ile Ile Asp Pro Phe Gly Thr Pro Val Ala Thr Ile Thr Cys Asn Leu
 90 95 100
 gct caa ggc cca ctg ctt gtt gat gaa cca gtg cag cgc tgg cag cag 451
 Ala Gln Gly Pro Leu Leu Val Asp Glu Pro Val Gln Arg Trp Gln Gln
 105 110 115
 atc cgc att act gcc ctg ggc att gat gtt gag gtc cac gac aat gca 499
 Ile Arg Ile Thr Ala Leu Gly Ile Asp Val Glu Val His Asp Asn Ala
 120 125 130
 gat gct tac atc cgc aat ggt ggc gaa act gtc ggc atg ctg gtt tct 547
 Asp Ala Tyr Ile Arg Asn Gly Gly Glu Thr Val His Met Leu Val Ser
 135 140 145
 gaa ggt gca gag aag att gcc agc ggc agc ggc gct gtc atc ccg gac 595
 Glu Gly Ala Glu Lys Ile Ala Ser Gly Ser Gly Ala Val Ile Pro Asp
 150 155 160 165
 gca tcc gca gag ttt tcc gca cgc gtg ttg tct gcg gag tac cgc acc 643
 Ala Ser Ala Glu Phe Ser Ala Arg Val Leu Ser Ala Glu Tyr Arg Thr
 170 175 180
 aac act ctt acc ggc cag cgt ttt atc cac gca aca gtt gat ggc ctc 691
 Asn Thr Leu Thr Gly Gln Arg Phe Ile His Ala Thr Val Asp Gly Leu
 185 190 195
 ttc gct ttt gat gtg tgc ctt cct gat gca cca gaa cta cct gcc cgt 739
 Phe Ala Phe Asp Val Cys Leu Pro Asp Ala Pro Glu Leu Pro Ala Arg
 200 205 210
 gac agc gtg ttg tct ggc aaa gtc atg ctg act gct gcc gtt atc ccc 787
 Asp Ser Val Leu Ser Gly Lys Val Met Leu Thr Ala Ala Val Ile Pro
 215 220 225
 act gag gtc acc ggc tgc ggt ggc tcc ggt ggc ggc tgt ggc tca ggt 835
 Thr Glu Val Thr Gly Cys Gly Gly Ser Gly Gly Cys Gly Ser Gly
 230 235 240 245
 agc tgt ggc tgc ggc gga cac taaaattctg cacaattttt taa 879
 Ser Cys Gly Cys Gly Gly His
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<210> 2652

<211> 252

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2652

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Asp Ala Val Glu Ala Ala Ile Ala Ser Gln Arg Leu Glu Val Thr Gly
          20              25              30

Glu Val Arg Gly Gly Gln Leu Ile Gln Phe Ser Asp Asp Ser Gly Ala
          35              40              45

Gln Ile Asn Ile Leu Ala Val Glu Pro Phe Ala Thr Phe Ala Gly Phe
 50              55              60

Asn Ser Ala Thr Val Ala Tyr Gly His Val Ser Met Ile Asn Asp Val
 65              70              75              80

Leu Ser Leu Val Asp Ile Ile Asp Pro Phe Gly Thr Pro Val Ala Thr
          85              90              95

Ile Thr Cys Asn Leu Ala Gln Gly Pro Leu Leu Val Asp Glu Pro Val
          100             105             110

Gln Arg Trp Gln Gln Ile Arg Ile Thr Ala Leu Gly Ile Asp Val Glu
          115             120             125

Val His Asp Asn Ala Asp Ala Tyr Ile Arg Asn Gly Gly Glu Thr Val
          130             135             140

Gly Met Leu Val Ser Glu Gly Ala Glu Lys Ile Ala Ser Gly Ser Gly
          145             150             155             160

Ala Val Ile Pro Asp Ala Ser Ala Glu Phe Ser Ala Arg Val Leu Ser
          165             170             175

Ala Glu Tyr Arg Thr Asn Thr Leu Thr Gly Gln Arg Phe Ile His Ala
          180             185             190

Thr Val Asp Gly Leu Phe Ala Phe Asp Val Cys Leu Pro Asp Ala Pro
          195             200             205

Glu Leu Pro Ala Arg Asp Ser Val Leu Ser Gly Lys Val Met Leu Thr
          210             215             220

Ala Ala Val Ile Pro Thr Glu Val Thr Gly Cys Gly Gly Ser Gly Gly
          225             230             235             240

Gly Cys Gly Ser Gly Ser Cys Gly Cys Gly Gly His
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<210> 2653

<211> 1656

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1633)

<223> RXA02244

<400> 2653

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ggcgcggtgg tgtccaactt gatcaggaag cgaaattcca atg agc cta gaa aaa 115
 Met Ser Leu Glu Lys
 1 5

tcc ggc gga ttc cgc tcc agg act cca aaa gcg cag cag gaa cct gct 163
 Ser Gly Gly Phe Arg Ser Arg Thr Pro Lys Ala Gln Gln Glu Pro Ala
 10 15 20

aag cag aag ccg cag gcg cgt aaa tct ccg tca aag aag gcc ccg gct 211
 Lys Gln Lys Pro Gln Ala Arg Lys Ser Pro Ser Lys Lys Ala Pro Ala
 25 30 35

cgg ggg cag ggg cag agt cag ggg cag cgc cag gcc caa agc agt ggc 259
 Arg Gly Gln Gly Gln Ser Gln Gly Gln Arg Gln Gly Gln Ser Ser Gly
 40 45 50

aaa ggc ggc gga aac cgc aag ccc cct gcg cag gcc agg gaa gtg agg 307
 Lys Gly Gly Gly Asn Arg Lys Pro Pro Ala Gln Ala Arg Glu Val Arg
 55 60 65

gct ctg ggc gtc gat aag ccg aga gaa att gcg ttt gag gtg ctt gat 355
 Ala Leu Gly Val Asp Lys Pro Arg Glu Ile Ala Phe Glu Val Leu Asp
 70 75 80 85

cgt gtg cgt acc ggt gag gcg tat gcc aac ttg gtg ttg cca cga ctg 403
 Arg Val Arg Thr Gly Glu Ala Tyr Ala Asn Leu Val Leu Pro Arg Leu
 90 95 100

ctg agc aag cac aat ctt tct ggc cgt gac gcg gcc ttt gct acg gaa 451
 Leu Ser Lys His Asn Leu Ser Gly Arg Asp Ala Ala Phe Ala Thr Glu
 105 110 115

att acc tac ggc acc ttg cgt aat gtc ggc ttg ctg gat gag gtc att 499
 Ile Thr Tyr Gly Thr Leu Arg Asn Val Gly Leu Leu Asp Glu Val Ile
 120 125 130

aag gct gca tct ggg cgt gaa ctg tct gat att gat cca gag gtt ttg 547
 Lys Ala Ala Ser Gly Arg Glu Leu Ser Asp Ile Asp Pro Glu Val Leu
 135 140 145

gac gtg ctg cgt ttg ggc gcg tac cag gtg atg ttt acc cgc gtg gag 595
 Asp Val Leu Arg Leu Gly Ala Tyr Gln Val Met Phe Thr Arg Val Glu
 150 155 160 165

gat cac gct gcg gtc gat act tca gta aag atg gtc ggt ggg ctg aag 643
 Asp His Ala Ala Val Asp Thr Ser Val Lys Met Val Gly Gly Leu Lys
 170 175 180

aaa ttc cag gcc act ggt ttt gcc aat gca att ttg cgc aac atc acg 691
 Lys Phe Gln Ala Thr Gly Phe Ala Asn Ala Ile Leu Arg Asn Ile Thr
 185 190 195

gcg aag gaa cca gag cag tgg ttg aag gaa ttg gag ccc gcg gaa gag 739
 Arg Lys Glu Pro Glu Gln Trp Leu Lys Glu Leu Glu Pro Ala Glu Glu
 200 205 210

ttg gct cgc gtt gcg ttc cgt act gcg cac cca cgc tgg att gcg cag 787

Leu Ala Arg Val Ala Phe Arg Thr Ala His Pro Arg Trp Ile Ala Gln	
215 220 225	
agt ttc tca cag gtg ctc ccg gca gat gag ttg gaa gca gcg ctt gct	835
Ser Phe Ser Gln Val Leu Pro Ala Asp Glu Leu Ala Ala Leu Ala	230 235 240 245
gcg gac tct gag cgc cca gtg gtg cac ttg gtg gct cgc cca ggt gag	883
Ala Asp Ser Glu Arg Pro Val Val His Leu Val Ala Arg Pro Gly Glu	250 255 260
atc agt gca gag gaa ttg gcg ctg atc acc ggt ggt gac gag ggc aag	931
Ile Ser Ala Glu Glu Leu Ala Leu Ile Thr Gly Gly Asp Glu Gly Lys	265 270 275
tat tcc cca tac gcg gtg tac ctc gag ggt ggc gac ccg ggt gat att	979
Tyr Ser Pro Tyr Ala Val Tyr Leu Glu Gly Gly Asp Pro Gly Asp Ile	280 285 290
gag cca gtg aag gat ggt ctt gca gca gtg caa gat gag ggt tct cag	1027
Glu Pro Val Lys Asp Gly Leu Ala Ala Val Gln Asp Glu Gly Ser Gln	295 300 305
ctg att gct cgc gcc ttg gtg gaa atc ccc gtg gag ggc acc gat gcc	1075
Leu Ile Ala Arg Ala Leu Val Glu Ile Pro Val Glu Gly Thr Asp Ala	310 315 320 325
ggc cgt tgg ctg gat atg tgt gca ggt cct ggc ggt aaa gcg gcg ctc	1123
Gly Arg Trp Leu Asp Met Cys Ala Gly Pro Gly Gly Lys Ala Ala Leu	330 335 340
att ggt gcg ttg gct cgc atg gat cgt gcc acc gtt gat gcc gtg gag	1171
Ile Gly Ala Leu Ala Arg Met Asp Arg Ala Thr Val Asp Ala Val Glu	345 350 355
gtc tct gat cac cgt gcc cga ctg att gaa aag tcc gtg cgt ggt ttg	1219
Val Ser Asp His Arg Ala Arg Leu Ile Glu Lys Ser Val Arg Gly Leu	360 365 370
ccc gtc aag gtt cat gtg ggc gat ggc cgc acc atc aac ttg acc ggt	1267
Pro Val Lys Val His Val Gly Asp Gly Arg Thr Ile Asn Leu Thr Gly	375 380 385
ggt tac gat cgt gcg cta gtc gat gcg ccg tgt tct ggt ttg ggt gca	1315
Gly Tyr Asp Arg Ala Leu Val Asp Ala Pro Cys Ser Gly Leu Gly Ala	390 395 400 405
ctg cgt cgt cgc cct gag gcg cgt tgg cgc aag cag gaa agc gac att	1363
Leu Arg Arg Arg Pro Glu Ala Arg Trp Arg Lys Gln Glu Ser Asp Ile	410 415 420
gtt gag ctc aac acc ctg cag tac gag ctg ctt gaa tcc gct gtg aac	1411
Val Glu Leu Asn Thr Leu Gln Tyr Glu Leu Leu Glu Ser Ala Val Asn	425 430 435
aag gtg cgt tcc ggt ggc gtg att gtg tac tcc aca tgt tca cct gat	1459
Lys Val Arg Ser Gly Gly Val Ile Val Tyr Ser Thr Cys Ser Pro Asp	440 445 450
ctg cgt gaa acc cgc gga atc gtg gac aag gca ctg ggg gct ctg gag	1507
Leu Arg Glu Thr Arg Gly Ile Val Asp Lys Ala Leu Gly Ala Leu Glu	

455 460 465

atc gaa gag ctt gag gct gcg gag ttc atg cca ggc atg acc gat acc 1555
 ile Glu Glu Leu Glu Ala Ala Glu Phe Met Pro Gly Met Thr Asp Thr
 470 475 480 485

ggc gat gag aaa tca gtg cag atg tgg cca cac cgc cac ggc acc gat 1603
 Gly Asp Glu Lys Ser Val Gln Met Trp Pro His Arg His Gly Thr Asp
 490 495 500

gcg atg ttt gtg gca gtg ctg cga aag aag tagacctgtg agctaagtgg 1653
 Ala Met Phe Val Ala Val Leu Arg Lys Lys
 505 510

ggt 1656

<210> 2654

<211> 511

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2654

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 20 25 30

Lys Lys Ala Pro Ala Arg Gly Gln Gly Gln Ser Gln Gly Gln Arg Gln
 35 40 45

Gly Gln Ser Ser Gly Lys Gly Gly Asn Arg Lys Pro Pro Ala Gln
 50 55 60

Ala Arg Glu Val Arg Ala Leu Gly Val Asp Lys Pro Arg Glu Ile Ala
 65 70 75 80

Phe Glu Val Leu Asp Arg Val Arg Thr Gly Glu Ala Tyr Ala Asn Leu
 85 90 95

Val Leu Pro Arg Leu Leu Ser Lys His Asn Leu Ser Gly Arg Asp Ala
 100 105 110

Ala Phe Ala Thr Glu Ile Thr Tyr Gly Thr Leu Arg Asn Val Gly Leu
 115 120 125

Leu Asp Glu Val Ile Lys Ala Ala Ser Gly Arg Glu Leu Ser Asp Ile
 130 135 140

Asp Pro Glu Val Leu Asp Val Leu Arg Leu Gly Ala Tyr Gln Val Met
 145 150 155 160

Phe Thr Arg Val Glu Asp His Ala Ala Val Asp Thr Ser Val Lys Met
 165 170 175

Val Gly Gly Leu Lys Lys Phe Gln Ala Thr Gly Phe Ala Asn Ala Ile
 180 185 190

Leu Arg Asn Ile Thr Arg Lys Glu Pro Glu Gln Trp Leu Lys Glu Leu
 195 200 205

Glu Pro Ala Glu Glu Leu Ala Arg Val Ala Phe Arg Thr Ala His Pro
 210 215 220
 Arg Trp Ile Ala Gln Ser Phe Ser Gln Val Leu Pro Ala Asp Glu Leu
 225 230 235 240
 Glu Ala Ala Leu Ala Ala Asp Ser Glu Arg Pro Val Val His Leu Val
 245 250 255
 Ala Arg Pro Gly Glu Ile Ser Ala Glu Glu Leu Ala Leu Ile Thr Gly
 260 265 270
 Gly Asp Glu Gly Lys Tyr Ser Pro Tyr Ala Val Tyr Leu Glu Gly Gly
 275 280 285
 Asp Pro Gly Asp Ile Glu Pro Val Lys Asp Gly Leu Ala Ala Val Gln
 290 295 300
 Asp Glu Gly Ser Gln Leu Ile Ala Arg Ala Leu Val Glu Ile Pro Val
 305 310 315 320
 Glu Gly Thr Asp Ala Gly Arg Trp Leu Asp Met Cys Ala Gly Pro Gly
 325 330 335
 Gly Lys Ala Ala Leu Ile Gly Ala Leu Ala Arg Met Asp Arg Ala Thr
 340 345 350
 Val Asp Ala Val Glu Val Ser Asp His Arg Ala Arg Leu Ile Glu Lys
 355 360 365
 Ser Val Arg Gly Leu Pro Val Lys Val His Val Gly Asp Gly Arg Thr
 370 375 380
 Ile Asn Leu Thr Gly Gly Tyr Asp Arg Ala Leu Val Asp Ala Pro Cys
 385 390 395 400
 Ser Gly Leu Gly Ala Leu Arg Arg Pro Glu Ala Arg Trp Arg Lys
 405 410 415
 Gln Glu Ser Asp Ile Val Glu Leu Asn Thr Leu Gln Tyr Glu Leu Leu
 420 425 430
 Glu Ser Ala Val Asn Lys Val Arg Ser Gly Gly Val Ile Val Tyr Ser
 435 440 445
 Thr Cys Ser Pro Asp Leu Arg Glu Thr Arg Gly Ile Val Asp Lys Ala
 450 455 460
 Leu Gly Ala Leu Glu Ile Glu Glu Leu Glu Ala Ala Glu Phe Met Pro
 465 470 475 480
 Gly Met Thr Asp Thr Gly Asp Glu Lys Ser Val Gln Met Trp Pro His
 485 490 495
 Arg His Gly Thr Asp Ala Met Phe Val Ala Val Leu Arg Lys Lys
 500 505 510

<210> 2655

<211> 1059

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1036)

<223> RXA02255

<400> 2655

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                               Val Ala Lys Asn Ser
                               1 5

gtt cgt gct gcg gaa gtg tct gca att tta agg ttt gct ggt gag atg 163
Val Arg Ala Ala Glu Val Ser Ala Ile Leu Arg Phe Ala Gly Glu Met
                               10 15 20

caa gct gtc ggc ggc aag ctg gtc atc gaa gca aat ttg gac agc atg 211
Gln Ala Val Gly Gly Lys Leu Val Ile Glu Ala Asn Leu Asp Ser Met
                               25 30 35

caa gtc ggt atg agg ctt cag gag ttt atc caa ggt ttg tac aac tct 259
Gln Val Gly Met Arg Leu Gln Glu Phe Ile Gln Gly Leu Tyr Asn Ser
                               40 45 50

cga gtc gat gtg cac acc gtg aac ccg act gtg agc agg aaa acg cca 307
Arg Val Asp Val His Thr Val Asn Pro Thr Val Ser Arg Lys Thr Pro
                               55 60 65

cgg tat ttg gtg cgc atc att gac aat gcc gat gaa att gcg cga cgc 355
Arg Tyr Leu Val Arg Ile Ile Asp Asn Ala Asp Glu Ile Ala Arg Arg
                               70 75 80 85

acc gga ctg gtc acc agg tct gga cat gtg gtt aaa ggt cta gcg cct 403
Thr Gly Leu Val Thr Arg Ser Gly His Val Val Lys Gly Leu Ala Pro
                               90 95 100

tct gtg gtc agc gga aca atc agt gac gct gaa gct gca tgg cgc ggt 451
Ser Val Val Ser Gly Thr Ile Ser Asp Ala Glu Ala Ala Trp Arg Gly
                               105 110 115

gcg ttt cta gcc aat gga tct tta agt gat cca ggt cgt tcc tct tcg 499
Ala Phe Leu Ala Asn Gly Ser Leu Ser Asp Pro Gly Arg Ser Ser Ser
                               120 125 130

ttg gag gtg ttg tgt cct ggt caa gaa tca gca ttg gca ctg gtt gga 547
Leu Glu Val Leu Cys Pro Gly Gln Glu Ser Ala Leu Ala Leu Val Gly
                               135 140 145

tgt gcg cga aga att ggg atc gcg gcg aaa acg aaa gat tct cga gga 595
Cys Ala Arg Arg Ile Gly Ile Ala Ala Lys Thr Lys Asp Ser Arg Gly
                               150 155 160 165

ttt gat cgc gtc aat gtt cgt gat gcg gaa gca att ggg gca ctg ctc 643
Phe Asp Arg Val Asn Val Arg Asp Ala Glu Ala Ile Gly Ala Leu Leu
                               170 175 180

act cga atg ggt gcc cag aaa act cgc atg ttg tgg gaa gaa aaa cgc 691
Thr Arg Met Gly Ala Gln Lys Thr Arg Met Leu Trp Glu Glu Lys Arg

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185	190	195	
atc aag cgg gaa agt cga act	ccg caa acc ggg ttg gcc aac ttc gac		739
Ile Lys Arg Glu Ser Arg Thr	Pro Gln Thr Gly Leu Ala Asn Phe Asp		
200	205	210	
gat gcc aat ctg cgc agg tca	gcc cga gca gca gtt gcc gct gca gcg		787
Asp Ala Asn Leu Arg Arg Ser	Ala Arg Ala Ala Val Ala Ala Ala Ala		
215	220	225	
agg gta gaa cgc gcc atg aag att ctt ggt gat gat gtt cct gag cat			835
Arg Val Glu Arg Ala Met Lys Ile Leu Gly Asp Val Pro Glu His			
230	235	240	245
ttg gct gag gct gga cag ctg cgt gtg cag cac cgt cag gca tcg ttg			883
Leu Ala Glu Ala Gly Gln Leu Arg Val Gln His Arg Gln Ala Ser Leu			
250	255	260	
gag gag ttg ggc cgg ttg gct gat cct caa atg acc aag gat gct gtg			931
Glu Glu Leu Gly Arg Leu Ala Asp Pro Gln Met Thr Lys Asp Ala Val			
265	270	275	
gcc ggt cgt att cgt cgt ctt ttg acg atg gca gat aag cgc gcc gaa			979
Ala Gly Arg Ile Arg Arg Leu Leu Thr Met Ala Asp Lys Arg Ala Glu			
280	285	290	
gat ctg aag att cct gat aca aat tct gtt gtg acg gaa gat ttg ttg			1027
Asp Leu Lys Ile Pro Asp Thr Asn Ser Val Val Thr Glu Asp Leu Leu			
295	300	305	
gaa gaa att tagatgattg aagcctaaaa acg			1059
Glu Glu Ile			
310			
<210> 2656			
<211> 312			
<212> PRT			
<213> <i>Corynebacterium glutamicum</i>			
<400> 2656			
Val Ala Lys Asn Ser Val Arg Ala Ala Glu Val Ser Ala Ile Leu Arg			
1 5 10 15			
Phe Ala Gly Glu Met Gln Ala Val Gly Gly Lys Leu Val Ile Glu Ala			
20 25 30			
Asn Leu Asp Ser Met Gln Val Gly Met Arg Leu Gln Glu Phe Ile Gln			
35 40 45			
Gly Leu Tyr Asn Ser Arg Val Asp Val His Thr Val Asn Pro Thr Val			
50 55 60			
Ser Arg Lys Thr Pro Arg Tyr Leu Val Arg Ile Ile Asp Asn Ala Asp			
65 70 75 80			
Glu Ile Ala Arg Arg Thr Gly Leu Val Thr Arg Ser Gly His Val Val			
85 90 95			
Lys Gly Leu Ala Pro Ser Val Val Ser Gly Thr Ile Ser Asp Ala Glu			
100 105 110			

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Ala Ala Trp Arg Gly Ala Phe Leu Ala Asn Gly Ser Leu Ser Asp Pro
  115                               120
Gly Arg Ser Ser Ser Leu Glu Val Leu Cys Pro Gly Gln Glu Ser Ala
  130                               135
Leu Ala Leu Val Gly Cys Ala Arg Arg Ile Gly Ile Ala Ala Lys Thr
  145                               150
Lys Asp Ser Arg Gly Phe Asp Arg Val Asn Val Arg Asp Ala Glu Ala
  165                               170
Ile Gly Ala Leu Leu Thr Arg Met Gly Ala Gln Lys Thr Arg Met Leu
  180                               185
Trp Glu Glu Lys Arg Ile Lys Arg Glu Ser Arg Thr Pro Gln Thr Gly
  195                               200
Leu Ala Asn Phe Asp Asp Ala Asn Leu Arg Arg Ser Ala Arg Ala Ala
  210                               215
Val Ala Ala Ala Ala Arg Val Glu Arg Ala Met Lys Ile Leu Gly Asp
  225                               230
Asp Val Pro Glu His Leu Ala Glu Ala Gly Gln Leu Arg Val Gln His
  245                               250
Arg Gln Ala Ser Leu Glu Glu Leu Gly Arg Leu Ala Asp Pro Gln Met
  260                               265
Thr Lys Asp Ala Val Ala Gly Arg Ile Arg Arg Leu Leu Thr Met Ala
  275                               280
Asp Lys Arg Ala Glu Asp Leu Lys Ile Pro Asp Thr Asn Ser Val Val
  290                               300
Thr Glu Asp Leu Leu Glu Glu Ile
  305                               310

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<210> 2657

<211> 636

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(613)

<223> RXA02266

<400> 2657

gaggaaaagta gcgctacatc tgcataatcta ccccttaaaa aatgaagcat aaaaccgccg 60

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tgtaccggcc ttttattgat ttgacgctaa gcttgaccgg atg act caa gat gaa 115
                               Met Thr Gln Asp Glu
                               1           5

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cac ccc cga cag gcc gac tcc cat ttc aac atg ctt tta ccg gat gga 163
His Pro Arg Gln Ala Asp Ser His Phe Asn Met Leu Leu Pro Asp Gly
      10           15           20

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aat gaa aac gca cac cag ctt tct gtc gct cta aat cag gtg gca cat 211
 Asn Glu Asn Ala His Gln Leu Ser Val Ala Leu Asn Gln Val Ala His
 25 30 35
 ctg ttg gcc tat gat gcg gac tct tca att cat cgg cct gat ggg cta 259
 Leu Leu Ala Tyr Asp Ala Asp Ser Ser Ile His Arg Pro Asp Gly Leu
 40 45 50
 agt ctg gcg tcc tat aga att ctc ttt tca ctg tgg act gat ggc ccg 307
 Ser Leu Ala Ser Tyr Arg Ile Leu Phe Ser Leu Trp Thr Asp Gly Pro
 55 60 65
 atg agt cca ctc cag gtg act gac aag act gga atg aaa aag tct gcg 355
 Met Ser Pro Leu Gln Val Thr Asp Lys Thr Gly Met Lys Lys Ser Ala
 70 75 80 85
 att tct aac ctg tta aag cca ttg ctc gct gaa tct ctg att gtg cag 403
 Ile Ser Asn Leu Leu Lys Pro Leu Leu Ala Gln Ser Leu Ile Val Gln
 90 95 100
 gtg acg gca gaa aat gat cga cgc tca aag gtt tta agc ctt agc gaa 451
 Val Thr Ala Glu Asn Asp Arg Arg Ser Lys Val Leu Ser Leu Ser Glu
 105 110 115
 aaa ggc act aca tac att cag aaa aca gcc acc cgc caa aat gct ttg 499
 Lys Gly Thr Thr Tyr Ile Gln Lys Thr Ala Thr Arg Gln Asn Ala Leu
 120 125 130
 gaa tcc gag tgg ttt ggc acc ctg acc gac atc gag cag gat tta ttg 547
 Glu Ser Glu Trp Phe Gly Thr Leu Thr Asp Ile Glu Gln Asp Leu Leu
 135 140 145
 gag tcg ttg ctc agg aaa ctg ctc gac tcc aac cgc gca tcc aag gtt 595
 Glu Ser Leu Leu Arg Lys Leu Leu Asp Ser Asn Arg Ala Ser Lys Val
 150 155 160 165
 cgt aaa aac cga tct aac tagcgtcgat ccttagggat gta 636
 Arg Lys Asn Arg Ser Asn
 170

<210> 2658

<211> 171

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2658

Met Thr Gln Asp Glu His Pro Arg Gln Ala Asp Ser His Phe Asn Met
 1 5 10 15
 Leu Leu Pro Asp Gly Asn Glu Asn Ala His Gln Leu Ser Val Ala Leu
 20 25 30
 Asn Gln Val Ala His Leu Leu Ala Tyr Asp Ala Asp Ser Ser Ile His
 35 40 45
 Arg Pro Asp Gly Leu Ser Leu Ala Ser Tyr Arg Ile Leu Phe Ser Leu
 50 55 60
 Trp Thr Asp Gly Pro Met Ser Pro Leu Gln Val Thr Asp Lys Thr Gly

65		70		75		80
Met Lys Lys Ser Ala Ile Ser Asn Leu Leu Lys Pro Leu Leu Ala Glu						
		85		90		95
Ser Leu Ile Val Gln Val Thr Ala Glu Asn Asp Arg Arg Ser Lys Val						
	100		105		110	
Leu Ser Leu Ser Glu Lys Gly Thr Thr Tyr Ile Gln Lys Thr Ala Thr						
	115		120		125	
Arg Gln Asn Ala Leu Glu Ser Glu Trp Phe Gly Thr Leu Thr Asp Ile						
	130		135		140	
Glu Gln Asp Leu Leu Glu Ser Leu Leu Arg Lys Leu Leu Asp Ser Asn						
	145	150		155		160
Arg Ala Ser Lys Val Arg Lys Asn Arg Ser Asn						
	165		170			

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<210> 2659
<211> 996
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(973)
<223> RXA02267

<400> 2659
tgcgctcggc aagtgttttg cttatcgacg tctccccaca taacaatccc aactogaagc 60
accaacgatt caagccttat cagttttgta caggaaaata gtg caa aaa tgg ggt 115
Val Gln Lys Trp Gly
1 5

tta agc ttc gtg gag agg att gtc atc gtg aac aac gtg caa cag ttt 163
Leu Ser Phe Val Glu Arg Ile Val Ile Val Asn Asn Val Gln Gln Phe
10 15 20

cat cga ttt ttt gat gat tcc gca gtc tat tat ccc tgc ttc gtc ccg 211
His Arg Phe Phe Asp Asp Ser Ala Val Tyr Tyr Pro Cys Phe Val Pro
25 30 35

ctt gac cga gcc atc gcc gaa cac ttt gat cgt cag aac aaa ccg atg 259
Leu Asp Arg Ala Ile Gly Glu His Phe Asp Arg Gln Asn Lys Pro Met
40 45 50

tcc aga ttc atc gga acg ctc att ctg ccg tta gcc aaa ctg gaa gaa 307
Ser Arg Phe Ile Gly Thr Leu Ile Leu Pro Leu Ala Lys Leu Glu Glu
55 60 65

gcc gcc caa tac acc gcc gat gaa gtc ctt cgc gtg tgc gca gta atc 355
Ala Ala Gln Tyr Thr Gly Asp Glu Val Leu Arg Val Ser Ala Val Ile
70 75 80 85

agt act gat ggg ctc gct gat ctg cga agg gat ttt tac gaa ctc ccc 403
Ser Thr Asp Gly Leu Ala Asp Leu Arg Arg Asp Phe Tyr Glu Leu Pro
90 95 100

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aac atc gac atc gcc tcg gtg gaa atc aag ctg gtc ggc gca gcc ctc 451
 Asn Ile Asp Ile Ala Ser Val Glu Ile Lys Leu Val Gly Ala Ala Leu
 105 110 115
 acc aac acc gct tgg ttg gga gat gtg gaa aaa ctc atc caa caa cat 499
 Thr Asn Thr Ala Trp Leu Gly Asp Val Glu Lys Leu Ile Gln Gln His
 120 125 130
 cgc aac act ttc gta tgg gtt gag att ccg aca gcc ctg gtc acc gca 547
 Arg Asn Thr Phe Val Trp Val Glu Ile Pro Thr Ala Leu Val Thr Ala
 135 140 145
 gat att gtc cga aaa ctc cgc cac atg gga gct ggc ctg aaa tac aga 595
 Asp Ile Val Arg Lys Leu Arg His Met Gly Ala Gly Leu Lys Tyr Arg
 150 155 160 165
 act gga ggt gat agg gaa gag ctc ttc ccc tca ccg cag gac ttg gtc 643
 Thr Gly Gly Asp Arg Glu Glu Leu Phe Pro Ser Pro Gln Asp Leu Val
 170 175 180
 act gtg ctg cgc acc gcc atc gat gct gca ttg ccg ttt aaa ctc act 691
 Thr Val Leu Arg Thr Ala Ile Asp Ala Ala Leu Pro Phe Lys Leu Thr
 185 190 195
 gca ggc ctg cat cgt gct ctc agg tat cgt gac gag aaa acc ggc cga 739
 Ala Gly Leu His Arg Ala Leu Arg Tyr Arg Asp Glu Lys Thr Gly Arg
 200 205 210
 ctt cac ttc gga ttc ctc aac att gca gcc gcc gtg gcg aca ctt cgt 787
 Leu His Phe Gly Phe Leu Asn Ile Ala Ala Val Ala Thr Leu Arg
 215 220 225
 gct gga aaa ggc gag gca gag gca ctg aag atc ctt gaa ggc gat gat 835
 Ala Gly Lys Gly Glu Ala Glu Ala Leu Lys Ile Leu Glu Gly Asp Asp
 230 235 240 245
 gcc gct ccg ctt att cac gca cta caa agc ggc gaa aac tgg cgg gat 883
 Ala Ala Pro Leu Ile His Ala Leu Gln Ser Gly Glu Asn Trp Arg Asp
 250 255 260
 tcc ttc cgc agc ttc agt acc tgc aat gtt gtt gaa cca ctc aac act 931
 Ser Phe Arg Ser Phe Ser Thr Cys Asn Val Val Glu Pro Leu Asn Thr
 265 270 275
 ctg att gat ctt gat gtg ttg gcg gaa gga gac gta cat ccc 973
 Leu Ile Asp Leu Asp Val Leu Ala Glu Gly Asp Val His Pro
 280 285 290
 taaggatcga cgctagttag atc 996

<210> 2660

<211> 291

<212> PRT

<213> Corynebacterium glutamicum

<400> 2660

 Val Gln Lys Trp Gly Leu Ser Phe Val Glu Arg Ile Val Ile Val Asn
 1 5 10 15

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Asn Val Gln Gln Phe His Arg Phe Phe Asp Asp Ser Ala Val Tyr Tyr
    20                                25                                30

Pro Cys Phe Val Pro Leu Asp Arg Ala Ile Gly Glu His Phe Asp Arg
    35                                40                                45

Gln Asn Lys Pro Met Ser Arg Phe Ile Gly Thr Leu Ile Leu Pro Leu
    50                                55                                60

Ala Lys Leu Glu Glu Ala Ala Gln Tyr Thr Gly Asp Glu Val Leu Arg
    65                                70                                75                                80

Val Ser Ala Val Ile Ser Thr Asp Gly Leu Ala Asp Leu Arg Arg Asp
    85                                90                                95

Phe Tyr Glu Leu Pro Asn Ile Asp Ile Ala Ser Val Glu Ile Lys Leu
   100                                105                                110

Val Gly Ala Ala Leu Thr Asn Thr Ala Trp Leu Gly Asp Val Glu Lys
   115                                120                                125

Leu Ile Gln Gln His Arg Asn Thr Phe Val Trp Val Glu Ile Pro Thr
   130                                135                                140

Ala Leu Val Thr Ala Asp Ile Val Arg Lys Leu Arg His Met Gly Ala
   145                                150                                155                                160

Gly Leu Lys Tyr Arg Thr Gly Gly Asp Arg Glu Glu Leu Phe Pro Ser
   165                                170                                175

Pro Gln Asp Leu Val Thr Val Leu Arg Thr Ala Ile Asp Ala Ala Leu
   180                                185                                190

Pro Phe Lys Leu Thr Ala Gly Leu His Arg Ala Leu Arg Tyr Arg Asp
   195                                200                                205

Glu Lys Thr Gly Arg Leu His Phe Gly Phe Leu Asn Ile Ala Ala Ala
   210                                215                                220

Val Ala Thr Leu Arg Ala Gly Lys Gly Glu Ala Glu Ala Leu Lys Ile
   225                                230                                235                                240

Leu Glu Gly Asp Asp Ala Ala Pro Leu Ile His Ala Leu Gln Ser Gly
   245                                250                                255

Glu Asn Trp Arg Asp Ser Phe Arg Ser Phe Ser Thr Cys Asn Val Val
   260                                265                                270

Glu Pro Leu Asn Thr Leu Ile Asp Leu Asp Val Leu Ala Glu Gly Asp
   275                                280                                285

Val His Pro
   290

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<210> 2661

<211> 776

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1) .. (753)

<223> RXA02280

<400> 2661

gcg gac ctg gct gaa acc atg ttg ggt ctt ctc acc ttg gag acc tcc	48
Ala Asp Leu Ala Glu Thr Met Leu Gly Leu Thr Leu Glu Thr Ser	
1 5 10 15	

cgt ggt cgc atc tcg atc ggt gag atc acc acg ttg tcc atc acc gag	96
Arg Gly Arg Ile Ser Ile Gly Glu Ile Thr Thr Leu Ser Ile Thr Glu	
20 25 30	

gat gtg tcg ctg cag ctg gct acc acg ttg gat gat ttc agg cag ctc	144
Asp Val Ser Leu Gln Leu Ala Thr Thr Leu Asp Asp Phe Arg Gln Leu	
35 40 45	

aac acc att gcg cgc ccg gac acc ttg att att aat ggc ggc tac att	192
Asn Thr Ile Ala Arg Pro Asp Thr Leu Ile Ile Asn Gly Gly Tyr Ile	
50 55 60	

cac gac agc gat ctg gct cgg ctc att ccc gtt cac tac cca ccg ctt	240
His Asp Ser Asp Leu Ala Arg Leu Ile Pro Val His Tyr Pro Pro Leu	
65 70 75 80	

acg gta tct act gct gac ctg cgc gaa tcc atg gat ctg atg gag ctt	288
Thr Val Ser Thr Ala Asp Leu Arg Glu Ser Met Asp Leu Met Glu Leu	
85 90 95	

ccg ccg ctg cag gac att gag aaa gcc aag gca ctg gat gcg cag gtc	336
Pro Pro Leu Gln Asp Ile Glu Lys Ala Lys Ala Leu Asp Ala Gln Val	
100 105 110	

acg gaa tca ttg aag gat ttt cag atc aag ggc gca acg agg gtt ttt	384
Thr Glu Ser Leu Lys Asp Phe Gln Ile Lys Gly Ala Thr Arg Val Phe	
115 120 125	

gaa ccc gca gat gtt cct gcc gtg gtg atc att gat tcc aag gcg cag	432
Glu Pro Ala Asp Val Pro Ala Val Val Ile Ile Asp Ser Lys Ala Gln	
130 135 140	

gcc tca cgg gat cgc aat gaa aca caa agc gca acc act gat cgt tgg	480
Ala Ser Arg Asp Arg Asn Glu Thr Gln Ser Ala Thr Thr Asp Arg Trp	
145 150 155 160	

gct gac att ttg gca acg gtg gat aac acg ttg agc cgt caa aca gcc	528
Ala Asp Ile Leu Ala Thr Val Asp Asn Thr Leu Ser Arg Gln Thr Ala	
165 170 175	

aac att cca cag gat cag gga ctg tcg gcg ttg tgc ttg aat tgg aac	576
Asn Ile Pro Gln Asp Gln Gly Leu Ser Ala Leu Cys Leu Asn Trp Asn	
180 185 190	

aat tcg ctg gtc agg aaa ttg gcg tcc act gat gac acc gcc gtg gtg	624
Asn Ser Leu Val Arg Lys Leu Ala Ser Thr Asp Asp Thr Ala Val Val	
195 200 205	

tcg cgc acg gtg cgt ttg ctc tac gtt cag gca ttg tcc acc aag	672
Ser Arg Thr Val Arg Leu Leu Tyr Val Gln Ala Leu Leu Ser Ser Lys	
210 215 220	

agg cca ctg cgg gtg aag gaa cgc gcg ctg ctt aat gat tgc ctg gca 720
 Arg Pro Leu Arg Val Lys Glu Arg Ala Leu Leu Asn Asp Ser Leu Ala
 225 230 235 240

gat ctg gtt tct ttg tct ttg tca tcc gat atc taagacaatc ctccgctaata 773
 Asp Leu Val Ser Leu Ser Leu Ser Ser Asp Ile
 245 250

ctt 776

<210> 2662

<211> 251

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2662

Ala Asp Leu Ala Glu Thr Met Leu Gly Leu Leu Thr Leu Glu Thr Ser
 1 5 10 15

Arg Gly Arg Ile Ser Ile Gly Glu Ile Thr Thr Leu Ser Ile Thr Glu
 20 25 30

Asp Val Ser Leu Gln Leu Ala Thr Thr Leu Asp Asp Phe Arg Gln Leu
 35 40 45

Asn Thr Ile Ala Arg Pro Asp Thr Leu Ile Ile Asn Gly Gly Tyr Ile
 50 55 60

His Asp Ser Asp Leu Ala Arg Leu Ile Pro Val His Tyr Pro Pro Leu
 65 70 75 80

Thr Val Ser Thr Ala Asp Leu Arg Glu Ser Met Asp Leu Met Glu Leu
 85 90 95

Pro Pro Leu Gln Asp Ile Glu Lys Ala Lys Ala Leu Asp Ala Gln Val
 100 105 110

Thr Glu Ser Leu Lys Asp Phe Gln Ile Lys Gly Ala Thr Arg Val Phe
 115 120 125

Glu Pro Ala Asp Val Pro Ala Val Val Ile Ile Asp Ser Lys Ala Gln
 130 135 140

Ala Ser Arg Asp Arg Asn Glu Thr Gln Ser Ala Thr Thr Asp Arg Trp
 145 150 155 160

Ala Asp Ile Leu Ala Thr Val Asp Asn Thr Leu Ser Arg Gln Thr Ala
 165 170 175

Asn Ile Pro Gln Asp Gln Gly Leu Ser Ala Leu Cys Leu Asn Trp Asn
 180 185 190

Asn Ser Leu Val Arg Lys Leu Ala Ser Thr Asp Asp Thr Ala Val Val
 195 200 205

Ser Arg Thr Val Arg Leu Leu Tyr Val Gln Ala Leu Leu Ser Ser Lys
 210 215 220

Arg Pro Leu Arg Val Lys Glu Arg Ala Leu Leu Asn Asp Ser Leu Ala
 225 230 235 240

Asp Leu Val Ser Leu Ser Leu Ser Ser Asp Ile
245 250

<210> 2663

<211> 672

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(649)

<223> RXA02286

<400> 2663

gcagcgcaca cgctttccccc tcagcctgct gatacccccg ttttgccacc taaaacaacc 60

tctcatcttc atttcatatt cacttcatag gggtgaatac atg aag aac gca aaa 115
Met Lys Asn Ala Lys
1 5

ctt ttc ctc gcg etc ata tcc gct cct ctt atc etc gct ggc tgc agc 163
Leu Phe Leu Ala Leu Ile Ser Ala Pro Leu Ile Leu Ala Gly Cys Ser
10 15 20

tcc acc gat act gga aca gca gaa tcc acc att tcc agc gaa act gct 211
Ser Thr Asp Thr Gly Thr Ala Glu Ser Thr Ile Ser Ser Glu Thr Ala
25 30 35

tct gca gta gat gcc acc act tct acc tcc tca agt acc gcc acc tct 259
Ser Ala Val Asp Ala Thr Thr Ser Thr Ser Ser Ser Thr Ala Thr Ser
40 45 50

gcc gtg att gat gac gat ccg gta ttc gac atc atc gac atc gtc ctt 307
Ala Val Ile Asp Asp Asp Pro Val Phe Asp Ile Ile Asp Ile Val Leu
55 60 65

gcc caa tac ccc gac agg atc atc acc gac att gac cgc gaa gac tcc 355
Ala Gln Tyr Pro Asp Arg Ile Ile Thr Asp Ile Asp Arg Glu Asp Ser
70 75 80 85

tcc gat caa tac gaa gtc gat gtt gtg gtt ggc caa gaa gtc ctt gaa 403
Ser Asp Gln Tyr Glu Val Asp Val Val Val Gly Gln Glu Val Leu Glu
90 95 100

ctt gat gtc acc acc agt ggc cag atc cat acc gac gac cgc gac aac 451
Leu Asp Val Thr Thr Ser Gly Gln Ile His Thr Asp Asp Arg Asp Asn
105 110 115

gat gat gat gac gac atc cgc gaa gct cac gca gcc aca gtc acc gca 499
Asp Asp Asp Asp Ile Arg Glu Ala His Ala Ala Thr Val Thr Ala
120 125 130

gct caa gcc att ggc cta gcg ctg gat caa tac cca gac gga att att 547
Ala Gln Ala Ile Gly Leu Ala Leu Asp Gln Tyr Pro Asp Gly Ile Ile
135 140 145

gat tct gtt gaa tta gac gaa gac gac ggc cag ctg aaa tgg aaa ata 595
Asp Ser Val Glu Leu Asp Glu Asp Asp Gly Gln Leu Lys Trp Lys Ile
150 155 160 165

gac ctc gat gac act tcc ggc aat gat ctt gct gac gtt gaa atc gca 643
 Asp Leu Asp Asp Thr Ser Gly Asn Asp Leu Ala Asp Val Glu Ile Ala
 170 175 180

gca gtt taagcagcgc caggaaagc cac 672
 Ala Val

<210> 2664

<211> 183

<212> PRT

<213> Corynebacterium glutamicum

<400> 2664

Met Lys Asn Ala Lys Leu Phe Leu Ala Leu Ile Ser Ala Pro Leu Ile
 1 5 10 15

Leu Ala Gly Cys Ser Ser Thr Asp Thr Gly Thr Ala Glu Ser Thr Ile
 20 25 30

Ser Ser Glu Thr Ala Ser Ala Val Asp Ala Thr Thr Ser Thr Ser Ser
 35 40 45

Ser Thr Ala Thr Ser Ala Val Ile Asp Asp Asp Pro Val Phe Asp Ile
 50 55 60

Ile Asp Ile Val Leu Ala Gln Tyr Pro Asp Arg Ile Ile Thr Asp Ile
 65 70 75 80

Asp Arg Glu Asp Ser Ser Asp Gln Tyr Glu Val Asp Val Val Val Gly
 85 90 95

Gln Glu Val Leu Glu Leu Asp Val Thr Thr Ser Gly Gln Ile His Thr
 100 105 110

Asp Asp Arg Asp Asn Asp Asp Asp Ile Arg Glu Ala His Ala
 115 120 125

Ala Thr Val Thr Ala Ala Gln Ala Ile Gly Leu Ala Leu Asp Gln Tyr
 130 135 140

Pro Asp Gly Ile Ile Asp Ser Val Glu Leu Asp Glu Asp Asp Gly Gln
 145 150 155 160

Leu Lys Trp Lys Ile Asp Leu Asp Asp Thr Ser Gly Asn Asp Leu Ala
 165 170 175

Asp Val Glu Ile Ala Ala Val
 180

<210> 2665

<211> 675

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(652)

<223> RXA02287

<400> 2665

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ttgaaaaagg aacattagtg ccagtaacaa gagcccagtt gaattcaagc gggcagagac 60
acatctggcc ctcaaaattt tccttttact ggagaccact gtg tac tca att tca 115
                               Val Tyr Ser Ile Ser 5
gaa act atc gcc cga act ctt atg ccc cgc acc gat cac gtt ttc gac 163
Glu Thr Ile Ala Arg Thr Leu Met Pro Arg Thr Asp His Val Phe Asp
                               10                               15                               20
ctg atg ggc aac gga aac gcc tgg ttc gtc gat gcc cta gaa cgc ctc 211
Leu Met Gly Asn Gly Asn Ala Trp Phe Val Asp Ala Leu Glu Arg Leu
                               25                               30                               35
ggg cga ggc atc atc acc gtc cgc ccc aca gtt gaa acc gtg gcc gcc 259
Gly Arg Gly Ile Ile Thr Val Arg Pro Thr Val Glu Thr Val Ala Ala
                               40                               45                               50
gcg gac acc tac cac cgc gtc acc cgc cgc ccg gcg gtc gct acc acc 307
Ala Asp Thr Tyr His Arg Val Thr Arg Arg Pro Ala Val Ala Thr Thr
                               55                               60                               65
acc tat ggt gct ggt ttc acc aac acc atg acc acg ctt gcc gac gtc 355
Thr Tyr Gly Ala Gly Phe Thr Asn Thr Met Thr Thr Leu Ala Asp Val
                               70                               75                               80                               85
gcc ctc tcc cgt atc cca ctt ctt tta gtt gtg ggc act gcc ccg agc 403
Ala Leu Ser Arg Ile Pro Leu Leu Leu Val Val Gly Thr Ala Pro Ser
                               90                               95                               100
gcc ggg cct cgc tgt ttc gac att gac cgg caa gga ctc gca cgt gcc 451
Ala Gly Pro Arg Cys Phe Asp Ile Asp Arg Gln Gly Leu Ala Arg Ala
                               105                               110                               115
gta ggt gtg gaa acc ttc acc gtg cat gca gat gac gtt gct gcg gta 499
Val Gly Val Glu Thr Phe Thr Val His Ala Asp Asp Val Ala Ala Val
                               120                               125                               130
act ctt cag gct tgg aat aat acg ccg gaa aac aca cac gtg atc ctg 547
Thr Leu Gln Ala Trp Asn Asn Thr Pro Glu Asn Thr His Val Ile Leu
                               135                               140                               145
gaa atc ccc tat gac cta gca gct gcc aca gcc acc gat cca aca gtg 595
Glu Ile Pro Tyr Asp Leu Ala Ala Ala Thr Ala Thr Asp Pro Thr Val
                               150                               155                               160                               165
act aca tac ctg ctg cgc ccc gga ttt cag aaa ctc ccg atg tca ccg 643
Thr Thr Tyr Leu Leu Arg Pro Gly Phe Gln Lys Leu Pro Met Ser Pro
                               170                               175                               180
acc ttg tcc tagctctacg caatgcccaa aat 675
Thr Leu Ser

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<210> 2666

<211> 184

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2666

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Val Tyr Ser Ile Ser Glu Thr Ile Ala Arg Thr Leu Met Pro Arg Thr
 1          5          10          15

Asp His Val Phe Asp Leu Met Gly Asn Gly Asn Ala Trp Phe Val Asp
          20          25          30

Ala Leu Glu Arg Leu Gly Arg Gly Ile Ile Thr Val Arg Pro Thr Val
          35          40          45

Glu Thr Val Ala Ala Ala Asp Thr Tyr His Arg Val Thr Arg Arg Pro
 50          55          60

Ala Val Ala Thr Thr Thr Tyr Gly Ala Gly Phe Thr Asn Thr Met Thr
 65          70          75          80

Thr Leu Ala Asp Val Ala Leu Ser Arg Ile Pro Leu Leu Leu Val Val
          85          90          95

Gly Thr Ala Pro Ser Ala Gly Pro Arg Cys Phe Asp Ile Asp Arg Gln
          100          105          110

Gly Leu Ala Arg Ala Val Gly Val Glu Thr Phe Thr Val His Ala Asp
          115          120          125

Asp Val Ala Ala Val Thr Leu Gln Ala Trp Asn Asn Thr Pro Glu Asn
          130          135          140

Thr His Val Ile Leu Glu Ile Pro Tyr Asp Leu Ala Ala Ala Thr Ala
          145          150          155          160

Thr Asp Pro Thr Val Thr Thr Tyr Leu Leu Arg Pro Gly Phe Gln Lys
          165          170          175

Leu Pro Met Ser Pro Thr Leu Ser
          180

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<210> 2667

<211> 498

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(475)

<223> RXA02294

<400> 2667

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atcctcggttt gtggcagggg acattcctag gatggggaggc atg gca aag aca aaa 115
                                     Met Ala Lys Thr Lys
                                     1          5

cta gaa agc atc tcc gag cgc aac tcg gat gat ccg ctt agt tac ccc 163
Leu Glu Ser Ile Ser Glu Arg Asn Ser Asp Asp Pro Leu Ser Tyr Pro
          10          15          20

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gac ctg act ctt gca cca ata tcc aca aca gtc aca gtc gtg gtc gcc 211
Asp Leu Thr 25 Leu Ala Pro Ile Ser Thr Thr Val Thr Val Val Ala
30 35

gaa gac acc cca aac gat aac ttc tca gaa ctt ctc ctc ggc gca gca 259
Glu Asp Thr Pro Asn Asp Asn Phe Ser Glu Leu Leu Leu Gly Ala Ala
40 45 50

gaa tca acc cgt ctt tta gga ctc gac gag ctc cac atc atc gct cca 307
Glu Ser Thr Arg Leu Leu Gly Leu Asp Glu Leu His Ile Ile Ala Pro
55 60 65

tca gtc cac cta ccc gct ctc gca gta gca gcc gcc gac atc gca cac 355
Ser Val His Leu Pro Ala Leu Ala Val Ala Ala Asp Ile Ala His
70 75 80 85

cat ctg cca gag aaa ttc caa ttc tgt gaa gcc gaa acc tgc act cat 403
His Leu Pro Glu Lys Phe Gln Phe Cys Glu Ala Glu Thr Cys Thr His
90 95 100

ctc cac ccc gac gat gac acc tat ctc acg gct gaa tcc gtt gct caa 451
Leu His Pro Asp Asp Thr Tyr Leu Thr Ala Glu Ser Val Ala Gln
105 110 115

ttg ggt acg aag ctg aag tct gcg tagttgtag gagccaccac aga 498
Leu Gly Thr Lys Leu Lys Ser Ala
120 125

<210> 2668
<211> 125
<212> PRT
<213> Corynebacterium glutamicum

<400> 2668
Met Ala Lys Thr Lys Leu Glu Ser Ile Ser Glu Arg Asn Ser Asp Asp
1 5 10 15
Pro Leu Ser Tyr Pro Asp Leu Thr Leu Ala Pro Ile Ser Thr Thr Val
20 25 30
Thr Val Val Val Ala Glu Asp Thr Pro Asn Asp Asn Phe Ser Glu Leu
35 40 45
Leu Leu Gly Ala Ala Glu Ser Thr Arg Leu Leu Gly Leu Asp Glu Leu
50 55 60
His Ile Ile Ala Pro Ser Val His Leu Pro Ala Leu Ala Val Ala Ala
65 70 75 80
Ala Asp Ile Ala His His Leu Pro Glu Lys Phe Gln Phe Cys Glu Ala
85 90 95
Glu Thr Cys Thr His Leu His Pro Asp Asp Asp Thr Tyr Leu Thr Ala
100 105 110
Glu Ser Val Ala Gln Leu Gly Thr Lys Leu Lys Ser Ala
115 120 125

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<210> 2669

<211> 903

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(880)

<223> RXA02295

<400> 2669

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gatgcaagac	tgataccggg	atgtgatagg	agcgcaccac	atg	ggg	ttg	gaa	tta	115
				Met	Gly	Leu	Glu	Leu	
				1				5	

gca	gct	agc	ggg	ttg	ggc	atc	ctc	atc	gca	ggc	gcc	gcc	gta	gcc	gga	163
Ala	Ala	Ser	Gly	Trp	Gly	Ile	Leu	Ile	Ala	Gly	Ala	Ala	Val	Ala	Gly	
			10						15					20		

ttg	atc	gac	gca	gta	atc	ggc	ggt	ggc	gga	ctc	gtc	ctc	atc	ccg	ctg	211
Trp	Ile	Asp	Ala	Val	Ile	Gly	Gly	Gly	Gly	Leu	Val	Leu	Ile	Pro	Leu	
			25				30						35			

atc	ctc	gcg	gtc	atg	ccg	caa	ctc	gca	cct	gtg	aca	gcg	ctg	gcc	tcc	259
Ile	Leu	Ala	Val	Met	Pro	Gln	Leu	Ala	Pro	Val	Thr	Ala	Leu	Ala	Ser	
			40				45					50				

aac	aaa	ctg	gca	gcc	gtc	acc	ggc	acg	gca	tcg	gcg	gca	ttc	acc	ctg	307
Asn	Lys	Leu	Ala	Ala	Val	Thr	Gly	Thr	Ala	Ser	Ala	Ala	Phe	Thr	Leu	
		55				60					65					

gtc	agg	cgc	gtc	aaa	ccc	gac	aaa	aaa	ctg	ctt	gcg	ctc	tac	gtt	ctg	355
Val	Arg	Arg	Val	Lys	Pro	Asp	Lys	Lys	Leu	Leu	Ala	Leu	Tyr	Val	Leu	
			70			75			80					85		

gtg	gca	gct	gtg	tgc	tcc	ggt	gca	ggc	gcc	ctg	gct	gcg	agt	ctc	att	403
Val	Ala	Ala	Val	Cys	Ser	Gly	Ala	Gly	Ala	Leu	Ala	Ala	Ser	Leu	Ile	
			90						95					100		

gac	aaa	caa	atc	atg	cga	ccg	ctg	atc	atc	gtg	ttg	atg	ctg	gtc	gtt	451
Asp	Lys	Gln	Ile	Met	Arg	Pro	Leu	Ile	Ile	Val	Leu	Met	Leu	Val	Val	
			105				110						115			

ggc	ctg	atc	gtg	gtg	ttc	aaa	cca	aac	ttc	gga	acc	ggc	gaa	agc	aaa	499
Gly	Leu	Ile	Val	Val	Phe	Lys	Pro	Asn	Phe	Gly	Thr	Gly	Glu	Ser	Lys	
			120				125					130				

gcc	ctg	ccc	acc	gga	tgg	aaa	cgc	tgg	gcc	gcc	atc	gtt	gca	gtc	gga	547
Ala	Leu	Pro	Thr	Gly	Trp	Lys	Arg	Trp	Ala	Ala	Ile	Val	Ala	Val	Gly	
		135				140					145					

ctc	atc	gca	gcc	tac	gac	ggc	atc	ttc	gga	ccc	gga	acc	ggc	atg	ttc	595
Leu	Ile	Ala	Ala	Tyr	Asp	Gly	Ile	Phe	Gly	Pro	Gly	Thr	Gly	Met	Phe	
			150		155				160					165		

ctc	atc	atg	gcg	ttc	acc	gca	ctg	ctc	tcc	caa	aat	ttc	ctg	tcc	tcc	643
Leu	Ile	Met	Ala	Phe	Thr	Ala	Leu	Leu	Ser	Gln	Asn	Phe	Leu	Ser	Ser	
			170					175						180		

gca	gcc	atg	gcg	aag	gtc	gta	aac	acc	gca	aca	aac	ctg	ggt	gcg	cta	691
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

```

Ala Ala Met Ala Lys Val Val Asn Thr Ala Thr Asn Leu Gly Ala Leu
      185                      190                      195

att gta ttc atc atc ggc ggc cac atg tgg tgg acc cta gga ctc gtg 739
ile Val Phe Ile Ile Gly Gly His Met Trp Trp Thr Leu Gly Leu Val
      200                      205                      210

ctg gca gtc gcc aat gtc gca ggc gca caa ctc ggt gcc cga acg gtg 787
Leu Ala Val Ala Asn Val Ala Gly Ala Gln Leu Gly Ala Arg Thr Val
      215                      220                      225

ctt ggt ggc ggt acc agg cta att aga tac gca cta cta acc ctg gtt 835
Leu Gly Gly Gly Thr Arg Leu Ile Arg Tyr Ala Leu Leu Thr Leu Val
      230                      235                      240                      245

gtc gtc atg agc gtc tac ctc acc tgg caa caa atc caa gga atg 880
Val Val Met Ser Val Tyr Leu Thr Trp Gln Gln Ile Gln Gly Met
      250                      255                      260

tagataagtc ggggcaaac cta 903

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<210> 2670
<211> 260
<212> PRT
<213> Corynebacterium glutamicum

<400> 2670
Met Gly Leu Glu Leu Ala Ala Ser Gly Trp Gly Ile Leu Ile Ala Gly
 1                      5                      10                      15

Ala Ala Val Ala Gly Trp Ile Asp Ala Val Ile Gly Gly Gly Gly Leu
      20                      25                      30

Val Leu Ile Pro Leu Ile Leu Ala Val Met Pro Gln Leu Ala Pro Val
      35                      40                      45

Thr Ala Leu Ala Ser Asn Lys Leu Ala Ala Val Thr Gly Thr Ala Ser
      50                      55                      60

Ala Ala Phe Thr Leu Val Arg Arg Val Lys Pro Asp Lys Lys Leu Leu
      65                      70                      75                      80

Ala Leu Tyr Val Leu Val Ala Ala Val Cys Ser Gly Ala Gly Ala Leu
      85                      90                      95

Ala Ala Ser Leu Ile Asp Lys Gln Ile Met Arg Pro Leu Ile Ile Val
      100                      105                      110

Leu Met Leu Val Val Gly Leu Ile Val Val Phe Lys Pro Asn Phe Gly
      115                      120                      125

Thr Gly Glu Ser Lys Ala Leu Pro Thr Gly Trp Lys Arg Trp Ala Ala
      130                      135                      140

Ile Val Ala Val Gly Leu Ile Ala Ala Tyr Asp Gly Ile Phe Gly Pro
      145                      150                      155                      160

Gly Thr Gly Met Phe Leu Ile Met Ala Phe Thr Ala Leu Leu Ser Gln
      165                      170                      175

```



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Asn Phe Leu Ser Ser Ala Ala Met Ala Lys Val Val Asn Thr Ala Thr
    180                      185                      190

Asn Leu Gly Ala Leu Ile Val Phe Ile Ile Gly Gly His Met Trp Trp
    195                      200                      205

Thr Leu Gly Leu Val Leu Ala Val Ala Asn Val Ala Gly Ala Gln Leu
    210                      215                      220

Gly Ala Arg Thr Val Leu Gly Gly Gly Thr Arg Leu Ile Arg Tyr Ala
    225                      230                      235                      240

Leu Leu Thr Leu Val Val Val Met Ser Val Tyr Leu Thr Trp Gln Gln
    245                      250                      255

Ile Gln Gly Met
    260

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<210> 2671

<211> 1260

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1237)

<223> RXA02297

<400> 2671

tgctgatcac gcctgactcc tatgaagtgt tgaccgattc cgctgctaaa gtgaagcgga 60

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cattatgaaa taaacgtgga tcaaggagtc cggtgcccaa ttg agc gat aaa gaa 115
                                Leu Ser Asp Lys Glu
                                1                      5

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cca gac ccc cac gaa caa att cca gag aag cca tcc cgc aag gtt att 163
Pro Asp Pro His Glu Gln Ile Pro Glu Lys Pro Ser Arg Lys Val Ile
    10                      15                      20

```

```

gca ctt cgt tgg tgc atc gta gcg ccg ctg tgc cta gcc gtg ggg tgg 211
Ala Leu Arg Trp Cys Ile Val Ala Pro Leu Ser Leu Ala Val Gly Trp
    25                      30                      35

```

```

ctt ttt act atg tgg ggt gtg cca gcc gca tgg atc ctc ggg gcg atc 259
Leu Phe Thr Met Trp Gly Val Pro Ala Ala Trp Ile Leu Gly Ala Ile
    40                      45                      50

```

```

ctt gtt gcc ggt gta tgt gcg ctg acc aca ggg caa gat ctt ccg atg 307
Leu Val Ala Gly Val Cys Ala Leu Thr Thr Gly Gln Asp Leu Pro Met
    55                      60                      65

```

```

gcc aag ggg gtg cat gtt ttt ggt cgc tca atc gtg gcg atg ctg gcg 355
Ala Lys Gly Val His Val Phe Gly Arg Ser Ile Val Ala Met Leu Ala
    70                      75                      80                      85

```

```

gcg ctg cct ttg att agt tct tct ggt tgc gaa ctt gtt cgt ttc ctc 403
Ala Leu Pro Leu Ile Ser Ser Ser Gly Ser Glu Leu Val Arg Phe Leu
    90                      95                      100

```

atc ccg ggt ctt gtg att tcc ttt ttc acc atc gcg gta ggc atc gtt 451

Ile	Pro	Gly	Leu	Val	Ile	Ser	Phe	Phe	Thr	Ile	Ala	Val	Gly	Ile	Val		
			105						110					115			
ggt	ggt	ttg	ttg	ctg	gca	aga	tcc	agg	ccg	gag	att	ttg	ccg	gaa	act	499	
Gly	Gly	Leu	Leu	Leu	Ala	Arg	Ser	Arg	Pro	Glu	Ile	Leu	Pro	Glu	Thr		
			120				125						130				
ggt	gtg	ctg	tcc	atg	ctg	gcg	ggt	ggc	gcg	tcg	gtg	atg	ccg	att	ctg	547	
Gly	Val	Leu	Ser	Met	Leu	Ala	Gly	Gly	Ala	Ser	Val	Met	Pro	Ile	Leu		
			135				140					145					
gcc	cga	gag	ttg	ggc	gct	gat	ttc	cgc	tat	gtg	gcg	ctg	acg	cag	tac	595	
Ala	Arg	Glu	Leu	Gly	Ala	Asp	Phe	Arg	Tyr	Val	Ala	Leu	Thr	Gln	Tyr		
			150			155				160					165		
ctc	agg	ttg	ttg	gtt	gtg	tcc	atg	acg	ttg	ccg	ctg	gtg	acg	cac	ttt	643	
Leu	Arg	Leu	Leu	Val	Val	Ser	Met	Thr	Leu	Pro	Leu	Val	Thr	His	Phe		
				170					175					180			
ttc	gtc	cct	ggc	ggg	gcg	gat	ttg	gga	tcg	ccg	cct	gag	aaa	tgg	ttg	691	
Phe	Val	Pro	Gly	Gly	Ala	Asp	Leu	Gly	Ser	Pro	Pro	Glu	Lys	Trp	Leu		
			185					190					195				
gac	gtg	ttg	agt	ttg	gga	gag	ttc	ggg	acg	tcg	ata	agc	gtt	tta	tcg	739	
Asp	Val	Leu	Ser	Leu	Gly	Glu	Phe	Gly	Thr	Ser	Ile	Ser	Val	Leu	Ser		
			200				205						210				
ctg	ctg	gtg	ctc	ttc	ggt	att	gtg	ctg	gcc	ggc	gaa	cct	ctc	ggc	agg	787	
Leu	Leu	Val	Leu	Phe	Gly	Ile	Val	Leu	Ala	Gly	Glu	Pro	Leu	Gly	Arg		
			215				220					225					
ttg	ctg	cgc	ttg	cct	gcc	cct	gcg	gtg	atg	ggg	ccg	ctg	atc	ctg	acc	835	
Leu	Leu	Arg	Leu	Pro	Ala	Pro	Ala	Val	Met	Gly	Pro	Leu	Ile	Leu	Thr		
			230			235				240					245		
gtg	ctg	gtg	agt	ttt	gtg	att	cca	gat	gat	ctc	agc	ctg	caa	ccg	cca	883	
Val	Leu	Val	Ser	Phe	Val	Ile	Pro	Asp	Asp	Leu	Ser	Leu	Gln	Pro	Pro		
				250				255						260			
acc	gtg	ttt	aag	att	atc	gcg	ttc	atg	gcg	atc	ggt	tgg	atg	tgt	ggc	931	
Thr	Val	Phe	Lys	Ile	Ile	Ala	Phe	Met	Ala	Ile	Gly	Trp	Met	Cys	Gly		
			265					270					275				
ggt	ccc	ttg	aat	atg	acc	gcg	ctg	aag	gtg	ttt	tct	aag	cag	ctt	ccg	979	
Gly	Pro	Leu	Asn	Met	Thr	Ala	Leu	Lys	Val	Phe	Ser	Lys	Gln	Leu	Pro		
			280				285					290					
gcc	acg	ttc	ttg	ttt	att	ttc	gcg	ctg	ctt	gcg	gtg	tgc	gca	ggt	gcg	1027	
Ala	Thr	Phe	Leu	Phe	Ile	Phe	Ala	Leu	Leu	Ala	Val	Cys	Ala	Gly	Ala		
			295				300					305					
gcg	ggg	ctg	ctc	acc	tgg	tgg	ttg	gat	atc	agc	ttc	ttc	gag	gct	tac	1075	
Ala	Gly	Leu	Leu	Thr	Trp	Trp	Leu	Asp	Ile	Ser	Phe	Phe	Glu	Ala	Tyr		
					315					320					325		
cta	gca	acc	agc	cct	gga	gct	ctg	gag	acg	gtg	ttg	gcg	ctg	tcc	tcg	1123	
Leu	Ala	Thr	Ser	Pro	Gly	Ala	Leu	Glu	Thr	Val	Leu	Ala	Leu	Ser	Ser		
				330					335					340			
gaa	gga	tct	gca	ggc	ccg	gtg	gtg	gtc	acg	atc	cag	atc	att	cga	cta	1171	
Glu	Gly	Ser	Ala	Gly	Pro	Val	Val	Val	Thr	Ile	Gln	Ile	Ile	Arg	Leu		

345

350

355

ctg gca atc ttg acc atc gcc ggt ttg atc ccc acg cta ctg cga cgc 1219
 Leu Ala Ile Leu Thr Ile Ala Gly Leu Ile Pro Thr Leu Leu Arg Arg
 360 365 370

att ttg cgt agg gat cgt taaaggcctt ctagttcagc acc 1260
 Ile Leu Arg Arg Asp Arg
 375

<210> 2672

<211> 379

<212> PRT

<213> Corynebacterium glutamicum

<400> 2672

Leu Ser Asp Lys Glu Pro Asp Pro His Glu Gln Ile Pro Glu Lys Pro
 1 5 10 15

Ser Arg Lys Val Ile Ala Leu Arg Trp Cys Ile Val Ala Pro Leu Ser
 20 25 30

Leu Ala Val Gly Trp Leu Phe Thr Met Trp Gly Val Pro Ala Ala Trp
 35 40 45

Ile Leu Gly Ala Ile Leu Val Ala Gly Val Cys Ala Leu Thr Thr Gly
 50 55 60

Gln Asp Leu Pro Met Ala Lys Gly Val His Val Phe Gly Arg Ser Ile
 65 70 75 80

Val Ala Met Leu Ala Ala Leu Pro Leu Ile Ser Ser Ser Gly Ser Glu
 85 90 95

Leu Val Arg Phe Leu Ile Pro Gly Leu Val Ile Ser Phe Phe Thr Ile
 100 105 110

Ala Val Gly Ile Val Gly Gly Leu Leu Leu Ala Arg Ser Arg Pro Glu
 115 120 125

Ile Leu Pro Glu Thr Gly Val Leu Ser Met Leu Ala Gly Gly Ala Ser
 130 135 140

Val Met Pro Ile Leu Ala Arg Glu Leu Gly Ala Asp Phe Arg Tyr Val
 145 150 155 160

Ala Leu Thr Gln Tyr Leu Arg Leu Leu Val Val Ser Met Thr Leu Pro
 165 170 175

Leu Val Thr His Phe Phe Val Pro Gly Gly Ala Asp Leu Gly Ser Pro
 180 185 190

Pro Glu Lys Trp Leu Asp Val Leu Ser Leu Gly Glu Phe Gly Thr Ser
 195 200 205

Ile Ser Val Leu Ser Leu Leu Val Leu Phe Gly Ile Val Leu Ala Gly
 210 215 220

Glu Pro Leu Gly Arg Leu Leu Arg Leu Pro Ala Pro Ala Val Met Gly
 225 230 235 240

Pro Leu Ile Leu Thr Val Leu Val Ser Phe Val Ile Pro Asp Asp Leu
245 250 255

Ser Leu Gln Pro Pro Thr Val Phe Lys Ile Ile Ala Phe Met Ala Ile
260 265 270

Gly Trp Met Cys Gly Gly Pro Leu Asn Met Thr Ala Leu Lys Val Phe
275 280 285

Ser Lys Gln Leu Pro Ala Thr Phe Leu Phe Ile Phe Ala Leu Leu Ala
290 295 300

Val Cys Ala Gly Ala Ala Gly Leu Leu Thr Trp Trp Leu Asp Ile Ser
305 310 315 320

Phe Phe Glu Ala Tyr Leu Ala Thr Ser Pro Gly Ala Leu Glu Thr Val
325 330 335

Leu Ala Leu Ser Ser Glu Gly Ser Ala Gly Pro Val Val Val Thr Ile
340 345 350

Gln Ile Ile Arg Leu Leu Ala Ile Leu Thr Ile Ala Gly Leu Ile Pro
355 360 365

Thr Leu Leu Arg Arg Ile Leu Arg Arg Asp Arg
370 375

<210> 2673

<211> 1782

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1759)

<223> RXA02298

<400> 2673

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aggtgggatt atgccgaaaa aatcgctacg atagccactt atg act ctt cag agt 115
Met Thr Leu Gln Ser
1 5

tct gat aaa cgt tct cct tca ctg tta gac gcc tcc tcc gag gtc ttt 163
Ser Asp Lys Arg Ser Pro Ser Leu Leu Asp Ala Ser Ser Glu Val Phe
10 15 20

gtc cat gat ttg gca gct ttg tct ccc act gat gcc act gca tgg ggt 211
Val His Asp Leu Ala Ala Leu Ser Pro Thr Asp Ala Thr Ala Trp Gly
25 30 35

atc tca ggc ttc gaa ggt gat ctt cag gat ttc tct cct gac tat tgg 259
Ile Ser Gly Phe Glu Gly Asp Leu Gln Asp Phe Ser Pro Asp Tyr Trp
40 45 50

aat gcc atc gcc gaa cgc aac cgc gac atg gtt gcc gat gtt gat gct 307
Asn Ala Ile Ala Glu Arg Asn Arg Asp Met Val Ala Asp Val Asp Ala
55 60 65

ttt gat gac ggc act gat gac aac gat gac gaa gaa gat ttc gat gac	355
Phe Asp Asp Gly Thr Asp Asp Asn Asp Asp Glu Asp Phe Asp Asp	
70 75 80 85	
ggt gac cgc gtc acc gct gat gtt ctc cgt gat cgc gta tgc ctg gat	403
Val Asp Arg Val Thr Ala Asp Val Leu Arg Asp Arg Val Cys Leu Asp	
90 95 100	
ctg gcc ctg cac cac cag ggc gaa acc tta cgc aat ctc aac aac att	451
Leu Ala Leu His His Gln Gly Glu Thr Leu Ala Asn Leu Asn Asn Ile	
105 110 115	
gat tcc cca gtc cag acc atc cgc gat acc ttc ctc atc atg ccc cgc	499
Asp Ser Pro Val Gln Thr Ile Arg Asp Thr Phe Leu Ile Met Pro Arg	
120 125 130	
gag acg gac gat gat gtg gaa aat ctc cgc gaa cgt ctc tcc cgc gtc	547
Glu Thr Asp Asp Asp Val Glu Asn Leu Arg Glu Arg Leu Ser Arg Val	
135 140 145	
ccc gac gct ctc cac gga tac tgt gaa tca ctc gct gag gct gcc agc	595
Pro Asp Ala Leu His Gly Tyr Cys Glu Ser Leu Ala Glu Ala Ala Ser	
150 155 160 165	
caa gcc cat gtt gca cgc gtc cgc cag gtg gaa gaa gtg gtg tgc caa	643
Gln Gly His Val Ala Ala Val Arg Gln Val Glu Glu Val Val Ser Gln	
170 175 180	
tgt gag gac ctc gct gat gag gac tcc gtt ttg cag cac ctt ggc ttg	691
Cys Glu Asp Leu Ala Asp Glu Asp Ser Val Leu Gln His Leu Gly Leu	
185 190 195	
gat gaa aat gat cca gta gtt gta gag gcc cag gaa gct ttt gca cga	739
Asp Glu Asn Asp Pro Val Val Val Glu Ala Gln Glu Ala Phe Ala Arg	
200 205 210	
ggt gcc ggt tgg tta gca gag caa ctg gct ccg cat gct cct cat gtg	787
Val Ala Gly Trp Leu Ala Glu Gln Leu Ala Pro His Ala Pro His Val	
215 220 225	
gat cgc gtt ggc cgg gat cgc tat gaa atg ttc tcc cac ctg cac gtc	835
Asp Ala Val Gly Arg Asp Arg Tyr Glu Met Phe Ser His Leu His Val	
230 235 240 245	
ggc gag ttt gta gat ctg gat gag gct tac caa tgg tcc ctg gaa cag	883
Gly Glu Phe Val Asp Leu Asp Glu Ala Tyr Gln Trp Ser Leu Glu Gln	
250 255 260	
ctg cgt gac att gat gct cag cag ctt cag gta gcc cag cag ctg tac	931
Leu Arg Asp Ile Asp Ala Gln Gln Leu Gln Val Ala Gln Gln Leu Tyr	
265 270 275	
ggc cct ggc acc acg atc cgt gag gcc atg aag aag ctc aat gct gat	979
Gly Pro Gly Thr Thr Ile Arg Glu Ala Met Lys Lys Leu Asn Ala Asp	
280 285 290	
gag cgc tac ctc atc cga ggc act gat gct ctg cag gag tgg atg caa	1027
Glu Arg Tyr Leu Ile Arg Gly Thr Asp Ala Leu Gln Glu Trp Met Gln	
295 300 305	

aag acc gct gat cag gca atc gct gat cta gat ggc gtt tcc ttc aac 1075
Lys Thr Ala Asp Gln Ala Ile Ala Asp Leu Asp Gly Val Ser Phe Asn
310 315 320 325

att cca gag cag gct cga cag gtt gag tgc ctc atc gat cct gct gga 1123
Ile Pro Glu Gln Ala Arg Gln Val Glu Cys Leu Ile Asp Pro Ala Gly
330 335 340

act ggc ggc att ttc tac acc cca cca agc gat gat ttc tcc agg cct 1171
Thr Gly Gly Ile Phe Tyr Thr Pro Pro Ser Asp Asp Phe Ser Arg Pro
345 350 355

ggc cgc atg tgg tgg tct gtg cct aaa acc cag gaa gtc ttc cac acc 1219
Gly Arg Met Trp Trp Ser Val Pro Lys Thr Gln Glu Val Phe His Thr
360 365 370

tgg caa gag ctc acc acc gtg ttc cac gag ggt gtt cct ggc cac cac 1267
Trp Gln Glu Leu Thr Thr Val Phe His Glu Gly Val Pro Gly His His
375 380 385

ctg cag atc tcc caa act ttg gtg gaa aag gat ctg aac ctg tgg cgt 1315
Leu Gln Ile Ser Gln Thr Leu Val Glu Lys Asp Leu Asn Leu Trp Arg
390 395 400 405

cga gtc gct tgc tgg aac tct ggc cac ggt gaa ggt tgg cgc ctg tac 1363
Arg Val Ala Cys Trp Asn Ser Gly His Gly Glu Gly Trp Ala Leu Tyr
410 415 420

gca gaa tct ctc atg aag gaa ttg gga tac cac gaa gat cca ggc aac 1411
Ala Glu Ser Leu Met Lys Glu Leu Gly Tyr His Glu Asp Pro Gly Asn
425 430 435

ctc atg ggc tac ctt gat gct cag cga ctc cgt gca gcc cgc gtg gcc 1459
Leu Met Gly Tyr Leu Asp Ala Gln Arg Leu Arg Ala Arg Val Ala
440 445 450

att gac atc gga att cac ctg aac aag agg aac cca gag tgc acc ggc 1507
Ile Asp Ile Gly Ile His Leu Asn Lys Arg Asn Pro Glu Cys Thr Gly
455 460 465

ctg tgg gat gcg tct tat gcg cgc agc ttc ctg cgt gaa aat acg tcc 1555
Leu Trp Asp Ala Ser Tyr Ala Arg Ser Phe Leu Arg Glu Asn Thr Ser
470 475 480 485

atg aat gaa gat gcg ctg tac ttt gag ctc aac cgt tac ctt ggt tgg 1603
Met Asn Glu Asp Ala Leu Tyr Phe Glu Leu Asn Arg Tyr Leu Gly Trp
490 495 500

cca ggt cag gcc gca tgc tat gcc att ggt cag cga ctc tgg ttg aac 1651
Pro Gly Gln Ala Ala Ser Tyr Ala Ile Gly Gln Arg Leu Trp Leu Asn
505 510 515

ctg cgc gat gag gcc att agc cag ggg caa acc ttg gcg caa ttc cac 1699
Leu Arg Asp Glu Ala Ile Ser Gln Gly Gln Thr Leu Ala Gln Phe His
520 525 530

agc aag gca ttg tcc tat ggc agc atc ccg atg ggc att ttg cgc gat 1747
Ser Lys Ala Leu Ser Tyr Gly Ser Ile Pro Met Gly Ile Leu Arg Asp
535 540 545

cag gtg ctg aac tagaaggcct ttaacgatcc cta 1782

Gln Val Leu Asn
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<210> 2674

<211> 553

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2674

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Ser Ser Glu Val Phe Val His Asp Leu Ala Ala Leu Ser Pro Thr Asp
20 25 30

Ala Thr Ala Trp Gly Ile Ser Gly Phe Glu Gly Asp Leu Gln Asp Phe
35 40 45

Ser Pro Asp Tyr Trp Asn Ala Ile Ala Glu Arg Asn Arg Asp Met Val
50 55 60

Ala Asp Val Asp Ala Phe Asp Asp Gly Thr Asp Asp Asn Asp Asp Glu
65 70 75 80

Glu Asp Phe Asp Asp Val Asp Arg Val Thr Ala Asp Val Leu Arg Asp
85 90 95

Arg Val Cys Leu Asp Leu Ala Leu His His Gln Gly Glu Thr Leu Ala
100 105 110

Asn Leu Asn Asn Ile Asp Ser Pro Val Gln Thr Ile Arg Asp Thr Phe
115 120 125

Leu Ile Met Pro Arg Glu Thr Asp Asp Asp Val Glu Asn Leu Arg Glu
130 135 140

Arg Leu Ser Arg Val Pro Asp Ala Leu His Gly Tyr Cys Glu Ser Leu
145 150 155 160

Ala Glu Ala Ala Ser Gln Gly His Val Ala Ala Val Arg Gln Val Glu
165 170 175

Glu Val Val Ser Gln Cys Glu Asp Leu Ala Asp Glu Asp Ser Val Leu
180 185 190

Gln His Leu Gly Leu Asp Glu Asn Asp Pro Val Val Val Glu Ala Gln
195 200 205

Glu Ala Phe Ala Arg Val Ala Gly Trp Leu Ala Glu Gln Leu Ala Pro
210 215 220

His Ala Pro His Val Asp Ala Val Gly Arg Asp Arg Tyr Glu Met Phe
225 230 235 240

Ser His Leu His Val Gly Glu Phe Val Asp Leu Asp Glu Ala Tyr Gln
245 250 255

Trp Ser Leu Glu Gln Leu Arg Asp Ile Asp Ala Gln Gln Leu Gln Val
260 265 270

Ala Gln Gln Leu Tyr Gly Pro Gly Thr Thr Ile Arg Glu Ala Met Lys
 275 280 285
 Lys Leu Asn Ala Asp Glu Arg Tyr Leu Ile Arg Gly Thr Asp Ala Leu
 290 295 300
 Gln Glu Trp Met Gln Lys Thr Ala Asp Gln Ala Ile Ala Asp Leu Asp
 305 310 315 320
 Gly Val Ser Phe Asn Ile Pro Glu Gln Ala Arg Gln Val Glu Cys Leu
 325 330 335
 Ile Asp Pro Ala Gly Thr Gly Gly Ile Phe Tyr Thr Pro Ser Asp
 340 345 350
 Asp Phe Ser Arg Pro Gly Arg Met Trp Trp Ser Val Pro Lys Thr Gln
 355 360 365
 Glu Val Phe His Thr Trp Gln Glu Leu Thr Thr Val Phe His Glu Gly
 370 375 380
 Val Pro Gly His His Leu Gln Ile Ser Gln Thr Leu Val Glu Lys Asp
 385 390 395 400
 Leu Asn Leu Trp Arg Arg Val Ala Cys Trp Asn Ser Gly His Gly Glu
 405 410 415
 Gly Trp Ala Leu Tyr Ala Glu Ser Leu Met Lys Glu Leu Gly Tyr His
 420 425 430
 Glu Asp Pro Gly Asn Leu Met Gly Tyr Leu Asp Ala Gln Arg Leu Arg
 435 440 445
 Ala Ala Arg Val Ala Ile Asp Ile Gly Ile His Leu Asn Lys Arg Asn
 450 455 460
 Pro Glu Cys Thr Gly Leu Trp Asp Ala Ser Tyr Ala Arg Ser Phe Leu
 465 470 475 480
 Arg Glu Asn Thr Ser Met Asn Glu Asp Ala Leu Tyr Phe Glu Leu Asn
 485 490 495
 Arg Tyr Leu Gly Trp Pro Gly Gln Ala Ala Ser Tyr Ala Ile Gly Gln
 500 505 510
 Arg Leu Trp Leu Asn Leu Arg Asp Glu Ala Ile Ser Gln Gly Gln Thr
 515 520 525
 Leu Ala Gln Phe His Ser Lys Ala Leu Ser Tyr Gly Ser Ile Pro Met
 530 535 540
 Gly Ile Leu Arg Asp Gln Val Leu Asn
 545 550

<210> 2675

<211> 1014

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(991)

<223> RXA02304

<400> 2675

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agtgcgaagt tttataaca gggcagtaac gtttactggt atg aaa act ccc cgt 115
Met Lys Thr Pro Arg
1 5

ctg ctg aag atc ctc agc gcg atg gtg gct gtc act gga ctt ctc att 163
Leu Leu Lys Ile Leu Ser Ala Met Val Ala Val Thr Gly Leu Leu Ile
10 15 20

cca acg gtg gtc ccc atg gcc gcc gct gat gct gct gaa ctg tcc gac 211
Pro Thr Val Val Pro Met Ala Ala Ala Asp Ala Ala Glu Leu Ser Asp
25 30 35

aac gtt ccc gat cgc acc caa att gcc atc atc aac cct gat ggc agc 259
Asn Val Pro Asp Arg Thr Gln Ile Ala Ile Ile Asn Pro Asp Gly Ser
40 45 50

gtg caa gaa tct gac aac gcc gaa gaa tcc cgc ccg gca tta tcc ctg 307
Val Gln Glu Ser Asp Asn Ala Glu Glu Ser Arg Pro Ala Leu Ser Leu
55 60 65

gcc aag ctg tat ttg ggt tat tat gtg ttg gct caa ggc gcg gaa gaa 355
Ala Lys Leu Tyr Leu Gly Tyr Tyr Val Leu Ala Gln Gly Ala Glu Glu
70 75 80 85

gat att gaa cta gtc cca gat atg atc cgc tac tct gat gat ttc acc 403
Asp Ile Glu Leu Val Pro Asp Met Ile Arg Tyr Ser Asp Asp Phe Thr
90 95 100

gcg gat tat ttg gag agc gaa tac ccg gaa gca att cct gag gtt att 451
Ala Asp Tyr Leu Glu Ser Glu Tyr Pro Glu Ala Ile Pro Glu Val Ile
105 110 115

gat gcc ttc gat ttg gaa gac acc gaa tgg gct ggt ttc tgg ggc aat 499
Asp Ala Phe Asp Leu Glu Asp Thr Glu Trp Ala Gly Phe Thr Gly Asn
120 125 130

gca act acc agt gcg gtg gat att gcg acg ttt gta gca gca ctc atc 547
Ala Thr Thr Ser Ala Val Asp Ile Ala Thr Phe Val Ala Ala Leu Ile
135 140 145

gac gat ccc acg gcg cag ccc ttg ctt gac gca atg tct gac acc gct 595
Asp Asp Pro Thr Ala Gln Pro Leu Leu Asp Ala Met Ser Asp Thr Ala
150 155 160 165

gag tat gcg gcg gat ggc tac gcc cag aac ttt ggc act ttt aca ttg 643
Glu Tyr Ala Ala Asp Gly Tyr Ala Gln Asn Phe Gly Thr Phe Thr Leu
170 175 180

tcc gat gtc acc ggt act aaa ttt ggt tgg tct gat tcc ctc gat gtg 691
Ser Asp Val Thr Gly Thr Lys Phe Gly Trp Ser Asp Ser Leu Asp Val
185 190 195

cat tca tcg gtc agc ttt ggc cct ggt ttt gtg atc gct gcc aac acc 739
His Ser Ser Val Ser Phe Gly Pro Gly Phe Val Ile Ala Ala Asn Thr

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200	205	210	
tac ggt gac gcc gaa acg ctc acc gaa gat gtc caa gat tcc gtg tct			787
Tyr Gly Asp Ala Glu Thr	Leu Thr Glu Asp Val	Gln Asp Ser Val Ser	
215	220	225	
tcg ctg tat ccg gag gaa gta acc acc gcg atc gag gag cag gtg gat			835
Ser Leu Tyr Pro Glu Glu Val Thr Thr Ala Ile Glu Glu Gln Val Asp			
230	235	240	245
cag ctg tgt gag tgc gct gca gag act acg cat ttg gga atg cac act			883
Gln Leu Cys Glu Cys Ala Ala Glu Thr Thr His Leu Gly Met His Thr			
250	255	260	
ggc gcg gag ctg aaa gca cag ctt gag ggc act att tat gga aaa acc			931
Gly Ala Glu Leu Cys Lys Ala Gln Leu Glu Gly Thr Ile Tyr Gly Lys Thr			
265	270	275	
ctc agc ttt tta cct aat tca gcc cca gcg cca gcg ttt att tac aac			979
Leu Ser Phe Leu Pro Asn Ser Ala Pro Ala Pro Ala Phe Ile Tyr Asn			
280	285	290	
ctg ctg gca cat tagcaaacag tttaaggaa ctc			1014
Leu Leu Ala His			
295			
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<211> 297			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 2676			
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Thr Gly Leu Leu Ile Pro Thr Val Val Pro Met Ala Ala Asp Ala			
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Ala Glu Leu Ser Asp Asn Val Pro Asp Arg Thr Gln Ile Ala Ile Ile			
35	40	45	
Asn Pro Asp Gly Ser Val Gln Glu Ser Asp Asn Ala Glu Glu Ser Arg			
50	55	60	
Pro Ala Leu Ser Leu Ala Lys Leu Tyr Leu Gly Tyr Tyr Val Leu Ala			
65	70	75	80
Gln Gly Ala Glu Glu Asp Ile Glu Leu Val Pro Asp Met Ile Arg Tyr			
85	90	95	
Ser Asp Asp Phe Thr Ala Asp Tyr Leu Glu Ser Glu Tyr Pro Glu Ala			
100	105	110	
Ile Pro Glu Val Ile Asp Ala Phe Asp Leu Glu Asp Thr Glu Trp Ala			
115	120	125	
Gly Phe Trp Gly Asn Ala Thr Thr Ser Ala Val Asp Ile Ala Thr Phe			
130	135	140	
Val Ala Ala Leu Ile Asp Asp Pro Thr Ala Gln Pro Leu Leu Asp Ala			


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55              60              65
gca gta atc cac gag gca gga gga acg atc aac aac att gtt tcc acc 355
Ala Val Ile His Glu Ala Gly Gly Thr Ile Asn Asn Ile Val Ser Thr
70              75              80              85

act act tat ctt gcc gat gtc acc gat gct ccc gtt gtt aac gct gct 403
Thr Thr Tyr Leu Ala Asp Val Thr Asp Ala Pro Val Val Asn Ala Ala
90              95              100

cgc tcc cgc tat ttc acc gga gaa gta ttg ccc acc cac acc gta att 451
Arg Ser Arg Tyr Phe Thr Gly Glu Val Leu Pro Thr His Thr Val Ile
105              110              115

gga gtt gct gct ctt gct cgg cca cag ttt cta gtc gag atc tca gcg 499
Gly Val Ala Ala Leu Ala Arg Pro Gln Phe Leu Val Glu Ile Ser Ala
120              125              130

gtg gcc tat ttg ggg gac ctt tca aaa gac tagatacatg attatttttg 549
Val Ala Tyr Leu Gly Asp Leu Ser Lys Asp
135              140

cat 552

<210> 2678
<211> 143
<212> PRT
<213> Corynebacterium glutamicum

<400> 2678
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Leu Pro Pro Gly Pro Ala Glu Arg Thr Val Tyr Ser Tyr Gly Val Arg
20              25              30

Ala Gly Asp Gln Val His Ile Leu Arg Met Glu Ala Phe Asp Ser Asp
35              40              45

Ala Asn Ile Val Gly Glu Arg Asp Ile Glu Ala His Ala Glu Gln Val
50              55              60

Phe Lys Asn Leu Gln Ala Val Ile His Glu Ala Gly Gly Thr Ile Asn
65              70              75              80

Asn Ile Val Ser Thr Thr Tyr Leu Ala Asp Val Thr Asp Ala Pro
85              90              95

Val Val Asn Ala Ala Arg Ser Arg Tyr Phe Thr Gly Glu Val Leu Pro
100              105              110

Thr His Thr Val Ile Gly Val Ala Ala Leu Ala Arg Pro Gln Phe Leu
115              120              125

Val Glu Ile Ser Ala Val Ala Tyr Leu Gly Asp Leu Ser Lys Asp
130              135              140

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<210> 2679

<211> 1209

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1186)

<223> RXA02324

<400> 2679

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cgactctatt gaaaaatgatt cccaaaagga gggctttcac atg gcc aca acg acc 115
 Met Ala Thr Thr Thr
 1 5

cca gtc acc gtg cta tca gga ttt ctc gcc tcc gga aaa acc aca ttg 163
 Pro Val Thr Val Leu Ser Gly Phe Leu Gly Ser Gly Lys Thr Thr Leu
 10 15 20

ctc aac cag atc ctc cac cac cga gga tcc cgg aaa atc gca gtc att 211
 Leu Asn Gln Ile Leu His His Arg Gly Ser Arg Lys Ile Ala Val Ile
 25 30 35

gtc aac gat ttt tca gaa atc aac atc gac gca gcc ctc atc gca tcc 259
 Val Asn Asp Phe Ser Glu Ile Asn Ile Asp Ala Ala Leu Ile Ala Ser
 40 45 50

gaa ggc cac ctc acc cgc ggc gaa gac cgc ttc gtg gaa ctg acc aac 307
 Glu Gly His Leu Thr Arg Gly Glu Asp Arg Phe Val Glu Leu Thr Asn
 55 60 65

gga tgc atc tgc tgc acc ctg cgc gaa gac ctc gtg gat tcc gtc ggc 355
 Gly Cys Ile Cys Cys Thr Leu Arg Glu Asp Leu Val Asp Ser Val Gly
 70 75 80 85

gaa ctc gcc agc agc gac cgc ttc gac cac atc gtc atc gaa tcc acg 403
 Glu Leu Ala Ser Ser Asp Arg Phe Asp His Ile Val Ile Glu Ser Thr
 90 95 100

ggt atc tcc gaa cca atg ccg gta gcc gcc aca ttt gaa tgg cag tgg 451
 Gly Ile Ser Glu Pro Met Pro Val Ala Ala Thr Phe Glu Trp Gln Trp
 105 110 115

gat gac ggc acc cgc ctg gct gac aaa gca ccg atc gac acc atg gtc 499
 Asp Asp Gly Thr Arg Leu Ala Asp Lys Ala Pro Ile Asp Thr Met Val
 120 125 130

acc ctg gtc gat gcc acc caa ttc atc gac ctc atc cgc aaa aac acc 547
 Thr Leu Val Asp Ala Thr Gln Phe Ile Asp Leu Ile Arg Lys Asn Thr
 135 140 145

tcc ctc acc gag gct gac atg ggc gca acc gag gac gat gaa cgc acc 595
 Ser Leu Thr Glu Ala Asp Met Gly Ala Thr Glu Asp Asp Glu Arg Thr
 150 155 160 165

atc gcc gac cta ctc acc gat caa atc gag ttc gcc gac cgc atc tac 643
 Ile Ala Asp Leu Leu Thr Asp Gln Ile Glu Phe Ala Asp Arg Ile Tyr
 170 175 180

atc acc aaa tcc gac ctg gtg gac cgc act gtc ctc gag caa acc cgc 691
 Ile Thr Lys Ser Asp Leu Val Asp Arg Thr Val Leu Glu Gln Thr Arg

185	190	195	
gca cta atc gcc agc atg agt cca cgc gcc cgc att gac tta ctc atc Ala Leu Ile Ala Ser Met Ser Pro Arg Ala Arg Ile Asp Leu Leu Ile 200 205 210			739
gat ggc ctc aat gac ggc tcc ccc atc acc gac gac atc ctc gga gct Asp Gly Leu Asn Asp Gly Ser Pro Ile Thr Asp Asp Ile Leu Gly Ala 215 220 225			787
ttc ctc tac gac gaa gcc acc gcc cgc gcc tac gag ggc tac acg gaa Phe Leu Tyr Asp Glu Ala Thr Ala Arg Ala Tyr Glu Gly Tyr Thr Glu 230 235 240 245			835
gaa ctc gaa aac ccg cac act ccc gaa acc gag gaa tac ggc atc agt Glu Leu Glu Asn Pro His Thr Pro Glu Thr Glu Glu Tyr Gly Ile Ser 250 255 260			883
tcc gtg gta ttc cgc tct gac cgg ccg ttc aac aag gat cgc cta ctt Ser Val Val Phe Arg Ser Asp Arg Pro Phe Asn Lys Asp Arg Leu Leu 265 270 275			931
cag gta ctg cgt tcc acc act gga ctc gtt cgc tcc aaa ggc tat tgc Gln Val Leu Arg Ser Thr Thr Gly Leu Val Arg Ser Lys Gly Tyr Cys 280 285 290			979
tgg atc gct gat cac ctc aac atc gtc cag gtc tgg cac caa gcc ggc Trp Ile Ala Asp His Leu Asn Ile Val Gln Val Trp His Gln Ala Gly 295 300 305			1027
ccc aat ttg agc att cgc ccg gcc gcc tat tgg gcc aat tca gag atc Pro Asn Leu Ser Ile Arg Pro Ala Ala Tyr Trp Ala Asn Ser Glu Ile 310 315 320 325			1075
acc ccc ggc act gaa ttg gtc ctg atc ggc atc cac atc gac ggc ccc Thr Pro Gly Thr Glu Leu Val Leu Ile Gly Ile His Ile Asp Gly Pro 330 335 340			1123
acc ttg ctc gca ctg cta caa ggc gcg acg ctt acc gat gcg gaa gtg Thr Leu Leu Ala Leu Leu Gln Gly Ala Thr Leu Thr Asp Ala Glu Val 345 350 355			1171
gcg gca ctg gtt ttg tgagttcctc aagtcctga att Ala Ala Leu Val Leu 360			1209

<210> 2680

<211> 362

<212> PRT

<213> Corynebacterium glutamicum

<400> 2680

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Gly	Lys	Thr	Thr	Leu	Leu	Asn	Gln	Ile	Leu	His	His	Arg	Gly	Ser	Arg
		20					25						30		

Lys	Ile	Ala	Val	Ile	Val	Asn	Asp	Phe	Ser	Glu	Ile	Asn	Ile	Asp	Ala
	35					40						45			

Ala Leu Ile Ala Ser Glu Gly His Leu Thr Arg Gly Glu Asp Arg Phe
 50 55 60
 Val Glu Leu Thr Asn Gly Cys Ile Cys Cys Thr Leu Arg Glu Asp Leu
 65 70 75 80
 Val Asp Ser Val Gly Glu Leu Ala Ser Ser Asp Arg Phe Asp His Ile
 85 90 95
 Val Ile Glu Ser Thr Gly Ile Ser Glu Pro Met Pro Val Ala Ala Thr
 100 105 110
 Phe Glu Trp Gln Trp Asp Asp Gly Thr Arg Leu Ala Asp Lys Ala Pro
 115 120 125
 Ile Asp Thr Met Val Thr Leu Val Asp Ala Thr Gln Phe Ile Asp Leu
 130 135 140
 Ile Arg Lys Asn Thr Ser Leu Thr Glu Ala Asp Met Gly Ala Thr Glu
 145 150 155 160
 Asp Asp Glu Arg Thr Ile Ala Asp Leu Leu Thr Asp Gln Ile Glu Phe
 165 170 175
 Ala Asp Arg Ile Tyr Ile Thr Lys Ser Asp Leu Val Asp Arg Thr Val
 180 185 190
 Leu Glu Gln Thr Arg Ala Leu Ile Ala Ser Met Ser Pro Arg Ala Arg
 195 200 205
 Ile Asp Leu Leu Ile Asp Gly Leu Asn Asp Gly Ser Pro Ile Thr Asp
 210 215 220
 Asp Ile Leu Gly Ala Phe Leu Tyr Asp Glu Ala Thr Ala Arg Ala Tyr
 225 230 235 240
 Glu Gly Tyr Thr Glu Glu Leu Glu Asn Pro His Thr Pro Glu Thr Glu
 245 250 255
 Glu Tyr Gly Ile Ser Ser Val Val Phe Arg Ser Asp Arg Pro Phe Asn
 260 265 270
 Lys Asp Arg Leu Leu Gln Val Leu Arg Ser Thr Thr Gly Leu Val Arg
 275 280 285
 Ser Lys Gly Tyr Cys Trp Ile Ala Asp His Leu Asn Ile Val Gln Val
 290 295 300
 Trp His Gln Ala Gly Pro Asn Leu Ser Ile Arg Pro Ala Ala Tyr Trp
 305 310 315 320
 Ala Asn Ser Glu Ile Thr Pro Gly Thr Glu Leu Val Leu Ile Gly Ile
 325 330 335
 His Ile Asp Gly Pro Thr Leu Leu Ala Leu Leu Gln Gly Ala Thr Leu
 340 345 350
 Thr Asp Ala Glu Val Ala Ala Leu Val Leu
 355 360

<210> 2681

<211> 993

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(970)

<223> RXA02325

<400> 2681

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tactgcaccc	gtctaata	gaa aatcattact	attaggtgtc	atg atg gac cat gca	115
				Met Met Asp His Ala	
				1 5	

cac gat tcc tgc tca cca act ctg cgc cgt gat ttg gag gtc act ggc	163
His Asp Ser Cys Ser Pro Thr Leu Arg Arg Asp Leu Glu Val Thr Gly	
10 15 20	

cag ctc caa cct gag aaa gct gtc gat tta gca gcg ccg cac gaa ggg	211
Gln Leu Gln Pro Glu Lys Ala Val Asp Leu Ala Ala Pro His Glu Gly	
25 30 35	

aag gtt gcc aat ata acg aag gtg acc tcc tca aat atg gag cac acc	259
Lys Val Ala Asn Ile Thr Lys Val Thr Ser Ser Asn Met Glu His Thr	
40 45 50	

atc acg cag gcc tca aaa gct aag gag gtg gtg gtg ctc att ggt cac	307
Ile Thr Gln Ala Ser Lys Ala Lys Glu Val Val Val Ile Gly His	
55 60 65	

tcc ctg ctg ccc aca ttt cag gat ttg gaa aaa gac att ctg cac ttt	355
Ser Leu Leu Pro Thr Phe Gln Asp Leu Glu Lys Asp Ile Leu His Phe	
70 75 80 85	

cag gca ggt aat aaa ggg cga ttt tct gta gcg att gtt gat cct gat	403
Gln Ala Gly Asn Lys Gly Arg Phe Ser Val Ala Ile Val Asp Pro Asp	
90 95 100	

gcg agt gca gat gtg gtt gcc aga ttt agg cca aaa cag att ccg gtg	451
Arg Ser Ala Asp Val Val Ala Arg Phe Arg Pro Lys Gln Ile Pro Val	
105 110 115	

gca tac gtg gtg aaa gat ggc gcc agc att gcg gag ttc aac tcg ctc	499
Ala Tyr Val Val Lys Asp Gly Ala Ser Ile Ala Glu Phe Asn Ser Leu	
120 125 130	

aac aag gag ccg gtt gca caa tgg ctt gat cat ttt gtg tcg ccg gaa	547
Asn Lys Glu Pro Val Ala Gln Trp Leu Asp His Phe Val Ser Arg Glu	
135 140 145	

acg atc ccc aat gaa aaa gag ggg gac gtc gat aag caa ata gac ccg	595
Thr Ile Pro Asn Glu Lys Glu Gly Asp Val Asp Lys Gln Ile Asp Pro	
150 155 160 165	

gcg ctg tgg ccg gca gcg gaa ttg gtg aac gcc ggt gat ttt cgc gcg	643
Arg Leu Trp Arg Ala Ala Glu Leu Val Asn Ala Gly Asp Phe Arg Ala	
170 175 180	

gcg ttg gcg ttg tat gag cag ttg ccg cag gat gcg acg gtg aag cgg 691
 Ala Leu Ala Leu Tyr Glu Gln Leu Pro Gln Asp Ala Thr Val Lys Arg
 185 190 195

gcg cac gcg gcg gtg tcg gta ttg gcg cgg atg tct gtg gcg gat cgg 739
 Ala His Ala Ala Val Ser Val Leu Ala Arg Met Ser Val Ala Asp Arg
 200 205 210

gga gag gat ccg atc gag aag tcg cgc cgg gat cca gac gat gtg aac 787
 Gly Glu Asp Pro Ile Glu Lys Ser Arg Arg Asp Pro Asp Asp Val Asn
 215 220 225

aag gcg ctg gcg gcg gcg gat atg tat gtg ttg atg aat cag ccg gac 835
 Lys Ala Leu Ala Ala Ala Asp Met Tyr Val Leu Met Asn Gln Pro Asp
 230 235 240 245

aca gcg ctc gcg cac ctt gca gca cta ttg cca aaa ccg gag gct gcc 883
 Thr Ala Leu Ala His Leu Ala Ala Leu Leu Pro Lys Pro Glu Ala Ala
 250 255 260

cgg cgg atc gtg gag ttg ctg aac ttg ttt gat ccg ctg gac ctg gtc 931
 Arg Arg Ile Val Glu Leu Leu Asn Leu Phe Asp Pro Leu Asp Leu Val
 265 270 275

gca ttg gaa atc agg gcg cag gtg ggg aat gca atg agc taagaaaaca 980
 Ala Leu Glu Ile Arg Ala Gln Val Gly Asn Ala Met Ser
 280 285 290

ctttaaatat tct 993

<210> 2682
 <211> 290
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2682
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 20 25 30

Ala Pro His Glu Gly Lys Val Ala Asn Ile Thr Lys Val Thr Ser Ser
 35 40 45

Asn Met Glu His Thr Ile Thr Gln Ala Ser Lys Ala Lys Glu Val Val
 50 55 60

Val Leu Ile Gly His Ser Leu Leu Pro Thr Phe Gln Asp Leu Glu Lys
 65 70 75 80

Asp Ile Leu His Phe Gln Ala Gly Asn Lys Gly Arg Phe Ser Val Ala
 85 90 95

Ile Val Asp Pro Asp Arg Ser Ala Asp Val Val Ala Arg Phe Arg Pro
 100 105 110

Lys Gln Ile Pro Val Ala Tyr Val Val Lys Asp Gly Ala Ser Ile Ala
 115 120 125

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Glu Phe Asn Ser Leu Asn Lys Glu Pro Val Ala Gln Trp Leu Asp His
130                      135                      140

Phe Val Ser Arg Glu Thr Ile Pro Asn Glu Lys Glu Gly Asp Val Asp
145                      150                      155                      160

Lys Gln Ile Asp Pro Arg Leu Trp Arg Ala Ala Glu Leu Val Asn Ala
165                      170                      175

Gly Asp Phe Arg Ala Ala Leu Ala Leu Tyr Glu Gln Leu Pro Gln Asp
180                      185                      190

Ala Thr Val Lys Arg Ala His Ala Ala Val Ser Val Leu Ala Arg Met
195                      200                      205

Ser Val Ala Asp Arg Gly Glu Asp Pro Ile Glu Lys Ser Arg Arg Asp
210                      215                      220

Pro Asp Asp Val Asn Lys Ala Leu Ala Ala Ala Asp Met Tyr Val Leu
225                      230                      235                      240

Met Asn Gln Pro Asp Thr Ala Leu Ala His Leu Ala Ala Leu Leu Pro
245                      250                      255

Lys Pro Glu Ala Ala Arg Arg Ile Val Glu Leu Leu Asn Leu Phe Asp
260                      265                      270

Pro Leu Asp Leu Val Ala Leu Glu Ile Arg Ala Gln Val Gly Asn Ala
275                      280                      285

Met Ser
290

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<210> 2683
<211> 489
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(466)
<223> RXA02331

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tcaactaaaa aggcgcact taaaaaacac tatggaacct atg gaa cta aac ggc 115
Met Glu Leu Asn Gly
1 5

ggt cgt ttc tac gcc cgc aag ctc acc tca gat aat cgg att gat gat 163
Gly Arg Phe Tyr Ala Arg Lys Leu Thr Ser Asp Asn Arg Ile Asp Asp
10 15 20

gtc ccg gcg ctc tca ctg atc ctt gcc gat gca gca cag ttc atc gcg 211
Val Pro Ala Leu Ser Leu Ile Leu Ala Asp Ala Ala Gln Phe Ile Ala
25 30 35

gac gcc acc aca gcc tgg cac gag gac acc gaa tac acc tgg gct atc 259

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Asp Ala Thr Thr Ala Trp His Glu Asp Thr Glu Tyr Thr Trp Ala Ile
      40                      45                      50

tgc gag cag acc agt gtt gaa cta ctg gca ctg gca cgc ctt gat ccc 307
Cys Glu Gln Thr Ser Val Glu Leu Leu Ala Leu Ala Arg Leu Asp Pro
      55                      60                      65

aag cag cgc aca ctc gag gtc gtg ccc gca ggt gat ccc gcc acc caa 355
Lys Gln Arg Thr Leu Glu Val Val Pro Ala Gly Asp Pro Ala Thr Gln
      70                      75                      80                      85

ttg ccc aat gat cca gtg ctc gct ccg aaa acc atc ggc gat gct gtg 403
Leu Pro Asn Asp Pro Val Leu Ala Pro Lys Thr Ile Gly Asp Ala Val
      90                      95                      100

gcg gag ggc cgc gac acc atc acc aga tgg gca caa ggc tat tta gaa 451
Ala Glu Gly Arg Asp Thr Ile Thr Arg Trp Ala Gln Gly Tyr Leu Glu
      105                      110                      115

atc agc ctc act gat taggttctct ccgaaatggg cac 489
Ile Ser Leu Thr Asp
      120

<210> 2684
<211> 122
<212> PRT
<213> Corynebacterium glutamicum

<400> 2684
Met Glu Leu Asn Gly Gly Arg Phe Tyr Ala Arg Lys Leu Thr Ser Asp
  1                      5                      10                      15

Asn Arg Ile Asp Asp Val Pro Ala Leu Ser Leu Ile Leu Ala Asp Ala
      20                      25                      30

Ala Gln Phe Ile Ala Asp Ala Thr Thr Ala Trp His Glu Asp Thr Glu
      35                      40                      45

Tyr Thr Trp Ala Ile Cys Glu Gln Thr Ser Val Glu Leu Leu Ala Leu
      50                      55                      60

Ala Arg Leu Asp Pro Lys Gln Arg Thr Leu Glu Val Val Pro Ala Gly
      65                      70                      75                      80

Asp Pro Ala Thr Gln Leu Pro Asn Asp Pro Val Leu Ala Pro Lys Thr
      85                      90                      95

Ile Gly Asp Ala Val Ala Glu Gly Arg Asp Thr Ile Thr Arg Trp Ala
      100                      105                      110

Gln Gly Tyr Leu Glu Ile Ser Leu Thr Asp
      115                      120

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<210> 2685
<211> 303
<212> DNA
<213> Corynebacterium glutamicum

<220>

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<221> CDS

<222> (101)..(280)

<223> RXA02336

<400> 2685

caaatccaca cgacacaatt acacaaattt taccttgtgc attgaaagcc gtcagccgat 60

tagcggttaaa gaaaataaaa aaccacaagg ggagcacacc atg aaa gac acc acc 115

Met Lys Asp Thr Thr
1 5

gag atc aac tgg caa ggc tac gcc gat gga acc gca atc cgc gaa gca 163

Glu Ile Asn Trp Gln Gly Tyr Ala Asp Gly Thr Ala Ile Arg Glu Ala
10 15 20

gtc atc cac tcc att gaa cga gaa gta tca cgc ggc gag cag cca acc 211

Val Ile His Ser Ile Glu Arg Glu Val Ser Ala Gly Glu Gln Pro Thr
25 30 35

cca aac gat ctt aaa ttt ctc ggg ctg ttc cag cac cgc gcc ggg tat 259

Pro Asn Asp Leu Lys Phe Leu Gly Leu Phe Gln His Arg Ala Gly Tyr
40 45 50

gtg ggc tcg ttg atc acc ggt taagtgtggg gagcaggctg gct 303

Val Gly Ser Leu Ile Thr Gly
55 60

<210> 2686

<211> 60

<212> PRT

<213> Corynebacterium glutamicum

<400> 2686

Met Lys Asp Thr Thr Glu Ile Asn Trp Gln Gly Tyr Ala Asp Gly Thr

1 5 10 15

Ala Ile Arg Glu Ala Val Ile His Ser Ile Glu Arg Glu Val Ser Ala

20 25 30

Gly Glu Gln Pro Thr Pro Asn Asp Leu Lys Phe Leu Gly Leu Phe Gln

35 40 45

His Arg Ala Gly Tyr Val Gly Ser Leu Ile Thr Gly

50 55 60

<210> 2687

<211> 444

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(421)

<223> RXA02347

<400> 2687

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aacgatgaag aaaaatcctt tggttgaatg ggtctgggtt atg gat gaa ctc ggg 115

	Met	Asp	Glu	Leu	Gly	
	1				5	
gtt ggc tgg tgc caa tgc gag aaa gat tcc atc acc gga aaa gca cca						163
Val Gly Trp Cys Gln Cys Glu Lys Asp Ser Ile Thr Gly Lys Ala Pro						
	10				20	
cat ccc gtg aac aag cca ctg gtc acc aaa tcc att atc agg gct cta						211
His Pro Val Asn Lys Pro Leu Val Thr Lys Ser Ile Arg Ala Leu						
	25				35	
ggc gat gtc ccc gat gtc atg agc aac cag gac atc agc ctt gtg gtg						259
Gly Asp Val Pro Asp Val Met Ser Asn Gln Asp Ile Ser Leu Val Val						
	40				50	
gtg gat ttg tgg aaa ttc gat acc att act cct cca atc gca gaa tcc						307
Val Asp Leu Trp Lys Phe Asp Thr Ile Thr Pro Pro Ile Ala Glu Ser						
	55				65	
ctc atg cgt tcc gtc aaa gct gtt aac ggt gag atg cac ccg cag tat						355
Leu Met Arg Ser Val Lys Ala Val Asn Gly Glu Met His Pro Gln Tyr						
	70				80	
ccc acc gcg aca gca atg gct gcg atc aag cat ttc tcc aac act ttt						403
Pro Thr Ala Thr Ala Met Ala Ala Ile Lys His Phe Ser Asn Thr Phe						
	90				100	
gat gga cag att aac gct taaaaggcct gttatagact gat						444
Asp Gly Gln Ile Asn Ala						
	105					
#						
<210> 2688						
<211> 107						
<212> PRT						
<213> Corynebacterium glutamicum						
#						
<400> 2688						
Met Asp Glu Leu Gly Val Gly Trp Cys Gln Cys Glu Lys Asp Ser Ile						
	1				10	15
Thr Gly Lys Ala Pro His Pro Val Asn Lys Pro Leu Val Thr Lys Ser						
	20				25	30
Ile Ile Arg Ala Leu Gly Asp Val Pro Asp Val Met Ser Asn Gln Asp						
	35				40	45
Ile Ser Leu Val Val Val Asp Leu Trp Lys Phe Asp Thr Ile Thr Pro						
	50				55	60
Pro Ile Ala Glu Ser Leu Met Arg Ser Val Lys Ala Val Asn Gly Glu						
	65				70	75
Met His Pro Gln Tyr Pro Thr Ala Thr Ala Met Ala Ala Ile Lys His						
	85				90	95
Phe Ser Asn Thr Phe Asp Gly Gln Ile Asn Ala						
	100				105	

<210> 2689

<211> 490

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(490)

<223> RXA02349

<400> 2689

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gagctatccc	tcaaaaaatt	actgatagtg	agggttttcgc	atg	tca	act	gca	tat	115
				Met	Ser	Thr	Ala	Tyr	
				1				5	

ttt att gcg cac gga aac gat acg tac cgc cca acg gag cat tcc agc	163
Phe Ile Ala His Gly Asn Asp Thr Tyr Arg Pro Thr Glu His Ser Ser	
10 15 20	

ggt gcg tgg cgc gat gat gaa ctc cac ctt gca cgg gtt gcc ggt ttg	211
Gly Ala Trp Arg Asp Asp Glu Leu His Leu Ala Pro Val Ala Gly Leu	
25 30 35	

gtg att cac cat atg gaa cgt tgg cgc agg gaa gtg gtt gcc gat gct	259
Val Ile His His Met Glu Arg Trp Arg Arg Glu Val Val Gly Asp Ala	
40 45 50	

ttg gtg ttc agc cgt ttt agt ttg gag gtc ttg gcc cag atc gct cgg	307
Leu Val Phe Ser Arg Phe Ser Leu Glu Val Leu Gly Gln Ile Ala Arg	
55 60 65	

gat gat gtc acc ttg aga aca gag atc gtt cgt ccc ggg cgc acc att	355
Asp Asp Val Thr Leu Arg Thr Glu Ile Val Arg Pro Gly Arg Thr Ile	
70 75 80 85	

gaa ctt att gaa acc gtg gct gaa atc aac gcc aga gtg acg att cgt	403
Glu Leu Ile Glu Thr Val Ala Glu Ile Asn Gly Arg Val Thr Ile Arg	
90 95 100	

gca cgc gcc tgg ttg ctg aag acc tct gat ctt gcc cat att tct gcc	451
Ala Arg Ala Trp Leu Leu Lys Thr Ser Asp Leu Ala His Ile Ser Gly	
105 110 115	

gat act ttt gaa gcg ttg cgg tca atg act gaa ctg gca	490
Asp Thr Phe Glu Ala Leu Pro Ser Met Thr Glu Leu Ala	
120 125 130	

<210> 2690

<211> 130

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2690

Met Ser Thr Ala Tyr Phe Ile Ala His Gly Asn Asp Thr Tyr Arg Pro
1 5 10 15

Thr Glu His Ser Ser Gly Ala Trp Arg Asp Asp Glu Leu His Leu Ala
20 25 30

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Pro Val Ala Gly Leu Val Ile His His Met Glu Arg Trp Arg Arg Glu
      35              40              45

Val Val Gly Asp Ala Leu Val Phe Ser Arg Phe Ser Leu Glu Val Leu
      50              55              60

Gly Gln Ile Ala Arg Asp Asp Val Thr Leu Arg Thr Glu Ile Val Arg
      65              70              75              80

Pro Gly Arg Thr Ile Glu Leu Ile Glu Thr Val Ala Glu Ile Asn Gly
      85              90              95

Arg Val Thr Ile Arg Ala Arg Ala Trp Leu Leu Lys Thr Ser Asp Leu
      100             105             110

Ala His Ile Ser Gly Asp Thr Phe Glu Ala Leu Pro Ser Met Thr Glu
      115             120             125

Leu Ala
      130

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<210> 2691
<211> 578
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (1)..(555)
<223> RXA02352

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<400> 2691
atc tac aac aca tcg agc acg ctc aac ggc ttc atc gca gac aaa gac      48
Ile Tyr Asn Thr Ser Ser Thr Leu Asn Gly Phe Ile Ala Asp Lys Asp
      1              5              10              15

aac tcc ctg caa tgg ctt ttc gac gtc ccc ggc agc gac ggt gcc tct      96
Asn Ser Leu Gln Trp Leu Phe Asp Val Pro Gly Ser Asp Gly Ala Ser
      20              25              30

gaa gac ttc ggt aat ttc ctt tca aaa gcc ggc acc atc gta atg gga      144
Glu Asp Phe Gly Asn Phe Leu Ser Lys Ala Gly Thr Ile Val Met Gly
      35              40              45

tcc acc acc tat gaa tgg ctg ctc aag gac cta gat ttc atc agc gat      192
Ser Thr Thr Tyr Glu Trp Leu Leu Lys Asp Leu Asp Phe Ile Ser Asp
      50              55              60

ccc cac aag tgg acc gat gtg tat ggc gat cgc ccc acg tgg gtg ttc      240
Pro His Lys Trp Thr Asp Val Tyr Gly Asp Arg Pro Thr Trp Val Phe
      65              70              75              80

agc agc agg aac ttg gaa acc ccg gaa gga aaa cct gtc aag gta gta      288
Ser Ser Arg Asn Leu Glu Thr Pro Glu Gly Lys Pro Val Lys Val Val
      85              90              95

aat gga gat gtc gcc gat gtt ctc ccc gcc ata ctg gaa gag agt cca      336
Asn Gly Asp Val Ala Asp Val Leu Pro Ala Ile Leu Glu Glu Ser Pro
      100             105             110

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gag aac act gat att tgg atc gtc ggt ggt ggc gat ctg gcg ggt caa 384
 Glu Asn Thr Asp Ile Trp Ile Val Gly Gly Gly Asp Leu Ala Gly Gln
 115 120 125
 ttc ttt gat gcg ggt gca ctc gat cgg atc atc ttg acc atg gcg cca 432
 Phe Phe Asp Ala Gly Ala Leu Asp Arg Ile Ile Leu Thr Met Ala Pro
 130 135 140
 gtg ttt ctc gat gaa ggg cag cca gcg atg ccc cgc cgg atc gaa agt 480
 Val Phe Leu Asp Glu Gly Gln Pro Ala Met Pro Arg Arg Ile Glu Ser
 145 150 155 160
 aat cgt ctc cgc acc gta aat gtc cgc gag gtt gga caa ttc acc gag 528
 Asn Arg Leu Arg Thr Val Asn Val Arg Glu Val Gly Gln Phe Thr Glu
 165 170 175
 atc acc ctg gag acg att aaa ggg gct taattgtag agttttgggc 575
 Ile Thr Leu Glu Thr Ile Lys Gly Ala
 180 185
 aga 578

<210> 2692

<211> 185

<212> PRT

<213> Corynebacterium glutamicum

<400> 2692

Ile Tyr Asn Thr Ser Ser Thr Leu Asn Gly Phe Ile Ala Asp Lys Asp
 1 5 10 15

Asn Ser Leu Gln Trp Leu Phe Asp Val Pro Gly Ser Asp Gly Ala Ser
 20 25 30

Glu Asp Phe Gly Asn Phe Leu Ser Lys Ala Gly Thr Ile Val Met Gly
 35 40 45

Ser Thr Thr Tyr Glu Trp Leu Leu Lys Asp Leu Asp Phe Ile Ser Asp
 50 55 60

Pro His Lys Trp Thr Asp Val Tyr Gly Asp Arg Pro Thr Trp Val Phe
 65 70 75 80

Ser Ser Arg Asn Leu Glu Thr Pro Glu Gly Lys Pro Val Lys Val Val
 85 90 95

Asn Gly Asp Val Ala Asp Val Leu Pro Ala Ile Leu Glu Glu Ser Pro
 100 105 110

Glu Asn Thr Asp Ile Trp Ile Val Gly Gly Gly Asp Leu Ala Gly Gln
 115 120 125

Phe Phe Asp Ala Gly Ala Leu Asp Arg Ile Ile Leu Thr Met Ala Pro
 130 135 140

Val Phe Leu Asp Glu Gly Gln Pro Ala Met Pro Arg Arg Ile Glu Ser
 145 150 155 160

Asn Arg Leu Arg Thr Val Asn Val Arg Glu Val Gly Gln Phe Thr Glu
 165 170 175

Ile Thr Leu Glu Thr Ile Lys Gly Ala
180 185

<210> 2693

<211> 1119

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1096)

<223> RXA02356

<400> 2693

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aaacccacaa tgtgtactgg tgctggtaat ttagtagaac atg gca acg gtc aca 115
Met Ala Thr Val Thr
1 5

ttc gac aag gtc aca atc cgg tac ccc gcc gcg gag cgc gca aca gtt 163
Phe Asp Lys Val Thr Ile Arg Tyr Pro Gly Ala Glu Arg Ala Thr Val
10 15 20

cat gag ctt gat tta gat atc gct gat gcc gag ttt ttg gtg ctc gtc 211
His Glu Leu Asp Leu Asp Ile Ala Asp Gly Glu Phe Leu Val Leu Val
25 30 35

ggc cct tcg ggt tgt ggt aaa tcc act acg ctg cgt gct ttg gcg ggg 259
Gly Pro Ser Gly Cys Gly Lys Ser Thr Thr Leu Arg Ala Leu Ala Gly
40 45 50

ctt gag gcc gtg gag tcg ggt gtg atc aaa att gat gcc aag gat gtc 307
Leu Glu Gly Val Glu Ser Gly Val Ile Lys Ile Asp Gly Lys Asp Val
55 60 65

act ggt cag gag ccg gcg gat cgc gat atc gcg atg gtg ttc cag aat 355
Thr Gly Gln Glu Pro Ala Asp Arg Asp Ile Ala Met Val Phe Gln Asn
70 75 80 85

tat gct ctg tac cct cac atg acg gtg gcg aag aat atg ggt ttt gcg 403
Tyr Ala Leu Tyr Pro His Met Thr Val Ala Lys Asn Met Gly Phe Ala
90 95 100

ctg aag ttg gct aag ctg ccg cag gcg cag atc gat gcg aag gtc aat 451
Leu Lys Leu Ala Lys Leu Pro Gln Ala Gln Ile Asp Ala Lys Val Asn
105 110 115

gag gct gcg gaa att ctt ggg ttg acg gag ttt ttg gat cgc aag cct 499
Glu Ala Ala Glu Ile Leu Gly Leu Thr Glu Phe Leu Asp Arg Lys Pro
120 125 130

aag gat tta tcg ggt ggt cag cgt cag cgt gtg gcg atg ggt cgc gcg 547
Lys Asp Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Met Gly Arg Ala
135 140 145

ttg gtg cgt gat ccg aag gtg ttc ctc atg gat gag ccg ctg tcc aac 595
Leu Val Arg Asp Pro Lys Val Phe Leu Met Asp Glu Pro Leu Ser Asn
150 155 160 165

ctg gat gcg aaa ttg cgc gtg caa acc cgc gcg gag gtc gct gct ttg 643
 Leu Asp Ala Lys Leu Arg Val Gln Thr Arg Ala Glu Val Ala Ala Leu
 170 175 180

cag cgt cgc ctg ggc acc acc acg gtg tat gtc acc cac gat cag gtt 691
 Gln Arg Arg Leu Gly Thr Thr Thr Arg Val Tyr Val Thr His Asp Gln Val
 185 190 195

gag gca atg acg atg ggc gat cgg gtt gcg gtg ctc aag gac ggg ttg 739
 Glu Ala Met Thr Met Gly Asp Arg Val Ala Val Leu Lys Asp Gly Leu
 200 205 210

ctg cag cag gtc gca ccg ccc agg gag ctt tac gac gcc ccg gtc aac 787
 Leu Gln Gln Val Ala Pro Pro Arg Glu Leu Tyr Asp Ala Pro Val Asn
 215 220 225

gaa ttc gtt gcg ggc ttc atc ggc tcg ccg tcc atg aac ctc ttc cct 835
 Glu Phe Val Ala Gly Phe Ile Gly Ser Pro Ser Met Asn Leu Phe Pro
 230 235 240 245

gcc aac ggg cac aag atg ggt gtg cgc ccg gag aag atg ctg gtc aat 883
 Ala Asn Gly His Lys Met Gly Val Arg Pro Glu Lys Met Leu Val Asn
 250 255 260

gag acc cct gag ggt ttc aca agc att gat gct gtg gtg gat atc gtc 931
 Glu Thr Pro Glu Gly Phe Thr Ser Ile Asp Ala Val Val Asp Ile Val
 265 270 275

gag gag ctt ggc tcc gaa tcg tat gtt tat gcc act tgg gag ggc cac 979
 Glu Glu Leu Gly Ser Glu Ser Tyr Val Tyr Ala Thr Trp Glu Gly His
 280 285 290

cgc ctg gtg gcc cgt tgg gtg gaa ggc ccc gtg cca gcc cct ggc acg 1027
 Arg Leu Val Ala Arg Trp Val Glu Gly Pro Val Pro Ala Pro Gly Thr
 295 300 305

cct gtg act ttt tcc tat gat gcg gcg gag gcg cat cat ttc gat ctg 1075
 Pro Val Thr Phe Ser Tyr Asp Ala Ala Gln Ala His His Phe Asp Leu
 310 315 320 325

gag tcg ggc gag cgt atc gct tagtttcgga cgtggggagg cgt 1119
 Glu Ser Gly Glu Arg Ile Ala
 330

<210> 2694

<211> 332

<212> PRT

<213> Corynebacterium glutamicum

<400> 2694

Met Ala Thr Val Thr Phe Asp Lys Val Thr Ile Arg Tyr Pro Gly Ala
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 20 25 30

Phe Leu Val Leu Val Gly Pro Ser Gly Cys Gly Lys Ser Thr Thr Leu
 35 40 45

Arg Ala Leu Ala Gly Leu Glu Gly Val Glu Ser Gly Val Ile Lys Ile
 50 55 60
 Asp Gly Lys Asp Val Thr Gly Gln Glu Pro Ala Asp Arg Asp Ile Ala
 65 70 75 80
 Met Val Phe Gln Asn Tyr Ala Leu Tyr Pro His Met Thr Val Ala Lys
 85 90 95
 Asn Met Gly Phe Ala Leu Lys Leu Ala Lys Leu Pro Gln Ala Gln Ile
 100 105 110
 Asp Ala Lys Val Asn Glu Ala Ala Glu Ile Leu Gly Leu Thr Glu Phe
 115 120 125
 Leu Asp Arg Lys Pro Lys Asp Leu Ser Gly Gly Gln Arg Gln Arg Val
 130 135 140
 Ala Met Gly Arg Ala Leu Val Arg Asp Pro Lys Val Phe Leu Met Asp
 145 150 155 160
 Glu Pro Leu Ser Asn Leu Asp Ala Lys Leu Arg Val Gln Thr Arg Ala
 165 170 175
 Glu Val Ala Ala Leu Gln Arg Arg Leu Gly Thr Thr Thr Val Tyr Val
 180 185 190
 Thr His Asp Gln Val Glu Ala Met Thr Met Gly Asp Arg Val Ala Val
 195 200 205
 Leu Lys Asp Gly Leu Leu Gln Gln Val Ala Pro Pro Arg Glu Leu Tyr
 210 215 220
 Asp Ala Pro Val Asn Glu Phe Val Ala Gly Phe Ile Gly Ser Pro Ser
 225 230 235 240
 Met Asn Leu Phe Pro Ala Asn Gly His Lys Met Gly Val Arg Pro Glu
 245 250 255
 Lys Met Leu Val Asn Glu Thr Pro Glu Gly Phe Thr Ser Ile Asp Ala
 260 265 270
 Val Val Asp Ile Val Glu Glu Leu Gly Ser Glu Ser Tyr Val Tyr Ala
 275 280 285
 Thr Trp Glu Gly His Arg Leu Val Ala Arg Trp Val Glu Gly Pro Val
 290 295 300
 Pro Ala Pro Gly Thr Pro Val Thr Phe Ser Tyr Asp Ala Ala Gln Ala
 305 310 315 320
 His His Phe Asp Leu Glu Ser Gly Glu Arg Ile Ala
 325 330

<210> 2695

<211> 414

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(391)

<223> RXA02358

<400> 2695

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tcgtccctag tacacccaaa gtttatgaaa gataaaaaatc atg gtt tct tat agc 115
Met Val Ser Tyr Ser
1 5

gtg cac ggc gca cta gat atc gac ggc agc ctc aaa aaa ctc acc ctc 163
Val His Gly Ala Leu Asp Ile Asp Gly Ser Leu Lys Lys Leu Thr Leu
10 15 20

gat ttc ctc aat aaa cta gcc acc aat cca gct tcc ccg ggg ctt cat 211
Asp Phe Leu Asn Lys Leu Ala Thr Asn Pro Ala Ser Pro Gly Leu His
25 30 35

att gag ccc atc aaa aac agc atc gac tcc cgc gtc cgc aca ggt cgg 259
Ile Glu Pro Ile Lys Asn Ser Ile Asp Ser Arg Val Arg Thr Gly Arg
40 45 50

gtc aat gat caa ttc cgc gca gtg ctt ttt gag ctt cac gac gaa ttt 307
Val Asn Asp Gln Phe Arg Ala Val Leu Phe Glu Leu His Asp Glu Phe
55 60 65

gat cat cac ttt gta gtg ggt ggg ttt atc ccc atg atg atg cca tca 355
Asp His His Phe Val Val Gly Gly Phe Ile Pro Met Met Met Pro Ser
70 75 80 85

cca agg cag gaa aaa tcc gcc ttg aag tca act ctg taacggcatt 401
Pro Arg Gln Glu Lys Ser Ala Leu Lys Ser Thr Leu
90 95

actcgactca tcg 414

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<210> 2696

<211> 97

<212> PRT

<213> Corynebacterium glutamicum

<400> 2696

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Lys Lys Leu Thr Leu Asp Phe Leu Asn Lys Leu Ala Thr Asn Pro Ala
20 25 30

Ser Pro Gly Leu His Ile Glu Pro Ile Lys Asn Ser Ile Asp Ser Arg
35 40 45

Val Arg Thr Gly Arg Val Asn Asp Gln Phe Arg Ala Val Leu Phe Glu
50 55 60

Leu His Asp Glu Phe Asp His His Phe Val Val Gly Gly Phe Ile Pro
65 70 75 80

Met Met Met Pro Ser Pro Arg Gln Glu Lys Ser Ala Leu Lys Ser Thr
85 90 95

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Leu

<210> 2697

<211> 3822

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(3799)

<223> RXA02362

<400> 2697

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aattatttga	tccgattctt	ccgttcaaag	gcctcattcc	gtg	act	atc	tct	cgc	115
				Val	Thr	Ile	Ser	Arg	
				1				5	

cga	ctc	aaa	caa	gag	cgc	agt	ttc	gct	gac	gat	ctt	caa	gat	ctc	aaa	163
Arg	Leu	Lys	Gln	Glu	Arg	Ser	Phe	Ala	Asp	Asp	Leu	Gln	Asp	Leu	Lys	
				10				15						20		

act	ctc	aat	gat	caa	ctg	cgg	ttt	aca	aac	gcc	aaa	ttg	caa	gct	cgc	211
Thr	Leu	Asn	Asp	Gln	Leu	Arg	Phe	Thr	Asn	Ala	Lys	Leu	Gln	Ala	Arg	
			25					30					35			

atc	agt	ggg	att	ggc	aat	gat	gga	aag	aaa	atc	acg	cgc	cct	acc	cca	259
Ile	Ser	Gly	Ile	Gly	Asn	Asp	Gly	Lys	Lys	Ile	Thr	Arg	Pro	Thr	Pro	
		40					45					50				

ctc	ctt	gcg	ctg	gat	ttt	cag	ctg	acc	gtt	gaa	gaa	tac	gaa	acg	atc	307
Leu	Leu	Ala	Leu	Asp	Phe	Gln	Leu	Thr	Val	Glu	Glu	Tyr	Glu	Thr	Ile	
		55				60						65				

att	gca	atc	ttg	gtg	gaa	gca	gtt	ggc	gga	aat	caa	tcc	aag	cca	gcg	355
Ile	Ala	Ile	Leu	Val	Glu	Ala	Val	Gly	Gly	Asn	Gln	Ser	Lys	Pro	Ala	
		70			75					80					85	

att	ctt	aaa	gat	ctg	ttt	ata	gaa	tat	cca	ctc	gtc	ttc	ctg	gca	gcg	403
Ile	Leu	Lys	Asp	Leu	Phe	Ile	Glu	Tyr	Pro	Leu	Val	Phe	Leu	Ala	Ala	
				90					95					100		

ctt	tct	gga	acc	gcc	atg	ctc	gat	gct	caa	gaa	ggg	ttc	tgg	cct	gcg	451
Leu	Ser	Gly	Thr	Ala	Met	Leu	Asp	Ala	Gln	Glu	Gly	Phe	Trp	Pro	Ala	
			105					110					115			

ttc	tgg	aaa	cgc	act	cag	gtg	tca	gtt	cca	gag	cat	gta	tac	gac	gcg	499
Phe	Trp	Lys	Arg	Thr	Gln	Val	Ser	Val	Pro	Glu	His	Val	Tyr	Asp	Ala	
		120						125					130			

atc	cgt	aaa	gaa	cta	gtt	aat	agc	atc	cgc	aaa	aat	ggc	cta	gaa	act	547
Ile	Arg	Lys	Glu	Leu	Val	Asn	Ser	Ile	Arg	Lys	Asn	Gly	Leu	Glu	Thr	
		135					140					145				

ttt	tct	ctc	gct	gac	ctc	aat	cga	cgc	gaa	tat	gtc	gga	ctc	atc	caa	595
Phe	Ser	Leu	Ala	Asp	Leu	Asn	Arg	Arg	Glu	Tyr	Val	Gly	Leu	Ile	Gln	
		150			155					160					165	

ctt cac agt ggc ctt tct gca aaa gac atg ctc gcc ttg gtc aaa ttt Leu His Ser Gly Leu Ser Ala Lys Asp Met Leu Ala Leu Val Lys Phe 170 175 180	643
atc gat cac act cga gca gaa aac caa gga tgg gat tct ggt gag gac Ile Asp His Thr Arg Ala Glu Asn Gln Gly Trp Asp Ser Gly Glu Asp 185 190 195	691
ttt gca tca tat gcg aag agt gtc ttc tcc tcc ggg gac aac cta tta Phe Ala Ser Tyr Ala Lys Ser Val Phe Ser Ser Gly Asn Leu Leu 200 205 210	739
acc acg gag tcg ctc aag caa tta gtc acc cac atc cct gcg cgt tcc Thr Thr Glu Ser Leu Lys Gln Leu Val Thr His Ile Pro Ala Arg Ser 215 220 225	787
gtc gac ttc atc gcc aga gtc tat gaa cta acc aat tgg tac cgc gac Val Asp Phe Ile Ala Arg Val Tyr Glu Leu Thr Asn Trp Tyr Arg Asp 230 235 240 245	835
ctc aaa gac ctc aat gaa gta gaa gcc ttc gta ggt act cat ggg ctg Leu Lys Asp Leu Asn Glu Val Glu Ala Phe Val Gly Thr His Gly Leu 250 255 260	883
ccg gaa ttg tct ttc aaa ttt ctt ctg gag tgt ctg agc ggc gaa gct Pro Glu Leu Ser Phe Lys Phe Leu Leu Glu Cys Leu Ser Gly Glu Ala 265 270 275	931
gaa caa att gcc gaa aag acg aaa gca gca cca gca agc ctg gaa aac Glu Gln Ile Ala Glu Lys Thr Lys Ala Ala Pro Ala Ser Leu Glu Asn 280 285 290	979
ctg gaa cct ccg cat ctc tat ctg gat cca cag agt ttt gaa ctc agt Leu Glu Pro Pro His Leu Tyr Leu Asp Pro Gln Ser Phe Glu Leu Ser 295 300 305	1027
ctt gtt ttc cca gcg atc tct aaa act gca gca ctt cag att cca gca Leu Val Phe Pro Ala Ile Ser Lys Thr Ala Ala Leu Gln Ile Pro Ala 310 315 320 325	1075
cca gaa tgg aca gtg att tat gac gga aac tcc att aaa gtt cgt ccc Pro Glu Trp Thr Val Ile Tyr Asp Gly Asn Ser Ile Lys Val Arg Pro 330 335 340	1123
gaa cag gac tgg tcc tac gga ggt ttc gcc gaa tac cgt ttg cct tta Glu Gln Asp Trp Ser Tyr Gly Gly Phe Ala Glu Tyr Arg Leu Pro Leu 345 350 355	1171
gac aaa ccg ctc tcc agc ttg aga gtc atc act cca aca gag aaa tcc Asp Lys Pro Leu Ser Ser Leu Arg Val Ile Thr Pro Thr Glu Lys Ser 360 365 370	1219
cta att ctg att gaa gga ttt ggc cac aag aat ccc att atg ttc ttt Leu Ile Leu Ile Glu Gly Phe Gly His Lys Asn Pro Ile Met Phe Phe 375 380 385	1267
aag aac aac ggt cag cca tat gca aac caa gaa atg ctc agt ggc aac Lys Asn Asn Gly Gln Pro Tyr Ala Asn Gln Glu Met Leu Ser Gly Asn 390 395 400 405	1315